

From: Holleran, Anne  
Sent: Friday, August 31, 2001 2:43 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search for 09/512,363

Please search the following sequences for 09/512,363:

1. commercial database and interference search for the following sequences:

SEQ ID NO: 2(aa)

2. commercial database and interference search of SEQ ID NO: 2(aa) against nucleotide databases
3. oligomer search, commercial and interference databases, for SEQ ID NO: 2(aa)
4. fragment search for SEQ ID NO: 2(aa):

/amino acids -25 - 137 (if aa -25 is numbered as "1", then 1-162)  
/amino acids 1-137 (" , then 26-162)  
amino acids 1-114 (" , then 26-139)  
amino acids -25-139 (" , then 1-164)  
amino acids 21-139 (" , then 46-164)  
amino acids 8-129 (" , then 33-154)  
amino acids 8-48 (" , then 33-73)  
amino acids 49-88 (" , then 74-113)  
amino acids 89-129 (" , then 114-154)

\* note for fragment search: the application lists the fragments using the numbering of the specification which includes negative numbers. I have listed the fragments using the fragment numbering as listed in the claims and also the fragment numbers that would correspond if the first aa is numbered "1" and not numbered "-25".

Thanks

Anne Holleran  
AU: 1642  
Tel: 308-8892  
Room: 8E03

**Point of Contact:**  
**Toby Port**  
**Technical Info. Specialist**  
**CM1 1E01 TEL: 308-3534**

RECEIVED  
SEP - 4 2001  
STIC

DT 28-JUL-1998 (first entry)  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; hematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /tag= a  
 FT /product= "human 312C2 protein"  
 XX  
 XX WO9806842-A1.  
 PN  
 XX  
 PD 9-FEB-1998.  
 XX  
 XX 14-AUG-1997; 97WO-US13931.  
 XX  
 XX 07-OCT-1996; 96US-0027901.  
 PR  
 XX 16-AUG-1996; 96US-0689943.  
 XX  
 XX (SCHE ) SCHERING CORP.  
 PA  
 XX Gorman DM, Randall TD, Zlotnik A;  
 PI  
 XX WPI; 1998-159534/14.  
 DR  
 DR N-PSDB; AAV19153.  
 XX  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 PT  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 XX  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 241 AA;  
 Query Match 100.0%; Score 246; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY " 1 DCASGTFSGGHEGHCKPWTDCTQFGFLTPPGNKNHNAVCV 41  
 DB 114 dcasgtfsgghegchckpwtcdctqfgfltpvpgnknthnavcv 154  
 RESULT 8  
 ID AAY06605  
 ID AAY06605 standard; Protein; 241 AA.  
 XX  
 AC AAY06605;  
 XX  
 XX 26-OCT-1999 (first entry)  
 DT  
 XX Human TNF receptor homologue PRO364.  
 DE PRO364; tumour necrosis factor receptor; human; apoptosis;  
 PRO364; tumour necrosis factor receptor; human; apoptosis;

KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /note= "signal peptide"  
 FT /note= "mature protein"  
 FT Modified-site 146  
 FT Domain /note= "N-glycosylated"  
 FT /note= "transmembrane domain"  
 XX  
 XX WO9940196-A1.  
 PN  
 XX  
 PD 12-AUG-1999.  
 XX  
 XX 09-FEB-1999; 99WO-US02642.  
 PF  
 XX 09-FEB-1998; 98US-0024087.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 PI Pitti RM, Wood WI;  
 XX WPI; 1999-494296/41.  
 DR  
 DR N-PSDB; AAX87670.  
 XX  
 XX Tumour necrosis factor receptor homologue - useful for, e.g.  
 PT modulating apoptosis and NF-KB activation and proinflammatory or  
 PT autoimmune responses  
 PT  
 XX  
 PS Claim 17; Fig 2A; 104pp; English.  
 XX  
 CC The present sequence represents human PRO364, a novel member of the  
 CC tumour necrosis factor receptor family. The sequence was deduced  
 CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
 CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or  
 CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.  
 XX  
 SQ Sequence 241 AA;  
 Query Match 100.0%; Score 246; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DCASGTFSGGHEGHCKPWTDCTQFGFLTPPGNKNHNAVCV 41  
 DB 114 dcasgtfsgghegchckpwtcdctqfgfltpvpgnknthnavcv 154  
 RESULT 9  
 ID AAB27651  
 ID AAB27651 standard; Protein; 241 AA.





PN WO9806842-A1.  
 XX  
 XX PD  
 XX PF 19-FEB-1998.  
 XX PR 14-AUG-1997; 97WO-US13931.  
 XX PR 07-OCT-1996; 96US-0027901.  
 XX PR 16-AUG-1996; 96US-0689943.  
 XX PA (SCHE ) SCHERING CORP.  
 XX PI Gorman DM, Randall TD, Zlotnik A;  
 XX WPI; 1998-159534/14.  
 XX DR N-PSDB; AAV19153.  
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 XX PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX PS other T cell disorders  
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 XX Claim 2; Pages 59-60; 71pp; English.  
 XX  
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 XX proliferation and cytokine production by T-cells, and potentiates T  
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 XX development, including abnormal proliferation, e.g. cancerous  
 XX conditions or degenerative conditions. They can be used in the  
 XX regulation or development of haematopoietic cells, e.g. lymphoid cells  
 XX which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 XX Sequence 241 AA:  
 SQ  
 Query Match 100.0%; Score 255; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPGRLLLTGTGTDARCCRVHTTRCCRDYPGECCEWDCM 41  
 DB 33 gcgpgrrlllgtgttdarccrvhttrccrdypgeccsewcdm 73  
 ID AAY06605  
 AC AAY06605  
 XX 26-OCT-1999 (first entry)  
 XX Human TNF receptor homologue PRO364.  
 XX PRO364; tumour necrosis factor receptor; human; apoptosis;  
 KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX Peptide 1..25  
 XX Protein 26..241  
 XX Modified-site 146  
 XX Domain /note= "N-glycosylated"  
 XX 162..180  
 XX /note= "transmembrane domain"  
 XX  
 XX WO9940196-A1.  
 XX  
 XX PD  
 XX PF 12-AUG-1999.  
 XX PR 09-FEB-1999; 99WO-US02642.  
 XX PR 09-FEB-1998; 98US-0024087.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 XX PI Pitti RM, Wood WI;  
 XX WPI; 1999-494296/41.  
 XX DR N-PSDB; AAX87670.  
 XX PT Tumour necrosis factor receptor homologue - useful for, e.g.  
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 XX PT autoimmune responses  
 XX PS Claim 17; Fig 2A; 104pp; English.  
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 XX mature protein) and 26-X of the present sequence, where X is any  
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 XX Sequence 241 AA:  
 SQ  
 Query Match 100.0%; Score 255; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPGRLLLTGTGTDARCCRVHTTRCCRDYPGECCEWDCM 41  
 DB 33 gcgpgrrlllgtgttdarccrvhttrccrdypgeccsewcdm 73  
 ID AAB27651  
 AC AAB27651  
 XX 26-JAN-2001 (first entry)  
 XX Human protein PRO364.  
 XX Cardiovascular; endothelial; angiogenic disorder; PRO179;  
 KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO333;  
 KW PRO840; PRO877; PRO878; PRO882; PRO885; PRO887;  
 KW gene therapy.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX Peptide 1..25

IncYTE clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic; anti-inflammatory; antiproliferative; anti-HIV; antiasthmatic; aneemia; dermatological; antidiabetic; nephrotropic; antichyroid; thyromimetic; immunosuppressive; osteopathic; antiarthritic; uropathic; antitumor; ophthalmological; diagnosis; treatment; prevention; immune disorder; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.

Homo sapiens.

Key Location/Qualifiers  
Region 1..19  
Region /label= Signature\_sequence  
Region 68..96  
Region /label= Signature\_sequence  
Region 109..147  
Region /label= Signature\_sequence  
Region 122..129  
Region /label= Signature\_sequence  
Region 157..175  
Region /label= Signature\_sequence  
Region 165..186  
Region /label= Signature\_sequence  
Modified-site 37  
Modified-site /note= "Potential phosphorylation site"  
Modified-site 48  
Modified-site /note= "Potential phosphorylation site"  
Modified-site 62  
Modified-site /note= "Potential phosphorylation site"  
Modified-site 82  
Modified-site /note= "Potential phosphorylation site"  
Modified-site 205  
Modified-site /note= "Potential phosphorylation site"  
Modified-site 223  
Modified-site /note= "Potential phosphorylation site"  
Modified-site 140  
Modified-site /note= "N-glycosylated"

WO200005374-A2.

03-FEB-2000.

21-JUL-1999; 99WO-US16637.

22-JUL-1998; 98US-0093827.

INCYTE PHARM INC.

IncYTE, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;

WPI; 2000-182699/16.

N-PSDB; AA249948.

Polypeptides and polynucleotides useful for treating and detecting cell proliferation disorders e.g. actinic keratosis, and immune disorders e.g. Crohn's disease

Claim 1; Pages 64-65; 67pp; English.

The present sequence is a molecule associated with cell proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMN0706 CDNA library. This sequence is expressed in cardiovascular and haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV, hepatotropic, antiinflammatory, antiproliferative, cytostatic, antiasthmatic, dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic, immunosuppressive, osteopathic, antiarthritic, uropathic, antitumor, and ophthalmological activities. The present sequence is useful in the diagnosis, treatment and prevention of cell proliferative disorders e.g. actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and anaemia.

Sequence 235 AA;

Query Match 100.0%; Score 753; DB 21; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.8e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCGPGRLLLTGTARCCRVHTTRCCRDYPCBECCEWDCMCVQPFHCGDPCCTCRHH 60  
Db 27 GCGPGRLLLTGTARCCRVHTTRCCRDYPCBECCEWDCMCVQPFHCGDPCCTCRHH 86  
QY 61 PCPPGQGVQSGKFSFGQCDACSGTSGGHEGCKPWTDOCTGFLTVFPGKTHNAV 120  
Db 87 PCPPGQGVQSGKFSFGQCDACSGTSGGHEGCKPWTDOCTGFLTVFPGKTHNAV 146  
QY 121 CV 122  
Db 147 CV 148

RESULT 5

AAW37839

ID AAW37839 standard; Protein; 241 AA.

AC AAW37839;

DT 28-JUL-1998 (first entry)

DE Amino acid sequence of the human 312C2 T cell protein.

KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.

OS Homo sapiens.

Key Location/Qualifiers

CDS 1..726

FT /\*tag= a

FT /product= "human 312C2 protein"

PN WO9806842-A1.

XX 19-FEB-1998.

XX 14-AUG-1997; 97WO-US13931.

XX 07-OCT-1996; 96US-0027901.

PR 16-AUG-1996; 96US-0689943.

XX (SCHE ) SCHERING CORP.

PI Gorman DM, Randall TD, Zlotnik A;

XX WPI; 1998-159534/14.

DR N-PSDB; AAV19153.

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PT other T cell disorders

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XX conditions or degenerative conditions. They can be used in the  
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CC which affect immunological responses, e.g. autoimmune disorders.  
 XX Sequence 241 AA;  
 SQ

Query Match 100.0%; Score 753; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDAACRCRVHTRCCRDYPCGECCSEWDCMCVQPEPHCGDPCCTTCRHH 60  
 DB 33 GCGPGRLLLTGTDAACRCRVHTRCCRDYPCGECCSEWDCMCVQPEPHCGDPCCTTCRHH 92  
 QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFGNKTHNAV 120  
 DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFGNKTHNAV 152

QY 121 CV 122  
 DB 153 CV 154

RESULT 6  
 ID AAY06605  
 XX AAY06605 standard; Protein; 241 AA.  
 AC AAY06605;

DT 26-OCT-1999 (first entry)

XX Human TNF receptor homologue PRO364.

XX PRO364; tumour necrosis factor receptor; human; apoptosis;  
 KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..25  
 FT /note= "signal peptide"  
 FT Protein 26..241  
 FT /note= "mature protein"  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "transmembrane domain"

XX PRO9940196-A1.

XX 12-AUG-1999.

XX 09-FEB-1999; 99WO-US02642.

XX 09-FEB-1998; 98US-0024087.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 PI Pitti RM, Wood WI;

DR WPI; 1999-494296/41.  
 DR N-PSDB; AAX87670.

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PS Claim 17; Fig 2A; 104pp; English.

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 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
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 CC inhibitors.  
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 SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDAACRCRVHTRCCRDYPCGECCSEWDCMCVQPEPHCGDPCCTTCRHH 60  
 DB 33 GCGPGRLLLTGTDAACRCRVHTRCCRDYPCGECCSEWDCMCVQPEPHCGDPCCTTCRHH 92

QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFGNKTHNAV 120  
 DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFGNKTHNAV 152

QY 121 CV 122  
 DB 153 CV 154

RESULT 7

AAB27651

ID AAB27651 standard; Protein; 241 AA.

XX AAB27651;

XX 26-JAN-2001 (first entry)

XX Human protein PRO364.

XX Cardiovascular; endothelial; angiogenic disorder; PRO179;

XX PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;

XX PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;

XX gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..25

XX /label= "signal peptide"

XX WO200053757-A2.

XX 14-SEP-2000.

XX 24-FEB-2000; 2000WO-US05004.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 02-JUN-1999; 99WO-US12252.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 01-SEP-1999; 99WO-US20111.

XX 15-SEP-1999; 99WO-US21090.

XX 30-NOV-1999; 99WO-US28313.

FT Region /label= Signature\_sequence  
 FT 68..96  
 FT /label= Signature\_sequence  
 FT 109..147  
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 FT 122..129  
 FT /label= Signature\_sequence  
 FT 157..175  
 FT /label= Signature\_sequence  
 FT 165..186  
 FT /label= Signature\_sequence  
 FT 37  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 48  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 62  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 82  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 205  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 223  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 140  
 FT Modified-site /note= "N-glycosylated"

XX WO200005374-A2.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-US16637.

XX 22-JUL-1998; 98US-0093827.

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XX Sequence 235 AA;

Query Match 100.0%; Score 737; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-54;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCRRVHTTRCCRDYPGECCESEWDCMCVQPFHCGDPCCTTCRHHPCPPGGVQSQK 60  
 DB 40 darcrrvhttrccrdypgeccsewdcmcvqpfhcgdpcccttcrrhhpcppggvqsqk 99  
 |||

QY 61 FSGFGQICDASGTFSGGHEGHCKPWTDCTQFGFLTVFPGKTHNAVVCVPGSPPAEPLG 119  
 DB |||

Db 100 fsfgfqicdasgtfsggheghckpwtcdtqfgfltvfpgkthnavcvpgspapeplg 158

RESULT 5

AAW37839

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XX AAW37839;

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Query Match 100.0%; Score 737; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCRRVHTTRCCRDYPGECCESEWDCMCVQPFHCGDPCCTTCRHHPCPPGGVQSQK 60  
 DB 46 darcrrvhttrccrdypgeccsewdcmcvqpfhcgdpcccttcrrhhpcppggvqsqk 105  
 |||

QY 61 FSGFGQICDASGTFSGGHEGHCKPWTDCTQFGFLTVFPGKTHNAVVCVPGSPPAEPLG 119  
 DB 106 fsfgfqicdasgtfsggheghckpwtcdtqfgfltvfpgkthnavcvpgspapeplg 164

XX N1 J, Ruben SM;  
XX WPI: 2000-061922/05.  
DR N-PSDB; AAZ37762.  
XX  
XX New tumour necrosis factor receptor-like polypeptides used to, e.g.  
XX treat Digeorge syndrome -  
XX  
XX Claim 14; Fig 1; 167pp; English.  
XX  
XX This is the amino acid sequence of the human tumour necrosis factor  
XX receptor-like protein (TR1L receptor). The invention relates to TR1L and  
XX two splice variants TR1LSV1 and TR1LSV2. The nucleotide sequences were  
XX determined by sequencing cloned cDNAs AAZ37765-237766. The TR1L receptor  
XX and its splice variants show homology to the murine glucocorticoid  
XX induced tumour necrosis factor receptor family-related gene (GTR).  
XX TR1L, TR1LSV1 and TR1LSV2 polypeptides may be involved in the regulation  
XX of cell-type specific receptor-mediated cell growth, differentiation,  
XX and ultimately, cell death. They can be used for screening for  
XX agonists/antagonists. The polypeptides, agonists or antagonists can be  
XX used for treating a disease state associated with aberrant cell  
XX survival. They can be used for treating immune deficiency disorders,  
XX Digeorge syndrome, HIV infection, severe combined immunodeficiency  
XX (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
XX platelet disorders or wounds resulting from trauma or surgery. They can  
XX also be used to treat heart attacks, strokes, Addison's disease,  
XX haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
XX disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
XX systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
XX diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
XX hypersensitivity to an antigenic molecule, organ rejection or graft  
XX versus host disease, inflammatory conditions, ischaemia-reperfusion  
XX injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
XX chemokine induced lung injury, inflammatory bowel disease, Crohn's  
XX disease, hyperproliferative disorders, or infections. They can also be  
XX used to repair, replace, or protect tissue damaged by congenital  
XX defects, trauma, age, disease, surgery, including cosmetic plastic  
XX surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
XX neuropathies, and central nervous system disease (e.g. Alzheimer's  
XX disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
XX sclerosis, and Shy-Drager syndrome). The products can also be used for  
XX detection, diagnosis and prognosis.  
XX  
XX Sequence 234 AA;

Query Match 100.0%; Score 979; DB 21; Length 234;  
Best Local Similarity 100.0%; Pred. No. 3.9e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAOHGAMGAFRALCGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 maqhgamafralcgallcalcslgqrptggpgcgprlllgtgtdarccrvhttrccrd 60  
QY 61 YPGEECCSEWDCMCVQPEFHCGPCCTTCRRHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
DB 61 ypgeccsewdcmcvqpefhcgpccttcrrhpcppggvgqsgkfsgfqcidasgtf 120  
QY 121 SGGHEGHCKPWTDCDTQFGFLTVFPGNKTNAVCVPGSPPAEPLG 164  
DB 121 sggheghckpwtcdtqfgfltvfpgnktnavcvcpgsppaeplg 164  
RESULT 3  
ID AAW37839  
AC AAW37839;  
XX 28-JUL-1998 (first entry)  
DT  
XX Amino acid sequence of the human 312C2 T cell protein.

XX Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX  
XX Homo sapiens.  
XX  
XX Location/Qualifiers  
FH 1..726  
FT /\*tag= a  
FT /product= "human 312C2 protein"  
XX  
XX WO9806842-A1.  
PN 19-FEB-1998.  
XX  
XX 14-AUG-1997; 97WO-US13931.  
PF 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Gorman DM, Randall TD, Zlotnik A;  
PI  
XX WPI: 1998-159534/14.  
DR N-PSDB; AAV19153.  
XX  
XX Isolated 312C2 T cell gene - used to develop products for treating,  
PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
XX  
XX Claim 2; Pages 59-60; 7lpp; English.  
XX  
XX This is the amino acid sequence encoding the human 312C2 T cell  
XX protein. The 312C2 proteins are expressed in thymus cells and are  
XX induced on T cells and spleen cells following activation. Engagement  
XX of 312C2 stimulates proliferation of T cell clones, antigen-specific  
XX proliferation and cytokine production by T-cells, and potentiates T  
XX cell expansion or apoptosis. The products can be used in the  
XX treatment of conditions associated with abnormal physiology or  
XX development, including abnormal proliferation, e.g. cancerous  
XX conditions or degenerative conditions. They can be used in the  
XX regulation or development of haematopoietic cells, e.g. lymphoid cells  
XX which affect immunological responses, e.g. autoimmune disorders.  
XX  
XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 19; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAOHGAMGAFRALCGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 maqhgamafralcgallcalcslgqrptggpgcgprlllgtgtdarccrvhttrccrd 60  
QY 61 YPGEECCSEWDCMCVQPEFHCGPCCTTCRRHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
DB 61 ypgeccsewdcmcvqpefhcgpccttcrrhpcppggvgqsgkfsgfqcidasgtf 120  
QY 121 SGGHEGHCKPWTDCDTQFGFLTVFPGNKTNAVCVPGSPPAEPLG 164  
DB 121 sggheghckpwtcdtqfgfltvfpgnktnavcvcpgsppaeplg 164  
RESULT 4  
ID AAY06605  
AC AAY06605;  
XX 28-JUL-1998 (first entry)  
DT  
XX Amino acid sequence of the human 312C2 T cell protein.

FT Region /label= Signature\_sequence  
FT 68..96  
FT /label= Signature\_sequence  
FT 109..147  
FT /label= Signature\_sequence  
FT 122..129  
FT /label= Signature\_sequence  
FT 157..175  
FT /label= Signature\_sequence  
FT 165..186  
FT /label= Signature\_sequence  
FT 37  
FT /note= "Potential phosphorylation site"  
FT 48  
FT /note= "Potential phosphorylation site"  
FT 62  
FT /note= "Potential phosphorylation site"  
FT 82  
FT /note= "Potential phosphorylation site"  
FT 205  
FT /note= "Potential phosphorylation site"  
FT 223  
FT /note= "Potential phosphorylation site"  
FT 140  
FT /note= "N-glycosylated"

XX WO200005374-A2.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-US16637.

XX 22-JUL-1998; 98US-0093827.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;

XX WPI; 2000-182699/16.

DR N-PSDB; AAZ49948.

XX Polypeptides and polynucleotides useful for treating and detecting cell  
PT proliferation disorders e.g. actinic keratosis, and immune disorders  
PT e.g. Crohn's disease

XX Claim 1; Pages 64-65; 67pp; English.

XX The present sequence is a molecule associated with cell  
CC proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06  
CC cDNA library. This sequence is expressed in cardiovascular and  
CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
CC hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
CC immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer,  
CC and ophthalmological activities. The present sequence is useful in the  
CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
CC anemia.

XX Sequence 235 AA;

Query Match 100.0%; Score 711; DB 21; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRTGGPGCGPGRLLGTGTARCCRVHTTRCCRDYFGEECCSEWDCMCVQPEFHCGDPC 60

.Db 20 qrptggpgcpgprlllgtgtardccrvhttrccrdypgeccscwcdmcvqpefhcgdp 79

Qy 61 CTTCRHHPCPPGGVOSQKFSFGFCIDCASGTFSGGHEGHCCKPWTDCQFGF 114

|||||

Db 80 cttcrhhpcppggvsgqkfsfgfcidcasgtfsggheghckpwtcdtqfgf 133

RESULT 5

AAW37839

ID AAW37839 standard; Protein; 241 AA.

XX AC AAW37839;

XX DT 28-JUL-1998 (first entry)

XX DE Amino acid sequence of the human 312C2 T cell protein.

XX KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT CDS 1..726  
FT /tag= a  
FT /product= "human 312C2 protein"

XX PN WO9806842-A1.

XX PD 19-FEB-1998.

XX PF 14-AUG-1997; 97WO-US13931.

XX PR 07-OCT-1996; 96US-0027901.

XX PR 16-AUG-1996; 96US-0689943.

XX PA (SCHE ) SCHERING CORP.

XX PI Gorman DM, Randall TD, Zlotnik A;

XX WPI; 1998-159534/14.

DR N-PSDB; AAV19153.

XX PT Isolated 312C2 T cell gene - used to develop products for treating,  
PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders

XX PS Claim 2; Pages 59-60; 71pp; English.

XX CC This is the amino acid sequence encoding the human 312C2 T cell  
CC protein. The 312C2 proteins are expressed in thymus cells and are  
CC induced on T cells and spleen cells following activation. Engagement  
CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
CC proliferation and cytokine production by T-cells, and potentiates T  
CC cell expansion or apoptosis. The products can be used in the  
CC treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.

XX Sequence 241 AA;

Query Match 100.0%; Score 711; DB 19; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRTGGPGCGPGRLLGTGTARCCRVHTTRCCRDYFGEECCSEWDCMCVQPEFHCGDPC 60

.Db 26 qrptggpgcpgprlllgtgtardccrvhttrccrdypgeccscwcdmcvqpefhcgdp 85

Qy 61 CTTCRHHPCPPGGVOSQKFSFGFCIDCASGTFSGGHEGHCCKPWTDCQFGF 114

|||||

KW Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;  
 KW anti-inflammatory; antiproliferative; anti-HIV; antiasthmatic; anaemia;  
 KW dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic;  
 KW immunosuppressive; osteopathic; antiarthritic; uropathic; antitumor;  
 KW ophthalmological; diagnosis; treatment; prevention; immune disorder;  
 KW cell proliferative disorder; actinic keratosis; arteriosclerosis;  
 KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.  
 XX Homo sapiens.

OS Key Location/Qualifiers  
 FH Region 1..19  
 FT Region /label= Signature\_sequence  
 FT Region 68..96  
 FT Region /label= Signature\_sequence  
 FT Region 109..147  
 FT Region /label= Signature\_sequence  
 FT Region 122..129  
 FT Region /label= Signature\_sequence  
 FT Region 157..175  
 FT Region /label= Signature\_sequence  
 FT Region 165..186  
 FT Region /label= Signature\_sequence  
 FT Modified-site 37  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT Modified-site 48  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT Modified-site 62  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT Modified-site 82  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT Modified-site 205  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT Modified-site 223  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT Modified-site 140  
 FT Modified-site /note= "N-glycosylated"

PN W0200005374-A2.

PD 03-FEB-2000.

PF 21-JUL-1999; 99WO-US16637.

PR 22-JUL-1998; 98US-0093827.

PA INCY- INCYTE PHARM INC.

PI Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 DR WPI: 2000-182699/16.  
 DR N-PSDB; AA249948.

XX Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease

PS Claim 1; Pages 64-65; 67pp; English.

XX The present sequence is a molecule associated with cell  
 CC proliferation. MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06  
 CC cDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotropic, antiinflammatory, antiproliferative, cytostatic, antiasthmatic,  
 CC immunosuppressive, osteopathic, nephrotropic, antithyroid, thyromimetic,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.

XX Sequence 235 AA;

Query Match 100.0%; Score 841; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRPFGGCGGGRLLGTGTARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 50  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 20 qrpfggpgcpgrrllgtgtardccrvhttrccrdypggeccsewdcmcvqpefhcgdpc 79  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 CTTCRHHPCCPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCCKEWTCTQFGFLTVFPG 120  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 80 cttcrhnpccpggvgqgkfsfgfcidcasgtfsgghegchckpwtctqfgfltvfpg 139  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 NKTHNAVCPGSPPAEP 137  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 140 nkthnavcpgspapap 156  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 5

AAW37839

ID AAW37839 standard; Protein; 241 AA.

XX AC AAW37839;

XX DT 28-JUL-1998 (first entry)

XX DE Amino acid sequence of the human 312C2 T cell protein.

XX KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..726

XX FT FT /\*tag= a

XX FT /product= "human 312C2 protein"

XX PN W09806842-A1.

XX PD 19-FEB-1998.

XX PF 14-AUG-1997; 97WO-US13931.

XX PR 07-OCT-1996; 96US-0027901.

XX PR 16-AUG-1996; 96US-0689943.

XX PA (SCHE ) SCHERING CORP.

XX PI Gorman DM, Randall TD, Zlotnik A;

XX DR WPI: 1998-159534/14.

XX DR N-PSDB; AAV19153.

XX PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 PS Claim 2; Pages 59-60; 71pp; English.

XX This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells





XX N1 J, Ruben SM;  
XX WPI: 2000-061922/05.  
XX N-PSDB; AAZ37762.  
XX  
XX New tumour necrosis factor receptor-like polypeptides used to, e.g.  
XX treat Digeorge syndrome.  
XX  
XX Claim 14; Fig 1; 167pp; English.  
XX  
XX This is the amino acid sequence of the human tumour necrosis factor  
XX receptor-like protein (TR11 receptor). The invention relates to TR11 and  
XX two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
XX determined by sequencing cloned cDNAs AAZ37765-237766. The TR11 receptor  
XX and its splice variants show homology to the murine glucocorticoid  
XX induced tumour necrosis factor receptor family-related gene (GTR).  
XX TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation  
XX of cell-type specific receptor-mediated cell growth, differentiation,  
XX and ultimately, cell death. They can be used for screening for  
XX agonists/antagonists. The polypeptides, agonists or antagonists can be  
XX used for treating a disease state associated with aberrant cell  
XX survival. They can be used for treating immune deficiency disorders,  
XX Digeorge syndrome, HIV infection, severe combined immunodeficiency  
XX (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
XX platelet disorders or wounds resulting from trauma or surgery. They can  
XX also be used to treat heart attacks, strokes, Addison's disease,  
XX haemolytic anaemia, rheumatoid arthritis, Goodpasture's syndrome, Grave's  
XX disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
XX systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
XX diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
XX hypersensitivity to an antigenic molecule, organ rejection or graft  
XX versus host disease, inflammatory conditions, ischaemia-reperfusion  
XX injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
XX chemokine induced lung injury, inflammatory bowel disease, Crohn's  
XX disease, hyperproliferative disorders, or infections. They can also be  
XX used to repair, replace, or protect tissue damaged by congenital  
XX defects, trauma, age, disease, surgery, including cosmetic plastic  
XX surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
XX neuropathies, and central nervous system disease (e.g. Alzheimer's  
XX disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
XX sclerosis, and Shy-Drager syndrome). The products can also be used for  
XX detection, diagnosis and prognosis.  
XX  
XX Sequence 234 AA;  
XX  
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XX Local Similarity 100.0%; Pred. No. 1.3e-69;  
XX Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 maqhgamaafraleglallcalalslgprtgpgcgprlllgtgttdarcrcrvhttrccrd 60  
QY 61 YPGEECCSEWDCMVQPEFHCGDPCTTCRHHPCCPGQGVQSGKFSFGQCIDCASGTF 120  
Db 61 ypgeeccewdcmcvqpefhcgdpcttcrrhpcppgqgvsgqgkfsfgqcidcasgtf 120  
QY 121 SGGHEGCHKPWTDCQTFGFLTVFPNGKTHNAVCPGSPPAEP 162  
Db 121 sgghegchckpwtcdtqfgfltvfpngkthnavcvpgsppaep 162  
RESULT 3  
ID AAW37839  
XX AAW37839 standard; Protein; 241 AA.  
XX  
XX AAW37839;  
XX  
XX 28-JUL-1998 (first entry)  
XX  
XX Amino acid sequence of the human 312C2 T cell protein.

XX Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
XX antigen-specific T cell proliferation; cytokine production by T-cell;  
XX apoptosis; cancer; haematopoietic cells; lymphoid cell;  
XX autoimmune disorders.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX 1..726  
XX CDS /tag- a  
XX /product- "human 312C2 protein"  
XX  
XX W09806842-A1.  
XX  
XX 19-FEB-1998.  
XX  
XX 14-AUG-1997; 97WO-US13931.  
XX  
XX 07-OCT-1996; 96US-0027901.  
XX  
XX 16-AUG-1996; 96US-0689943.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Gorman DM, Randall TD, Zlotnik A;  
XX  
XX WPI: 1998-159534/14.  
XX  
XX N-PSDB; AAV19153.  
XX  
XX Isolated 312C2 T cell gene - used to develop products for treating,  
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XX other T cell disorders  
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XX Claim 2; Pages 59-60; 71pp; English.  
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XX This is the amino acid sequence encoding the human 312C2 T cell  
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XX induced on T cells and spleen cells following activation. Engagement  
XX of 312C2 stimulates proliferation of T cell clones, antigen-specific  
XX proliferation and cytokine production by T-cells, and potentiates T  
XX cell expansion or apoptosis. The products can be used in the  
XX treatment of conditions associated with abnormal physiology or  
XX development, including abnormal proliferation, e.g. cancerous  
XX conditions or degenerative conditions. They can be used in the  
XX regulation or development of haematopoietic cells, e.g. lymphoid cells  
XX which affect immunological responses, e.g. autoimmune disorders.  
XX  
XX Sequence 241 AA;  
XX  
XX Query Match 100.0%; Score 969; DB 19; Length 241;  
XX Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
XX Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGMAGAFRALCGALICALSLGQRTGGCGGGRLLLTGTGTDARCCRVHTTRCCRD 60  
Db 1 maqhgamaafraleglallcalalslgprtgpgcgprlllgtgttdarcrcrvhttrccrd 60  
QY 61 YPGEECCSEWDCMVQPEFHCGDPCTTCRHHPCCPGQGVQSGKFSFGQCIDCASGTF 120  
Db 61 ypgeeccewdcmcvqpefhcgdpcttcrrhpcppgqgvsgqgkfsfgqcidcasgtf 120  
QY 121 SGGHEGCHKPWTDCQTFGFLTVFPNGKTHNAVCPGSPPAEP 162  
Db 121 sgghegchckpwtcdtqfgfltvfpngkthnavcvpgsppaep 162  
RESULT 4  
ID AAY06605  
XX AAY06605 standard; Protein; 241 AA.  
XX  
XX AAY06605;  
XX

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:34 ; Search time 65.86 Seconds  
(without alignments)  
50.647 Million cell updates/sec

Title: us-09-512-363-2\_COPY\_1\_162

Perfect score: 969

Sequence: 1 MAQHGAMGAFRALGLALIC.....FPGKTHNAVCPGSPPAEP 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scored: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued\_Patents\_AA.\*

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3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	937	96.7	228	3	Sequence 4, Appl
3	937	96.7	311	3	Sequence 6, Appl
4	605	62.4	232	3	Sequence 8, Appl
5	506	52.2	228	3	Sequence 7, Appl
6	255	26.3	89	4	Sequence 2, Appl
7	166.5	17.2	206	1	Sequence 191, App
8	166.5	17.2	206	1	Sequence 7, Appl
9	166.5	17.2	438	1	Sequence 11, Appl
10	166.5	17.2	438	1	Sequence 11, Appl
11	162	16.7	277	2	Sequence 2, Appl
12	162	16.7	277	4	Sequence 2, Appl
13	160.5	16.6	255	1	Sequence 8, Appl
14	160.5	16.6	255	2	Sequence 8, Appl
15	160.5	16.6	255	5	Sequence 9, Appl
16	158.5	16.4	219	2	Sequence 8, Appl
17	153	15.8	191	3	Sequence 2, Appl
18	153	15.8	256	1	Sequence 52, Appl
19	153	15.8	256	5	Sequence 6, Appl
20	153	15.8	300	2	Sequence 2, Appl
21	151	15.6	205	3	Sequence 2, Appl
22	149	15.4	140	4	Sequence 51, Appl
23	141.5	14.6	401	3	Sequence 17, Appl
24	139.5	14.4	139	2	Sequence 2, Appl
25	139.5	14.4	401	3	Sequence 8, Appl
26	139.5	14.4	401	4	Sequence 4, Appl
27	138.5	14.3	451	3	Sequence 13, Appl

28	138.5	14.3	451	4	US-08-995-659-4	Sequence 4, Appl
29	138.5	14.3	616	3	US-08-996-139-6	Sequence 6, Appl
30	138.5	14.3	616	4	US-08-995-659-6	Sequence 6, Appl
31	135.5	14.0	197	3	US-08-974-022-49	Sequence 49, Appl
32	135.5	14.0	289	4	US-09-042-785A-11	Sequence 11, Appl
33	133	13.7	401	3	US-08-974-022-6	Sequence 6, Appl
34	133	13.7	401	4	US-09-042-785A-12	Sequence 12, Appl
35	131	13.5	591	3	US-08-996-139-2	Sequence 2, Appl
36	131	13.5	591	4	US-08-995-659-2	Sequence 2, Appl
37	129.5	13.4	253	4	US-09-042-785A-4	Sequence 4, Appl
38	129.5	13.4	605	4	US-09-042-785A-23	Sequence 23, Appl
39	129.5	13.4	655	3	US-08-959-382-2	Sequence 2, Appl
40	123	12.7	625	3	US-08-996-139-15	Sequence 15, Appl
41	123	12.7	625	4	US-08-995-659-15	Sequence 15, Appl
42	121	12.5	227	3	US-08-974-022-48	Sequence 48, Appl
43	121	12.5	461	4	US-09-042-785A-7	Sequence 7, Appl
44	119	12.3	461	1	US-08-385-229-2	Sequence 2, Appl
45	119	12.3	461	6	5395760-2	Patent No. 5395760

## ALIGNMENTS

RESULT 1  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; STREET: DNAX Research Institute  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 969; DB 3; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.3e-77;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAFAFALGALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRD 60  
DB 1 MAQHGAFAFALGALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRD 60

QY 61 YPGECCSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTF 120  
DB 61 YPGECCSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTF 120

QY 121 SGGHEGCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162  
DB 121 SGGHEGCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162

RESULT 2  
US-08-911-423-6  
Sequence 6, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-6

Query Match 96.7%; Score 937; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3e-74;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRDYPGEEC 66  
DB 1 MGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRDYPGEEC 66

QY 121 SGGHEGCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162  
DB 121 SGGHEGCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162

Best Local Similarity 100.0%; Pred. No. 5.3e-77;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAFAFALGALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRD 60  
DB 1 MAQHGAFAFALGALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRD 60

QY 61 YPGECCSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTF 120  
DB 61 YPGECCSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTF 120

QY 121 SGGHEGCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162  
DB 121 SGGHEGCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162

RESULT 2  
US-08-911-423-6  
Sequence 6, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-6

Query Match 96.7%; Score 937; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3e-74;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRDYPGEEC 66  
DB 1 MGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRDYPGEEC 66

QY 121 SGGHEGCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162  
DB 121 SGGHEGCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162

QY 67 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTFSGGHEG 120

QY 127 HCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162  
DB 121 HCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 156

RESULT 3  
US-08-911-423-8  
Sequence 8, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 96.7%; Score 937; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 4e-74;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRDYPGEEC 66  
DB 1 MGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTCCRDYPGEEC 60

QY 67 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTFSGGHEG 120

QY 127 HCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162

Query Match 100.0%; Score 841; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.2e-66;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 60  
DB 20 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 79

QY 61 CTTCHRHPCPPGGVQSGKFSFGQICDASGTFSGHGHCKPWTDTCTQFGFLTVPFG 120  
DB 80 CTTCHRHPCPPGGVQSGKFSFGQICDASGTFSGHGHCKPWTDTCTQFGFLTVPFG 139

QY 121 NKTHNAVCPGSPAP 137  
DB 140 NKTHNAVCPGSPAP 156

RESULT 2  
US-08-911-423-4  
Sequence 4, Application US/08911423  
Patent No. 611090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 841; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 60  
DB 26 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 85

QY 61 CTTCHRHPCPPGGVQSGKFSFGQICDASGTFSGHGHCKPWTDTCTQFGFLTVPFG 120  
DB 86 CTTCHRHPCPPGGVQSGKFSFGQICDASGTFSGHGHCKPWTDTCTQFGFLTVPFG 145

QY 121 NKTHNAVCPGSPAP 137  
DB 146 NKTHNAVCPGSPAP 162

RESULT 3  
US-08-911-423-8  
Sequence 8, Application US/08911423  
Patent No. 611090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 841; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 4.2e-66;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 60  
DB 20 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 79

QY 61 CTTCHRHPCPPGGVQSGKFSFGQICDASGTFSGHGHCKPWTDTCTQFGFLTVPFG 120  
DB 80 CTTCHRHPCPPGGVQSGKFSFGQICDASGTFSGHGHCKPWTDTCTQFGFLTVPFG 139

QY 121 NKTHNAVCPGSPAP 137

Query Match 100.0%; Score 711; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.2e-54;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGGPGRLLLGTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPC 60  
DB 20 QRTGGPGGPGRLLLGTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPC 79

QY 61 CTTCHHPCPPGGVQSGKSFQFCIDCASGTFSGGHEGCHKPWTCTQFGF 114  
DB 80 CTTCHHPCPPGGVQSGKSFQFCIDCASGTFSGGHEGCHKPWTCTQFGF 133

RESULT 2  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 611090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; INFORMATION FOR SEQ ID NO: 4:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: linear  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 711; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGGPGRLLLGTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPC 60  
DB 26 QRTGGPGGPGRLLLGTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPC 85

QY 61 CTTCHHPCPPGGVQSGKSFQFCIDCASGTFSGGHEGCHKPWTCTQFGF 114  
DB 86 CTTCHHPCPPGGVQSGKSFQFCIDCASGTFSGGHEGCHKPWTCTQFGF 139

RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 611090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 711; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.8e-54;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGGPGRLLLGTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPC 60  
DB 20 QRTGGPGGPGRLLLGTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPC 79

QY 61 CTTCHHPCPPGGVQSGKSFQFCIDCASGTFSGGHEGCHKPWTCTQFGF 114  
DB 80 CTTCHHPCPPGGVQSGKSFQFCIDCASGTFSGGHEGCHKPWTCTQFGF 133

RESULT 4  
US-08-911-423-7  
; Sequence 7, Application US/08911423  
; Patent No. 611090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert

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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:36 ; Search time 65.86 Seconds  
(without alignments)  
51.273 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_164

Perfect score: 979  
Sequence: 1 MAQHGAMGAPRALCGLALLC.....GNKTHNAVCPGSPAPPLG 164

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Sehed: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	979	100.0	241	3	US-08-911-423-4
2	947	96.7	228	3	US-08-911-423-6
3	947	96.7	311	3	US-08-911-423-8
4	605	61.8	232	3	US-08-911-423-7
5	510	52.1	228	3	US-08-911-423-2
6	255	26.0	89	4	US-09-188-930-191
7	165.5	17.0	206	1	US-08-097-827-7
8	165.5	17.0	206	1	US-08-494-574-7
9	165.5	17.0	438	1	US-08-097-827-11
10	165.5	17.0	438	1	US-08-494-574-11
11	162	16.5	277	2	US-08-147-784-2
12	162	16.5	277	2	US-08-195-967-2
13	160.5	16.4	255	1	US-08-236-918A-8
14	160.5	16.4	255	2	US-08-816-605-9
15	160.5	16.4	255	5	PCT-US96-03965-8
16	158.5	16.2	219	2	US-08-816-605-2
17	153	15.6	191	3	US-08-974-022-52
18	153	15.6	256	1	US-08-236-918A-6
19	153	15.6	256	5	PCT-US96-03965-2
20	153	15.6	300	2	US-08-794-796-2
21	151	15.4	205	3	US-08-974-022-51
22	149	15.2	140	4	US-08-477-347-17
23	141.5	14.5	401	3	US-08-974-022-2
24	139.5	14.2	139	2	US-08-219-237B-8
25	139.5	14.2	401	3	US-08-974-022-4
26	139.5	14.2	401	4	US-09-042-785A-13
27	138.5	14.1	451	3	US-08-996-139-4

28	138.5	14.1	451	4	US-08-995-659-4	Sequence 4, Appl
29	138.5	14.1	616	3	US-08-996-139-6	Sequence 6, Appl
30	138.5	14.1	616	4	US-08-995-659-6	Sequence 6, Appl
31	137	14.0	401	3	US-08-974-022-6	Sequence 6, Appl
32	137	14.0	401	3	US-09-042-785A-12	Sequence 12, Appl
33	135.5	13.8	197	3	US-08-974-022-49	Sequence 49, Appl
34	135.5	13.8	289	4	US-09-042-785A-11	Sequence 11, Appl
35	131	13.4	591	3	US-08-996-139-2	Sequence 2, Appl
36	131	13.4	591	4	US-08-995-659-2	Sequence 2, Appl
37	129.5	13.2	253	4	US-09-042-785A-4	Sequence 4, Appl
38	129.5	13.2	605	4	US-09-042-785A-23	Sequence 23, Appl
39	129.5	13.2	655	3	US-08-959-382-2	Sequence 2, Appl
40	123	12.6	625	3	US-08-996-139-15	Sequence 15, Appl
41	123	12.6	625	4	US-08-995-659-15	Sequence 15, Appl
42	121	12.4	197	2	US-08-505-606-1	Sequence 1, Appl
43	121	12.4	227	3	US-08-974-022-48	Sequence 48, Appl
44	121	12.4	461	4	US-09-042-785A-7	Sequence 7, Appl
45	119	12.2	461	6	5395760-2	Patent No. 5395760

## ALIGNMENTS

RESULT 1  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 979; DB 3; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.7e-78;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAFAFALCGALLCALSLGQRPTGGPGGPGRLLLGTGTDCRCRHHVTRCCRD 60  
DB 1 MAQHGAFAFALCGALLCALSLGQRPTGGPGGPGRLLLGTGTDCRCRHHVTRCCRD 60  
QY 61 YPEECCSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSQKFSFGFCIDCASGTF 120  
DB 61 YPEECCSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSQKFSFGFCIDCASGTF 120  
QY 121 SGHGHCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 164  
DB 121 SGHGHCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 164

## RESULT 2

US-08-911-423-6  
Sequence 6, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-911-423-6

Query Match 96.7%; Score 947; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.2e-75;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFAFALCGALLCALSLGQRPTGGPGGPGRLLLGTGTDCRCRHHVTRCCRDYPGEEC 66  
DB 1 MGAFAFALCGALLCALSLGQRPTGGPGGPGRLLLGTGTDCRCRHHVTRCCRDYPGEEC 60

QY 67 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSQKFSFGFCIDCASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSQKFSFGFCIDCASGTFSGGHEG 120  
QY 127 HCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 164  
DB 121 HCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 158

## RESULT 3

US-08-911-423-8  
Sequence 8, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-911-423-8

Query Match 96.7%; Score 947; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 4.3e-75;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFAFALCGALLCALSLGQRPTGGPGGPGRLLLGTGTDCRCRHHVTRCCRDYPGEEC 66  
DB 1 MGAFAFALCGALLCALSLGQRPTGGPGGPGRLLLGTGTDCRCRHHVTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSQKFSFGFCIDCASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSQKFSFGFCIDCASGTFSGGHEG 120  
QY 127 HCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 164



Query Match 100.0%; Score 737; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.2e-58;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGVQSQGK 60  
DB 40 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGVQSQGK 99  
QY 61 FSGFQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVFPNGKTHNAVCPGSPPAEPLG 119  
DB 100 FSGFQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVFPNGKTHNAVCPGSPPAEPLG 158

RESULT 2  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 737; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.2e-58;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGVQSQGK 60  
DB 46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGVQSQGK 105  
QY 61 FSGFQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVFPNGKTHNAVCPGSPPAEPLG 119  
DB 106 FSGFQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVFPNGKTHNAVCPGSPPAEPLG 164

RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 737; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.5e-58;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGVQSQGK 60  
DB 40 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGVQSQGK 99  
QY 61 FSGFQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVFPNGKTHNAVCPGSPPAEPLG 119  
DB 100 FSGFQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVFPNGKTHNAVCPGSPPAEPLG 158

RESULT 4  
US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert

Query Match 100.0%; Score 753; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6e-60;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGPRLLLTGTDAACRCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60  
|||||  
Db 27 CGGPRLLLTGTDAACRCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 86  
|||||

QY 61 PCPPGQVQSGKFSFGQICDASGTFSGGHEGCKPWTDCQFGFLTVFPGNKTHNAV 120  
|||||  
Db 87 PCPPGQVQSGKFSFGQICDASGTFSGGHEGCKPWTDCQFGFLTVFPGNKTHNAV 146  
|||||

QY 121 CV 122  
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Db 147 CV 148

RESULT 2  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 753; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 6.3e-60;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGPRLLLTGTDAACRCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60  
|||||  
Db 33 CGGPRLLLTGTDAACRCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 92  
|||||

QY 61 PCPPGQVQSGKFSFGQICDASGTFSGGHEGCKPWTDCQFGFLTVFPGNKTHNAV 120  
|||||  
Db 93 PCPPGQVQSGKFSFGQICDASGTFSGGHEGCKPWTDCQFGFLTVFPGNKTHNAV 152  
|||||

QY 121 CV 122  
||  
Db 153 CV 154

RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 753; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 7.9e-60;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGPRLLLTGTDAACRCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60  
|||||  
Db 27 CGGPRLLLTGTDAACRCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 86  
|||||

QY 61 PCPPGQVQSGKFSFGQICDASGTFSGGHEGCKPWTDCQFGFLTVFPGNKTHNAV 120  
|||||  
Db 87 PCPPGQVQSGKFSFGQICDASGTFSGGHEGCKPWTDCQFGFLTVFPGNKTHNAV 146  
|||||

QY 121 CV 122

**GENERAL INFORMATION:**

Query Match 100.0%; Score 252; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.4e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCI 40  
Db 68 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCI 107

## RESULT 2

US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0., Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 252; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.5e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCI 40  
Db 74 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCI 113

## RESULT 3

US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.

APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0., Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 252; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 3.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCI 40  
Db 68 CVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCI 107

## RESULT 4

US-08-911-423-7  
; Sequence 7, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:

APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

Query Match 100.0%; Score 246; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.2e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 41  
Db 108 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 148

## RESULT 2

US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023.419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027.901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 246; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 41  
Db 114 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 154

## RESULT 3

US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.

APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911.423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023.419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027.901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 246; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 41  
Db 108 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 148

## RESULT 4

US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.  
 AC Q9Y5U5;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.  
 GN TNFRSF18  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BONE MARROW;  
 RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,  
 RA Gurdin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,  
 RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.,  
 RT "Identification of a new member of the tumor necrosis factor family  
 and its receptor, a human ortholog of mouse GITR.";  
 RL Curr. Biol. 0:0-0(1999).  
 DR EMBL; AF125304; AAD22635.1; -.  
 DR InterPro; IPR001368; -.  
 DR SMART; SM00208; TNFR; 1.  
 SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 711; DB 4; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-70;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRTGPGCGGPGRLLLGTGTDAACRCRVHTRCCRDYDPEGECSSWDCMCVQPEFHCGDPC 60  
 DB 26 QRTGPGCGGPGRLLLGTGTDAACRCRVHTRCCRDYDPEGECSSWDCMCVQPEFHCGDPC 85  
 QY 61 CTTCTRHHPCCPPGGVSGQKFSFGFCIDCASGTFSGHGHCKPWTDCQTQFGF 114  
 DB 86 CTTCTRHHPCCPPGGVSGQKFSFGFCIDCASGTFSGHGHCKPWTDCQTQFGF 139

RESULT 3  
 Q9NYJ9  
 ID Q9NYJ9 PRELIMINARY; PRT; 255 AA.  
 AC Q9NYJ9;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE GITR-D.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RA Nocentini G., Bartoli A., Ronchetti S., Mastroiaca E., Riccardi C.,  
 RT "Identification of a soluble human GITR splicing (hGITR-D).";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF241229; AAF63506.1; -.  
 SQ SEQUENCE 255 AA; 26827 MW; C98652AC97AF2CC CRC64;

Query Match 96.1%; Score 683; DB 4; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-67;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRTGPGCGGPGRLLLGTGTDAACRCRVHTRCCRDYDPEGECSSWDCMCVQPEFHCGDPC 60  
 DB 26 QRTGPGCGGPGRLLLGTGTDAACRCRVHTRCCRDYDPEGECSSWDCMCVQPEFHCGDPC 85  
 QY 61 CTTCTRHHPCCPPGGVSGQKFSFGFCIDCASGTFSGHGHCKPWTDC 109  
 DB 86 CTTCTRHHPCCPPGGVSGQKFSFGFCIDCASGTFSGHGHCKPWTDC 134

RESULT 4  
 Q9JKR2  
 ID Q9JKR2 PRELIMINARY; PRT; 222 AA.  
 AC Q9JKR2;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE GITR-C.  
 GN TNFRSF18  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
 RA Migliorati G., Riccardi C.,  
 RT "Identification of three novel mRNA splice variants of GITR.";  
 RL Cell Death Differ. 0:0-0(2000).  
 DR EMBL; AF229433; AAF61567.1; -.  
 DR InterPro; IPR000561; -.  
 DR SMART; SM00181; EGF; 1.  
 SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 52.5%; Score 373.5; DB 11; Length 222;  
 Best Local Similarity 53.7%; Pred. No. 1.8e-33;  
 Matches 58; Conservative 19; Mismatches 24; Indels 7; Gaps 1;  
 QY 7 PGGPGRLLLGTGTDAACRCRVHTRCCRDYDPEGECSSWDCMCVQPEFHCGDPCCTTGRH 66  
 DB 27 PGGPGKQVSGNTRCCSLYA-----PKEDCPKRCICVTPHYHCGDPCQCKICKH 79  
 QY 67 HPCPPGQVSGQKFSFGFCIDCASGTFSGHGHCKPWTDCQTQFGF 114  
 DB 80 YPCPPGQVSGQKFSFGFCIDCASGTFSGHGHCKPWTDCQTQFGF 127

RESULT 5  
 Q35714  
 ID Q35714 PRELIMINARY; PRT; 228 AA.  
 AC Q35714;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE GLUCOCORTICOID-INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.  
 GN TNFRSF18 OR GITR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/HEJ;  
 RX MEDLINE=97322352; PubMed=9177197;  
 RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,  
 RA Moraca R., Migliorati G., Riccardi C.,  
 RT "A new member of the tumor necrosis factor/nerve growth factor  
 receptor family inhibits T cell receptor-induced apoptosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/C;  
 RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., CuPELLI A.,  
 RA Migliorati G., Riccardi C.,  
 RT "Gene structure and chromosomal assignment of GITR, a mouse member of  
 the tumor necrosis factor/nerve growth factor receptor family.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U82534; AAB81243.1; -.  
 DR EMBL; AF109216; AAF14231.1; -.  
 DR MGI; 894675; Tnfrsf18.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:30 ; Search time 133.1 Seconds  
(without alignments)  
113.319 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_139

Perfect score: 711  
Sequence: 1 QRTGPGGCGPRLLLGTGT.....FSGHGEGCKPWTDCQFGF 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- SPTREMBL16:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_unclassified:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	711	100.0	234	4 Q95851	Q95851 homo sapien
2	711	100.0	241	4 Q9Y5U5	Q9Y5U5 homo sapien
3	683	96.1	255	4 Q9NYJ9	Q9NYJ9 homo sapien
4	373.5	52.5	222	11 Q9JRR2	Q9JRR2 mus musculu
5	373.5	52.5	228	11 Q35714	Q35714 mus musculu
6	373.5	52.5	294	11 Q9JRR3	Q9JRR3 mus musculu
7	339.5	47.7	132	11 Q9JRR1	Q9JRR1 mus musculu
8	130.5	18.4	267	6 O02764	O02764 oryctolagus
9	122	17.2	107	11 Q9JKE0	Q9JKE0 rattus norv
10	119	16.7	276	13 Q9DDD2	Q9DDD2 gallus gall
11	117	16.5	300	4 Q95407	Q95407 homo sapien
12	112	15.8	152	5 Q9XVX3	Q9XVX3 caenorhabdi
13	108.5	15.3	2906	11 Q9WUH9	Q9WUH9 rattus norv
14	108	15.2	616	4 Q9Y6Q6	Q9Y6Q6 homo sapien
15	107	15.0	164	5 Q22048	Q22048 caenorhabdi
16	106	14.9	625	11 Q35305	Q35305 mus musculu
17	105	14.8	1574	11 Q88281	Q88281 rattus norv
18	104.5	14.7	655	4 Q75509	Q75509 homo sapien
19	104	14.6	1522	5 Q22685	Q22685 caenorhabdi

20	104	14.6	4601	5 Q9V383	Q9V383 drosophila
21	103.5	14.6	126	10 Q9S9F4	Q9S9F4 phytolacca
22	103.5	14.6	655	11 Q9EP05	Q9EP05 mus musculu
23	102.5	14.4	188	5 Q18238	Q18238 caenorhabdi
24	102.5	14.4	283	6 Q9XSZ8	Q9XSZ8 cercopithec
25	102.5	14.4	1308	5 Q9GPM8	Q9GPM8 caenorhabdi
26	102	14.3	401	11 Q08727	Q08727 rattus norv
27	102	14.3	870	6 Q02660	Q02660 bos taurus
28	101	14.2	401	11 Q08712	Q08712 mus musculu
29	99.5	14.0	1764	11 Q35806	Q35806 rattus norv
30	99	13.9	372	4 Q9UHP4	Q9UHP4 homo sapien
31	99	13.9	401	4 Q00300	Q00300 homo sapien
32	97	13.6	1587	4 Q00508	Q00508 homo sapien
33	96.5	13.6	410	11 Q63720	Q63720 rattus norv
34	96.5	13.6	469	11 Q63721	Q63721 rattus norv
35	96.5	13.6	1821	4 Q14767	Q14767 homo sapien
36	96	13.5	1511	4 Q75412	Q75412 homo sapien
37	96	13.5	1963	6 Q28019	Q28019 bos taurus
38	95.5	13.4	1698	5 Q94438	Q94438 chironomus
39	95.5	13.4	1792	13 Q57484	Q57484 gallus gall
40	95	13.4	1537	5 Q9VAI2	Q9VAI2 drosophila
41	94.5	13.3	830	4 Q43701	Q43701 homo sapien
42	94.5	13.3	830	4 Q14162	Q14162 homo sapien
43	94.5	13.3	1833	11 Q08999	Q08999 mus musculu
44	94	13.2	1203	11 Q06008	Q06008 mus musculu
45	94	13.2	1637	6 Q9XSU8	Q9XSU8 bos taurus

ALIGNMENTS

RESULT 1					
Q95851					
ID Q95851	PRELIMINARY;	PRT;	234 AA.		
AC Q95851;					
DT 01-MAY-1999 (Tremblrel. 10, Created)					
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)					
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)					
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.					
OS Homo sapiens (human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=99156876; PubMed=10037686;					
RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,					
Liu D., Wang S.X., Kwon B.S.;					
RT "Identification of a novel activation-inducible protein of the tumor					
RT necrosis factor receptor superfamily and its ligand."					
RL J. Biol. Chem. 274:6056-6061(1999).					
DR EMBL; AF117297; AAD19694.1; -					
DR InterPro; IPR001368; -					
DR SMART; SM00208; TNFR; 1.					
KW Receptor.					
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;					
Query Match 100.00%; Score 711; DB 4; Length 234;					
Best Local Similarity 100.00%; Pred. No. 2e-70;					
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1 QRTGPGGCGPRLLLGTGTDCRCRVHTTRCRRDTPGEECCSEWDCMCVQPFHCGDPC 60					
Db 26 QRTGPGGCGPRLLLGTGTDCRCRVHTTRCRRDTPGEECCSEWDCMCVQPFHCGDPC 85					
QY 61 CTTCTRHHPGPGGVQSGKFSFGFCIDCASCTFSGGEGHCKPWTDCQFGF 114					
Db 86 CTTCTRHHPGPGGVQSGKFSFGFCIDCASCTFSGGEGHCKPWTDCQFGF 139					
RESULT 2					
Q9Y5U5					

Q9JKE0	PRELIMINARY;	PRT;	107 AA.
Q9JKE0;			
AC	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)		
DE	CD40 PROTEIN (FRAGMENT).		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
NCBI_TaxID=101116;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=WISTAR; TISSUE=SMOOTH MUSCLE, AORTA;		
RA	MEDLINE=99930195; PubMed=10403401;		
RX	Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;		
RL	"Cytokine-inducible CD40 gene expression in vascular smooth muscle		
RT	cells is mediated by nuclear factor kappaB and signal transducer and		
RT	activation of transcription-1.";		
FEBS Lett. 453:191-196(1999).			
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=WISTAR; TISSUE=SMOOTH MUSCLE, AORTA;		
RA	Krzesz R., Hecker M.;		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
EMBL; AF241231; AAF43717.1; -			
InterPro: IPR001368; -			
DR	PROSITE; PS50050; TNFR_NGFR_2; 1.		
FT	NON_TER 1		
FT	NON_TER 107		
SEQUENCE	107 AA; 11819 MW; 55BFF8327A0933B2 CRC64; -		
Query Match	17.2%;	Score 122;	DB 11; Length 107;
Best Local Similarity	33.3%;	Pred. No. 3.3e-06;	
Matches	31; Conservative	6; Mismatches	46; Indels 10; Gaps
QY	26 RVHTTCCRDYPGEE-----CCSEWDCMCVQPFHCQDPCCCTC-RHHPCPPGQGVQSQ 78		
Db	14 RCHQRRHCELNQLQVKKEGTAVSDTVCTKEGQ-HCASKECETCAQHRPCGPGFGVQM 72		
QY	79 GKFSFGQCIDCASGTFSGGHE--GHCKPWTD 109		
Db	73 ATETDTVCQPCVPVGFSGSSLFKCHPWTC 105		
RESULT 10			
Q9DD2	PRELIMINARY;	PRT;	276 AA.
ID	Q9DD2;		
AC	Q9DD2;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)		
DE	HUMAN CD40-HOMOLOGUE.		
GN	TNFSF5.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
NCBI_TaxID=9031;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	Tregaskes C.A.;		
RA	Thesis (2001), University of Reading, Reading, UNITED KINGDOM.		
DR	EMBL; AJ293700; CAC20218.1; -		
SEQUENCE	276 AA; 30009 MW; 4040B7E0DB82454E CRC64;		
Query Match	16.7%;	Score 119;	DB 13; Length 276;
Best Local Similarity	26.7%;	Pred. No. 1.6e-05;	
Matches	43; Conservative	7; Mismatches	49; Indels 62; Gaps
QY	14 LLLGTGT--DARGCR----VHTTRCC-RDYPGECGCE-----WD 46		

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Db      13 LLLCGCGGDAVNCSDQYEHKGRCCNRCOPGGKKLASECNDTDSVCTPCENGQOYHSWT   72
QY      47 -----CMCVQPEFHGCDPCCTTC-RHHPPCPGQG- 74
Db      73 KERHCTPHEICEDNAGLVIVKRHNATHNTVCQC-RAGMHCSADSCQTGVENEPCKOGFGF   131
QY      75 VQSQRFSFSGFCIDCASGTFS--GGHGHCXKPWTDCTQFG 113
Db      132 VAAMAEARMTSPCEPCAEGTSFTSVSSKTPECFHWFTSCEEKG 172

RESULT 11
095407 PRELIMINARY; PRT; 300 AA.
ID AC 095407;
DT DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DE DECOY RECEPTOR_3 (M68) (M68C) (M68E) (DJ583PL5.1.1).
GN GN DCR3 OR TR6 OR TNFRSF6B.
OS OS Homo sapiens (human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN RN [1]
SEQUENCE FROM N.A.
RX RX MEDLINE=99087326; PubMed=9872321;
RA RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RT RT Nature 396:699-703(1998).
[2]
SEQUENCE FROM N.A.
RX RX TISSUE=BLOOD;
RC RC MEDLINE=99253915; PubMed=10318773;
RA RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
[3]
SEQUENCE FROM N.A.
RX RX TISSUE=PANCREAS;
RC RC MEDLINE=20122600; PubMed=10655513;
RA RA Bai C., Connolly B., Metzker M.B., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Gallowsay S.M., Liu Q., Austin C.P., Caskey C.T.;
RT RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
[4]
SEQUENCE FROM N.A.
RA RA Matthews L.;
RL RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR DR ENBL; AF104419; AAD03056.1; -
DR DR ENBL; AF134240; AAD29688.1; -
DR DR ENBL; AF217796; AAF35244.1; -
DR DR ENBL; AF217793; AAF33685.1; -
DR DR ENBL; AF217794; AAF33686.1; -
DR DR ENBL; AL121845; CAC03668.1; -
DR DR HSP; P25942; ICDP.
DR DR InterPro: IPR000561; -
DR DR InterPro: IPR001368; -
DR DR Pfam: PF00020; TNFR_C6; 4.
DR DR ProDom: PD000771; -; 1.
DR DR PROSITE; PS01186; EGF_2; UNKNOWN_1
DR DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW KW Receptor.
SQ SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;
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DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
KW Signal; Receptor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY
FT RELATED PROTEIN.
SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259. CRC64;

Query Match 52.5%; Score 373.5; DB 11; Length 228;
Best Local Similarity 53.7%; Pred. No. 1.8e-33;
Matches 58; Conservative 19; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRH 66
Db 27 PGCGPGKVGQSGNNTCCSLYA-----PGKEDCPKERCICVTPYHCGDPQCKICKH 79

QY 67 HPCPPGGVQSGQKFSFGFCQIDCASGTFSGGHEGHCXKPTDCTQFG 114
Db 80 YPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCLWNTCSQFG 127

RESULT 6
Q9JKR3 PRELIMINARY; PRT; 294 AA.
AC Q9JKR3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229432; AAF61566.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 52.5%; Score 373.5; DB 11; Length 294;
Best Local Similarity 53.7%; Pred. No. 2.2e-33;
Matches 58; Conservative 19; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRH 66
Db 27 PGCGPGKVGQSGNNTCCSLYA-----PGKEDCPKERCICVTPYHCGDPQCKICKH 79

QY 67 HPCPPGGVQSGQKFSFGFCQIDCASGTFSGGHEGHCXKPTDCTQFG 114
Db 80 YPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCLWNTCSQFG 127

RESULT 7
Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229432; AAF61566.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 52.5%; Score 373.5; DB 11; Length 294;
Best Local Similarity 53.7%; Pred. No. 2.2e-33;
Matches 58; Conservative 19; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRH 66
Db 27 PGCGPGKVGQSGNNTCCSLYA-----PGKEDCPKERCICVTPYHCGDPQCKICKH 79

QY 67 HPCPPGGVQSGQKFSFGFCQIDCASGTFSGGHEGHCXKPTDCTQFG 114
Db 80 YPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCLWNTCSQFG 127

RESULT 7
Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229432; AAF61566.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;
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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61568.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5404BIDFEDE CRC64;

Query Match 47.7%; Score 339.5; DB 11; Length 132;
Best Local Similarity 52.5%; Pred. No. 6e-30;
Matches 53; Conservative 17; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRH 66
Db 27 PGCGPGKVGQSGNNTCCSLYA-----PGKEDCPKERCICVTPYHCGDPQCKICKH 79

QY 67 HPCPPGGVQSGQKFSFGFCQIDCASGTFSGGHEGHCXKPT 107
Db 80 YPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCLWNT 120

RESULT 8
O02764 PRELIMINARY; PRT; 267 AA.
AC O02764;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHBB;HM;
RA Isono T., Seto A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -.
DR HSP; P19438; IEXT.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00208; TNFR; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 18 POTENTIAL.
FT CHAIN 19 267 OX40.
SQ SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;

Query Match 18.4%; Score 130.5; DB 6; Length 267;
Best Local Similarity 32.8%; Pred. No. 8.3e-07;
Matches 38; Conservative 7; Mismatches 50; Indels 21; Gaps 6;

QY 9 CGPGRLLLTGTDAACRCRVHTTRCCRDYPG--EECCSEWDCM-CVQ-----PEFHCG 57
Db 40 CQP-----GYGMVSRGNRSQDTTCHPECPGYNEAVNYQACKPCTCQNRSGSEPOQECT 94

QY 58 DPCCTTCRHHPGPPGGVQSGQKFSFGFCQIDCASGTFSGGHEGHCXKPTDCTQFG 113
Db 95 HTRDVTVC---CRP--GTQPLNGYKHGVDCAPCPQGHFSEGNRNACRPWTNCTLAG 145

RESULT 9
Q9JKEO
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RESULT 13  
 Q9WUH9 PRELIMINARY; PRT; 2906 AA.  
 ID Q9WUH9  
 AC Q9WUH9  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE FIBRILLIN-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yang Q., Ota K., Tian Y., Kumar A., Wada J., Kashiwara N.,  
 RA Wallner E.I., Kanwar Y.S.;  
 RT "Cloning of rat fibrillin-2 cDNA and its role in branching  
 RT morphogenesis of rat embryonic lung."  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF135060; AAD34439.1; -;  
 DR HSSP; P35555; IEMN.  
 DR InterPro; IPR000152; -;  
 DR InterPro; IPR000561; -;  
 DR InterPro; IPR001438; -;  
 DR InterPro; IPR001881; -;  
 DR InterPro; IPR002086; -;  
 DR InterPro; IPR002212; -;  
 DR Pfam; PF00008; EGF\_46;  
 DR Pfam; PF00683; TB; 9;  
 DR PRINTS; PR00010; EGFBL00D.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 43.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_2.  
 DR PROSITE; PS01186; EGF\_2; 36.  
 DR PROSITE; PS01187; EGF\_CA; 43.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat  
 KW SEQUENCE 2906 AA; 313372 MW; 9EE64E727044EF58 CRC64;  
 SQ  
 Query Match 15.3%; Score 108.5; DB 11; Length 2906;  
 Best Local Similarity 25.2%; Pred. No. 0.0016;  
 Matches 31; Conservative 15; Mismatches 38; Indels 39; Gaps  
 QY 9 CGPGRLLLGTTDARCC-----RVHTTCCRDYDGECCSEWDCMCVQPEFHCG 57  
 DB 676 CPPG---LAVGVGRVCVDTHMRSTCYGEIKKGVCRPFPG--AVTIKCCANPDVGFG 730  
 QY 58 DPCCTCRHHPPGPGVQSGQKFSFGF-----QC-ID---CAGS---TFSGGHE 100  
 DB 731 EPC-----QCPKAKNSAEFHGLSGGVITVDGRDINECALDPDICANGICENLRGSYR 780  
 QY 101 GHC 103  
 DB 785 CNC 787  
 RESULT 14  
 Q9Y6Q6 PRELIMINARY; PRT; 616 AA.  
 ID Q9Y6Q6  
 AC Q9Y6Q6;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-  
 DE INDUCED CYTOKINE RECEPTOR) (RANK).  
 GN TNFRSF11A OR RANK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Search completed: September 4, 2001, 16:14:30  
Job time: 1217 sec

DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
 DE (OCIF).  
 GN TNFRSF11B OR OPG.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=INTESTINE;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation  
 RT of bone density.";  
 RL Cell 89:309-319(1997).  
 CC -|- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -|- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 CC SIMILARITY).  
 CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; U94330; AAB53707.1; -;  
 DR HSSP; P25942; ICDF.  
 DR InterPro; IPR000488; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR ProDom; PD000771; -; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 DR SMART; SM00005; DEATH; 1.  
 KW Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 401 OSTEOPROTEGERIN.  
 FT DOMAIN 23 201 4 X TNFR-CYS.  
 FT REPEAT 23 63 TNFR-CYS 1.  
 FT REPEAT 64 106 TNFR-CYS 2.  
 FT REPEAT 107 143 TNFR-CYS 3.  
 FT REPEAT 144 201 TNFR-CYS 4.  
 FT DOMAIN 306 365 DEATH DOMAIN.  
 FT DISULFID 41 54 BY SIMILARITY.  
 FT DISULFID 44 62 BY SIMILARITY.  
 FT DISULFID 65 80 BY SIMILARITY.  
 FT DISULFID 83 97 BY SIMILARITY.  
 FT DISULFID 87 105 BY SIMILARITY.  
 FT DISULFID 118 142 BY SIMILARITY.  
 FT DISULFID 145 160 BY SIMILARITY.  
 FT CARBOHYD 98 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 165 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 401 AA; 46192 MW; FEC6A31F1D4E573A CRC64;

Query Match 10.6%; Score 141.5; DB 11; Length 401;  
 Best Local Similarity 27.2%; Pred. No. 2.2e-06;  
 Matches 46; Conservative 11; Mismatches 63; Indels 49; Gaps 8;  
 QY 15 GLALCALSLGQRITGGPGCGPGRLLLTGTGDACCRVHTTRC--CRDY-----PGEE 65  
 DB 36 GRQLLC-----DKCAPGYL-----KQHTVRRKTLCPVCPDYSTDSWHTSDE 79  
 QY 66 C-----CSEWD-----CMCVQPEHFHCGDPCCTTCRHHPCPGPGVQSGKGF 106  
 DB 80 CVYCSPVCKELQTVQECNRTHNRVCECEGRYLELEFC---LKHRSCTPGGLVQLQAGTP 136

QY 107 SFGFOCIDCASGTFSG--GHEGCHKPWTCTQFGELTVFPGNKTHNAV 153  
 DB 137 ERNTVKRCPDGFFSGETSSKAPCRKHTNCSSGLLLIQGNATHDNVC 185  
 RESULT 13  
 O08712  
 ID O08712 PRELIMINARY; PRT; 401 AA.  
 AC O08712; O70202;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
 DE (OCIF).  
 GN TNFRSF11B OR OPG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=KIDNEY;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation  
 RT of bone density.";  
 RL Cell 89:309-319(1997).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=129/Ola, AND NIH SWISS;  
 RX MEDLINE=98382527; PubMed=9714833;  
 RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,  
 RA Higashio K.;  
 RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)  
 RT gene and its expression in embryogenesis.";  
 RL Gene 215:339-343(1998).  
 CC -|- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -|- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).  
 CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -|- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND  
 CC PLACENTA. NOT DETECTED IN SPLEEN.  
 CC -|- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
 CC 15 TO DAY 17.  
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; U94331; AAB53708.1; -;  
 DR EMBL; AB013898; BAA28269.1; -;  
 DR EMBL; AB013903; BAA33388.1; -;  
 DR EMBL; AB013899; BAA33388.1; JOINED.  
 DR EMBL; AB013900; BAA33388.1; JOINED.  
 DR EMBL; AB013901; BAA33388.1; JOINED.  
 DR EMBL; AB013902; BAA33388.1; JOINED.  
 DR HSSP; P25942; ICDF.  
 DR MGI; MGI:109587; Tnfrsf11b.  
 DR InterPro; IPR000488; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR ProDom; PD000771; -; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR SMART; SM00005; DEATH; 1.  
 KW Glycoprotein; Repeat; Cytokine; Signal.







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QY 66 CCSEWDCMCVQPEHCHGDDPCTTCRHHPCPGPGQVQSGKFSFGQCIDCASGTFSGGHE 125
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 54 DCPKERICVTPYHCGDPQCKICKHYPCQPGQVQSGQDILVFGRCVACAMGTFSGAGD 113
QY 126 GHCKPWT 132
| ||| : ||
Db 114 GHCLWT 120

RESULT 8
O02764 PRELIMINARY; PRT; 267 AA.
AC O02764;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHB:HM;
RA Isono T., Seto A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: A8003911; BAA20059.1; -.
DR HSSP: P19438; 1EXT.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_c6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00050; TNFR_NGFR_2; 2.
DR SMART: SM00208; TNFR; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 18 POTENTIAL.
FT CHAIN 19 267 OX40.
SQ SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;

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Query Match 13.6%; Score 182.5; DB 6; Length 267;
Best Local Similarity 27.8%; Pred. No. 1.1e-10;
Matches 76; Conservative 22; Mismatches 94; Indels 81; Gaps 16;

QY 12 ALGCLA-LICALSLGQRTGPGCG-----GPGRLLL-----GTGTDARCCRVHTTRCCRD 60
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 4 AALGLALLLLGLLGAEP--PDCVGTYPGGDRCCLECPQGYGNVSRNRSQDTICHPC 61
QY 61 YPG--EECCSEWDCM-CVQ-----PEFHGDPCCCTTCRHHPCPGPGQVQSGKFSFG 109
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 62 EPGFYNAVNYQACKPCTQCNRSSGSEPPQECTHTRDTVCR---CRP--GTQPLNGYKHG 116
QY 110 FQCIDCASGTFSGGHEGCHPWTCTQFGFLTVFPGKNTNNAVC-----VPGS 157
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 117 VDCAPCPQGHFSEGNRACRPWTNCTLAGKRTLQPASSISDAVCEDRSSLATQPWETPSA 176
QY 158 PPAEP-----LGV-----LNVVL-LAAVACVLLTSAQLGLHI--- 189
Db 177 PYRPTARTAMPRTAAGSTPTLEASKGFLAIVLSLGLGLLALLAALALYLHQR 236
QY 190 -WOLRKTQLLLEVPPTEDARSCQFP--EEERGE 220
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 237 AWR-----PPKLPGGSGSFTPIQEEQAD 259

RESULT 9
Q9DD2 PRELIMINARY; PRT; 276 AA.
AC Q9DD2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

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DE HUMAN CD40-HOMOLOGUE.
OS TNFSF5.
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tregaskes C.A.;
RL Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
DR EMBL: AJ293700; CAC20218.1; -.
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

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Query Match 13.6%; Score 182.5; DB 13; Length 276;
Best Local Similarity 25.5%; Pred. No. 1.1e-10;
Matches 73; Conservative 20; Mismatches 94; Indels 99; Gaps 15;

QY 16 LALLCALSLGQRTGPGCG-PGRLLLTGTGDARCCR-----VHTTRCC-RDYPGEECCSE 69
| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 7 LGLLCALLL-----GGQPG-----DAVNCSDKQYEHKGRCCNRCQPKKLASE 50
QY 70 -----WD-----CMCVQPEF 79
Db 51 CNDTDSVCTPCENGQYQHSWTKERHCTPHEICEDNAGLIVKRHNATHNTVCQC-RAGM 109
QY 80 HCGDPCCTTC-RHHPCPGQG--VQSGKFSFGQCIDCASGTF--GGHEGCHKPWTCT 135
Db 110 HCSASCQTCVENEPCQKQGFVAAAEARMTSPCECAEGTFSNVSSKTEPCHEWTSCE 169
QY 136 QFGFLTVFPGKNTNNAVCVPGSPPAEPLGWLTVLLVAACVLLTSAQLGLHIHQLRKT 195
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 170 EKGLVVKVKGNTSDVIC--ESSRRSSLSVLIPITAAVVTCL-----VGICVCLVHT 220
QY 196 QLLEVPFS-----TEDARSCQPEER-----GERSAEKGR 228
Db 221 DLRRGPKQAEAPRELVTQOPEEVDFPVQETLLGGQPVQAEQDGK 266

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RESULT 10
O95407 PRELIMINARY; PRT; 300 AA.
AC O95407;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).
GN DCR3 OR TR6 OR TNFRSF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
colon cancer."
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
superfamily (TR6) suppresses LIGHT-mediated apoptosis."
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.

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GenCore version 4.5  
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# OW protein - protein search, using sw model

Run on: September 4, 2001, 15:54:13 ; Search time 133.1 Seconds  
(without alignments)  
232.602 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 1340  
Sequence: 1 MAQHGAMGAFRALCGLALLC.....EEERGSABEKGRLGIWV 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

SPTREMBL\_16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1340	100.0	234	4	O95851 homo sapien
2	1322.5	98.7	241	4	O9y5u5 homo sapien
3	815	60.8	255	4	O9nrj9 homo sapien
4	703	52.5	228	11	O35714 mus musculus
5	625.5	46.7	294	11	O9jkr3 mus musculus
6	618	46.1	222	11	O9jkr2 mus musculus
7	380	28.4	132	11	O9jkr1 mus musculus
8	182.5	13.6	267	6	O02764 oryctolagus
9	182.5	13.6	276	13	O9ddd2 gallus galli
10	153	11.4	300	4	O95407 homo sapien
11	150	11.2	616	4	O9y6q6 homo sapien
12	141.5	10.6	401	11	O08727 rattus norv
13	139.5	10.4	401	11	O08712 mus musculus
14	139.5	10.4	439	4	Q16042 homo sapien
15	138	10.3	372	4	O9uhp4 homo sapien
16	138	10.3	401	4	O00300 homo sapien
17	134.5	10.0	625	11	O35305 mus musculus
18	129.5	9.7	655	4	O75509 homo sapien
19	125	9.3	655	11	O9epu5 mus musculus

20	122	9.1	107	11	O9JKE0	O9jke0 rattus norv
21	121	9.0	302	13	O9PUS0	O9pus0 salvelinus
22	120.5	9.0	459	11	O62327	O62327 mus musculus
23	120.5	9.0	482	11	O88734	O88734 mus musculus
24	119.5	8.9	1587	4	O00508	O00508 homo sapien
25	119.5	8.9	1637	6	O9XSV8	O9xsv8 bos taurus
26	119	8.9	1574	11	O88281	O88281 rattus norv
27	118.5	8.8	1511	4	O75412	O75412 homo sapien
28	116	8.7	4123	4	O75851	O75851 homo sapien
29	115.5	8.6	1371	11	O9QVW4	O9qvW4 rattus sp.
30	115	8.6	1687	11	O61204	O61204 mus musculus
31	114.5	8.5	2906	11	O9WUH9	O9wuh9 rattus norv
32	113.5	8.5	283	6	O9XSZ8	O9xsZ8 cercopithec
33	112	8.4	152	5	O9XVX3	O9xvX3 caenorhabdi
34	111.5	8.3	1764	11	O35806	O35806 rattus norv
35	111	8.3	147	11	O9ER63	O9er63 mus musculus
36	111	8.3	1111	5	O9XWD6	O9xwD6 caenorhabdi
37	111	8.3	1792	13	O57484	O57484 gallus galli
38	110.5	8.2	870	6	O02660	O02660 bos taurus
39	110	8.2	1522	5	O22685	O22685 caenorhabdi
40	110	8.2	1537	5	O9VA12	O9vaI2 drosophila
41	110	8.2	1698	5	O94438	O94438 chironomus
42	109.5	8.2	164	5	O22048	O22048 caenorhabdi
43	109.5	8.2	4601	5	O9V383	O9v383 drosophila
44	108.5	8.1	2319	11	O9R172	O9r172 rattus norv
45	108	8.1	176	14	O68396	O68396 human cytom

## ALIGNMENTS

### RESULT 1

O95851 ID O95851 PRELIMINARY; PRT; 234 AA.  
AC O95851;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99156876; PubMed=10037686;  
RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,  
RA Liu D., Wang S.X., Kwon B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor  
RT necrosis factor receptor superfamily and its ligand.";  
RL J. Biol. Chem. 274:6036-6061(1999).  
DR EMBL; AF117297; AAD19694.1; -;  
DR InterPro; IPR001368; -;  
DR SMART; SM00208; TNFR; 1.  
KW Receptor.  
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 1340; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 8.9e-128;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAQHGAMGAFRALCGLALLCALSIGQRTGPGCGPGRLLLTGTGTARCCRVHTTRCCRD 60

Db 1 MAQHGAMGAFRALCGLALLCALSIGQRTGPGCGPGRLLLTGTGTARCCRVHTTRCCRD 60

OY 61 YPGEECCSEWDCMCVQPEFFHCGDPCCTTCRHHPCPGPGVQSGKFSFGFCIDCASGTF 120

Db 61 YPGEECCSEWDCMCVQPEFFHCGDPCCTTCRHHPCPGPGVQSGKFSFGFCIDCASGTF 120

OY 121 SGGHEGHCKPWTDCQTQFGFTLVFFGNKTHNAVCPGSPAPPLGWLTVVLLAVACVLL 180

Db 121 SGGHEGHCKPWTDCQTQFGFTLVFFGNKTHNAVCPGSPAPPLGWLTVVLLAVACVLL 180

QY 181 TSAQLGLHIWLRKLTQTLLEVPVPPSTEDARSCQFPPEERGERSAEKGRLGDLWV 234  
 |||||  
 Db 181 TSAQLGLHIWLRKLTQTLLEVPVPPSTEDARSCQFPPEERGERSAEKGRLGDLWV 234

## RESULT 2

Q9Y5U5  
 ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.  
 AC Q9Y5U5  
 DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.  
 GN TNFRSF18.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BONE MARROW;  
 RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,  
 RA Baldwin D.T., Gray A.M., Dowd K.P., Brush J., Heldens S., Schow P.,  
 RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;  
 RT "Identification of a new member of the tumor necrosis factor family  
 and its receptor, a human ortholog of mouse GTR.";  
 RL Curr. Biol. 0:0-0(1999).  
 DR EMBL; AF125304; AAD22635.1; -.  
 DR InterPro; IPR001368; -.  
 DR SMART; SM00208; TNFR; 1.  
 SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E92CBE CRC64;

Query Match 98.7%; Score 1322.5; DB 4; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 5.4e-126;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGAAGAFRALCGLALLCALSLGQRTGPGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
 |||||  
 Db 1 MAQHGAAGAFRALCGLALLCALSLGQRTGPGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
 |||||  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
 |||||  
 Db 61 YPGECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
 |||||  
 QY 121 SGGHEGCHKPWTDCQTFGFLTVFPGNKTHNAVCPGSPAPPLGLWLTVLLAVACVLL 180  
 |||||  
 Db 121 SGGHEGCHKPWTDCQTFGFLTVFPGNKTHNAVCPGSPAPPLGLWLTVLLAVACVLL 180  
 |||||  
 QY 181 TSAQLGLHIWLRKLTQTLLEVPVPPSTEDARSCQFPPEERGERSAEKGRLGDLW 233  
 |||||  
 Db 181 TSAQLGLHIWLRKLTQTLLEVPVPPSTEDARSCQFPPEERGERSAEKGRLGDLW 240  
 |||||  
 QY 234 V 234  
 |||||  
 Db 241 V 241

## RESULT 3

Q9NYJ9  
 ID Q9NYJ9 PRELIMINARY; PRT; 255 AA.  
 AC Q9NYJ9  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
 DE GTR-D.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

## RC TISSUE=THYMUS;

RA Nocentini G., Bartoli A., Ronchetti S., Mastroiaca E., Riccardi C.;  
 RT "Identification of a soluble human GTR splicing (hgtr-D).";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF241229; AAF63506.1; -.  
 SQ SEQUENCE 255 AA; 26827 MW; C98652AC97AF2CC CRC64;

Query Match 60.8%; Score 815; DB 4; Length 255;

Best Local Similarity 75.1%; Pred. No. 1.2e-74;  
 Matches 142; Conservative 2; Mismatches 9; Indels 36; Gaps 2;

QY 1 MAQHGAAGAFRALCGLALLCALSLGQRTGPGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
 |||||  
 Db 1 MAQHGAAGAFRALCGLALLCALSLGQRTGPGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
 |||||  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
 |||||  
 Db 61 YPGECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
 |||||  
 QY 121 SGGHEGCHKPWTDCQTFGFLTVFPGNKTHNAV 153  
 |||||  
 Db 121 SGGHEGCHKPWTDCQTFGFLTVFPGNKTHNAV 171  
 |||||  
 QY 154 YPSPAPAP 162  
 |||||  
 Db 172 EPGRP 180

## RESULT 4

Q35714  
 ID Q35714 PRELIMINARY; PRT; 228 AA.  
 AC Q35714;  
 DT 01-JAN-1998 (Tremblrel. 05, Created)  
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.  
 GN TNFRSF18 OR GTR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/HEJ;  
 RX MEDLINE=97322352; PubMed=9177197;  
 RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,  
 RA Moraca R., Migliorati G., Riccardi C.;  
 RT "A new member of the tumor necrosis factor/nerve growth factor  
 receptor family inhibits T cell receptor-induced apoptosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/C;  
 RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,  
 RA Migliorati G., Riccardi C.;  
 RT "Gene structure and chromosomal assignment of GTR, a mouse member of  
 the tumor necrosis factor/nerve growth factor receptor family.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U82534; AAB81243.1; -.  
 DR EMBL; AF109216; AAF14231.1; -.  
 DR MGI; 894675; Tnfrsf18.  
 DR InterPro; IPR000561; -.  
 DR SMART; SM00181; EGF; 1.  
 KW Signal; Receptor.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY  
 FT RELATED PROTEIN.  
 SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 52.5%; Score 703; DB 11; Length 228;  
 Best Local Similarity 54.9%; Pred. No. 2.2e-63;

```

DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR."
RL Curr. Biol. 0:0-0(1999).
DR EMBL: AF125304; AAD22635.1; -.
DR InterPro: IPR001368; -.
DR SMART: SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7B92CBE CRC64;

Query Match 100.0%; Score 246; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 3e-27;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAVCV 41
Db 114 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAVCV 154

RESULT 3
ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR."
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229433; AAF61567.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 78.0%; Score 192; DB 11; Length 222;
Best Local Similarity 75.0%; Pred. No. 1.3e-19;
Matches 30; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 CASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAVCV 41
Db 103 CAMGTFSAGRGHCRWNTCSQFGFLTVPFGKTHNAVCI 142

RESULT 4
ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)

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DE GLUCOCORTICOID-INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RX MEDLINE=97322352; PubMed=9177197;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Riccardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis."
RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA Migliorati G., Riccardi C.;
RT "Gene structure and chromosomal assignment of GTR, a mouse member of
RT the tumor necrosis factor/nerve growth factor receptor family."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U82534; AAB81243.1; -.
DR EMBL: AF109216; AAF14231.1; -.
DR MGI: 894675; Tnfrsf18.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
KW Signal; Receptor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY
FT RELATED PROTEIN.
SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 78.0%; Score 192; DB 11; Length 228;
Best Local Similarity 75.0%; Pred. No. 1.4e-19;
Matches 30; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 CASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAVCV 41
Db 103 CAMGTFSAGRGHCRWNTCSQFGFLTVPFGKTHNAVCI 142

RESULT 5
ID Q9JKR3 PRELIMINARY; PRT; 294 AA.
AC Q9JKR3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR."
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229432; AAF61566.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 78.0%; Score 192; DB 11; Length 294;
Best Local Similarity 75.0%; Pred. No. 1.8e-19;
Matches 30; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

```

GenCore version 4.5

Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:33 ; Search time 133.1 Seconds  
(without alignments)  
40.755 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_114\_154

Perfect score: 246

Sequence: 1 DCASGTFSGHEGCKPWT.....TQFGFLTVFPNGKTHNAVCV 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_unclassified:\*

13: sp\_vertebrate:\*

14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	246	100.0	234	4	Q95851 homo sapien
2	246	100.0	241	4	Q9Y5U5 homo sapien
3	192	78.0	222	11	Q9JKR2 mus musculu
4	192	78.0	228	11	Q35714 mus musculu
5	192	78.0	294	11	Q9JKR3 mus musculu
6	135	54.9	255	4	Q9NYJ9 homo sapien
7	96	39.0	267	6	O02764 oryctolagus
8	83	33.7	401	11	O08727 rattus norv
9	83	33.7	401	11	O08712 mus musculu
10	79	32.1	132	11	Q9JKR1 mus musculu
11	78	31.7	300	4	O95407 homo sapien
12	77	31.3	267	14	O90257 fish lympho
13	77	31.3	372	4	Q9UHP4 homo sapien
14	77	31.3	401	4	O00300 homo sapien
15	75	30.5	625	11	O35305 mus musculu
16	74	30.1	616	4	O9Y6Q6 homo sapien
17	74	30.1	655	4	O75509 homo sapien
18	70	28.5	276	13	Q9DD02 gallus gall
19	65	26.4	655	11	Q9EPU5 mus musculu

20	63	25.6	650	4	Q9NQ78	Q9nq78 homo sapien
21	63	25.6	653	4	Q9NQ79	Q9nq79 homo sapien
22	63	25.6	661	4	Q9NQ80	Q9nq80 homo sapien
23	62	25.2	193	11	Q9QX63	Q9qx63 rattus norv
24	61	24.8	175	11	Q9WUL4	Q9wul4 rattus norv
25	61	24.8	351	14	O57117	O57117 cowpox viru
26	61	24.8	439	4	Q16042	Q16042 homo sapien
27	61	24.8	459	11	O62327	O62327 mus musculu
28	61	24.8	482	11	O88734	O88734 mus musculu
29	59	24.0	897	14	O96631	O96631 black beetl
30	59	24.0	998	14	O66929	O66929 flock house
31	57.5	23.4	135	13	Q9IAM1	Q9iam1 agkistrodon
32	56.5	23.0	131	13	Q9PSM9	Q9psm9 echis carin
33	56.5	23.0	146	13	Q9DG31	Q9dg31 agkistrodon
34	55.5	22.6	146	13	Q9I840	Q9i840 agkistrodon
35	55	22.4	1283	4	O95451	O95451 homo sapien
36	55	22.4	1594	4	O9HC84	O9hc84 homo sapien
37	54.5	22.2	350	2	Q9Z377	Q9z377 pseudomonas
38	54	22.0	175	14	Q9PZS0	Q9pzs0 human cytom
39	54	22.0	176	14	Q68396	Q68396 human cytom
40	54	22.0	176	14	Q9PZR9	Q9pzs9 human cytom
41	54	22.0	176	14	Q9PZR8	Q9pzs8 human cytom
42	54	22.0	176	14	Q9PZQ7	Q9pzs7 human cytom
43	54	22.0	176	14	Q9PX59	Q9px59 human cytom
44	54	22.0	176	14	Q9PX08	Q9px08 human cytom
45	54	22.0	176	14	Q9PWX6	Q9pwx6 human cytom

## ALIGNMENTS

RESULT 1

Q95851 ID O95851 PRELIMINARY; PRT; 234 AA.  
AC O95851;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99156876; PubMed=10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor

RT necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AADI9694.1; -

DR InterPro; IPR001368; -

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE. 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match

Best Local Similarity 100.0%; Score 246; DB 4; Length 234;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGHEGCKPWTCTQFGFLTVFPNGKTHNAVCV 41

|||||

Db 114 DCASGTFSGHEGCKPWTCTQFGFLTVFPNGKTHNAVCV 154

RESULT 2

Q9Y5U5 ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.

AC Q9Y5U5;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

Best Local Similarity 39.08; Pred. No. 0.00079;  
Matches 16; Conservative 6; Mismatches 17; Indels 2; Gaps 1;

QY 2 CASGTFSG--GHEGCKPWTCTQFGFLTVFPNGKTHNAV 40  
DB 145 CPDFFSGEISSKAPCRKHTNCSSGLLLLIQGNATHDNVC 185

RESULT 9  
O08712 PRELIMINARY; PRT; 401 AA.

AC O08712; 070202;  
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
DE (OCIF)  
GN TNFRSF11B OR OPG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN-BALB/C; TISSUE-KIDNEY;  
RX MEDLINE=97262071; PubMed=9108485;  
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
Ra Luehly R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimanoto G.,  
Ra Daroe M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,  
Ra Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
Ra Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
Ra Suggs S., Boyle W.J.;  
RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
of bone density."  
RL Cell 89:309-319(1997).  
RN [2]  
SEQUENCE FROM N.A.  
RC STRAIN=129/OLA, AND NIH SWISS;  
RX MEDLINE=98382527; PubMed=9714833;  
RA Higashio K.;  
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,  
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)  
gene and its expression in embryogenesis."  
RL Gene 215:339-343(1998).  
CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).  
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND  
PLACENTA. NOT DETECTED IN SPLEEN.  
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
15 TO DAY 17.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; U94331; AAB53708.1; -;  
DR EMBL; AB013898; BAA28469.1; -;  
DR EMBL; AB013903; BAA33388.1; -;  
DR EMBL; AB013899; BAA33388.1; JOINED.  
DR EMBL; AB013900; BAA33388.1; JOINED.  
DR EMBL; AB013901; BAA33388.1; JOINED.  
DR EMBL; AB013902; BAA33388.1; JOINED.  
DR HSP; P25942; ICDF.  
DR MGD; MG1:109587; Tnfslf1b.  
DR InterPro; IPR000488; -;  
DR InterPro; IPR001368; -;  
DR Pfam; PF00020; TNFR\_C6; 3.  
DR ProDom; PD000771; -; 1.  
DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
KW SMART; SMO0005; DEATH; 1.  
KW Glycoprotein; Repeat; Cytokine; Signal.  
FT SIGNAL 1 21 OSTEOPROTEGERIN.  
FT CHAIN 22 401 4 X TNFR-CYS.  
FT DOMAIN 23 201 TNFR-CYS 1.  
FT REPEAT 23 63 TNFR-CYS 2.  
FT REPEAT 64 106 TNFR-CYS 3.  
FT REPEAT 107 143 TNFR-CYS 4.  
FT REPEAT 144 201 DEATH DOMAIN.  
FT DOMAIN 306 365 BY SIMILARITY.  
FT DISULFID 41 54 BY SIMILARITY.  
FT DISULFID 44 62 BY SIMILARITY.  
FT DISULFID 65 80 BY SIMILARITY.  
FT DISULFID 83 97 BY SIMILARITY.  
FT DISULFID 87 105 BY SIMILARITY.  
FT DISULFID 118 142 BY SIMILARITY.  
FT DISULFID 145 160 BY SIMILARITY.  
FT CARBOHYD 98 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 178 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 289 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARIANT 138 R -> P (IN STRAINS 129/OLA AND NIH  
SWISS).  
FT VARIANT 161 I -> R (IN STRAINS 129/OLA AND NIH  
SWISS).  
FT VARIANT 165 N -> D (IN STRAINS 129/OLA AND NIH  
SWISS).  
FT VARIANT 288 S -> A (IN STRAINS 129/OLA AND NIH  
SWISS).  
FT VARIANT 296 L -> R (IN STRAINS 129/OLA AND NIH  
SWISS).  
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 33.7%; Score 83; DB 11; Length 401;  
Best Local Similarity 41.5%; Pred. No. 0.00079;  
Matches 17; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

QY 2 CASGTFSG--GHEGCKPWTCTQFGFLTVFPNGKTHNAV 40  
DB 145 CPDFFSGEISSKAPCRKHTNCSSGLLLLIQGNATHDNVC 185

RESULT 10  
Q0JKR1 PRELIMINARY; PRT; 132 AA.

AC Q0JKR1;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE GTR-D.  
GN TNFRSF18.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RC TISSUE=THYMUS;  
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
RA Migliorati G., Riccardi C.;  
RT "Identification of three novel mRNA splice variants of GTR."  
RL Cell Death Differ. 0:0-0(2000).  
DR EMBL; AF229434; AAF61568.1; -;  
DR InterPro; IPR000561; -;  
DR SMART; SMO0181; EGF; 1.  
SQ SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;

Query Match 32.1%; Score 79; DB 11; Length 132;  
Best Local Similarity 66.7%; Pred. No. 0.00094;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;





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Query Match      31.3%; Score 77; DB 4; Length 372;
Best Local Similarity 36.6%; Pred. No. 0.0052;
Matches 15; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

OY 2 CASGTFSG--GHEGHCKPWTDCTQFGFLTVFPFGKNTNNAVC 40
Db 124 CPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNIC 164

RESULT 14
OQ0300
ID OQ0300 PRELIMINARY; PRT; 401 AA.
AC OQ0300; O60236;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF1B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luthy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Dorsey M., Elliott R., Colombero A., Tan H.-L., Trall G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RT Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC EMBL; AB021446; BAA25910.1; -
CC EMBL; AB008822; BAA32076.1; -
CC EMBL; AB008821; BAA32076.1; JOINED.
CC EMBL; U94332; AAB53709.1; -

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DR HSP; P25942; ICDF.
DR MIM; 602643; -.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; -; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM0005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT DOMAIN 23 183
FT REPEAT 23 63
FT REPEAT 23 106
FT REPEAT 107 143
FT REPEAT 144 201
FT DOMAIN 306 365
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 118 142
FT DISULFID 145 160
FT CARBOHYD 98
FT CARBOHYD 152 152
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT CONFLICT 263 263
SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;

Query Match      31.3%; Score 77; DB 4; Length 401;
Best Local Similarity 36.6%; Pred. No. 0.0056;
Matches 15; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

OY 2 CASGTFSG--GHEGHCKPWTDCTQFGFLTVFPFGKNTNNAVC 40
Db 145 CPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNIC 185

RESULT 15
ID O35305 PRELIMINARY; PRT; 625 AA.
AC O35305;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
DE INDUCED CYTOKINE RECEPTOR) (RANK).
GN TNFRSF1A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER EPITHELIUM;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tonetsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC EMBL; AF019046; AAB86810.1; -
CC HSP; P25942; ICDF.
CC MGD; MGI:1314891; Tnfrsf1a.

```

Query Match 31.7%; Score 78; DB 4; Length 300;  
Best Local Similarity 34.1%; Pred. No. 0.003;  
Matches 14; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

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Query Match      30.58; Score 75; DB 11; Length 625;
Best Local Similarity 39.08; Pred. No. 0.017;
Matches 16; Conservative 2; Mismatches 21; Indels 2; Gaps 1;

QY  2  CASCTFSG--GHEGHCKPWTCTQTQFGFLTVPFGKNTHNVC  40
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB  155  CLLGFFSDVFSSTOKCKPWTNCTLLGKLEAHQGTITESDVC  195

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Search completed: September 4, 2001, 16:14:33  
Job time: 1220 sec

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DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Gray S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RL Curr. Biol. 0:0-0(1999).
DR EMBL; AF125304; AAD22635.1; -.
DR InterPro; IPR001368; -.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 252; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.6e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVOPEFHCGDPCCTTCRRHHPCPPGGVQSGKFSFGFCI 40
Db 74 CVOPEFHCGDPCCTTCRRHHPCPPGGVQSGKFSFGFCI 113

RESULT 3
ID Q9NYJ9 PRELIMINARY; PRT; 255 AA.
AC Q9NYJ9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE GTR-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Mastrodicasa E., Riccardi C.;
RT "Identification of a soluble human GTR splicing (hGTR-D).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241229; AAF63506.1; -.
SQ SEQUENCE 255 AA; 26027 MW; C986652AC97AF2CC CRC64;

Query Match 100.0%; Score 252; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.9e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVOPEFHCGDPCCTTCRRHHPCPPGGVQSGKFSFGFCI 40
Db 74 CVOPEFHCGDPCCTTCRRHHPCPPGGVQSGKFSFGFCI 113

RESULT 4
ID Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-D.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61568.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;

Query Match 66.7%; Score 168; DB 11; Length 132;
Best Local Similarity 62.5%; Pred. No. 4.2e-15;
Matches 25; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CVOPEFHCGDPCCTTCRRHHPCPPGGVQSGKFSFGFCI 40
Db 62 CVTPEVHCDDPCKICKHYPCQPGQVRVESQGDIVFGRCV 101

RESULT 5
ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 66.7%; Score 168; DB 11; Length 222;
Best Local Similarity 62.5%; Pred. No. 6.5e-15;
Matches 25; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CVOPEFHCGDPCCTTCRRHHPCPPGGVQSGKFSFGFCI 40
Db 62 CVTPEVHCDDPCKICKHYPCQPGQVRVESQGDIVFGRCV 101

RESULT 6
ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:32 ; Search time 133.1 Seconds  
(without alignments)  
39.761 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_74\_113

Perfect score: 252

Sequence: 1 CVQPEFHCGDPCCTCRHHPCPGQGVQSGKFSFGFCI 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_unclassified.\*

13: sp\_vertebrate.\*

14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	252	100.0	234	4	O95851 homo sapien
2	252	100.0	241	4	O9Y5U5 homo sapien
3	252	100.0	255	4	O9NVJ9 homo sapien
4	168	66.7	132	11	O9JKR1 mus musculus
5	168	66.7	222	11	O9JKR2 mus musculus
6	168	66.7	228	11	O35714 mus musculus
7	168	66.7	294	11	O9JKR3 mus musculus
8	72	28.6	1574	11	O88281 rattus norv
9	66.5	26.4	107	11	O9JKE0 rattus norv
10	64	25.4	473	11	O9SESO rattus norv
11	64	25.4	643	11	O9ERV6 mus musculus
12	64	25.4	655	11	O9WVF5 mus musculus
13	64	25.4	1210	11	O9EP98 mus musculus
14	63	25.0	62	5	O77419 ascaris suu
15	63	25.0	283	4	O92956 homo sapien
16	63	25.0	404	4	O9UM65 homo sapien
17	62.5	24.8	1077	3	O74853 schizosacch
18	62.5	24.8	1283	4	O95451 homo sapien
19	62.5	24.8	1594	4	O9HC84 homo sapien

20	61.5	24.4	4123	4	O75851
21	61	24.2	2319	11	O9RL72
22	60.5	24.0	216	13	O9PSN7
23	60.5	24.0	850	4	O14425
24	60.5	24.0	1300	11	O9WTL4
25	60.5	24.0	1373	4	O75372
26	60.5	24.0	4547	5	O9W343
27	60	23.8	405	4	O92795
28	60	23.8	628	4	O9H2C9
29	60	23.8	657	4	O14226
30	60	23.8	705	4	O9GZX1
31	60	23.8	1209	11	O9QX70
32	59.5	23.6	62	6	O9TUI5
33	59.5	23.6	152	4	O43831
34	59.5	23.6	809	5	O9U3W7
35	59.5	23.6	4601	5	O9V383
36	59	23.4	266	10	O43391
37	59	23.4	267	6	O02764
38	59	23.4	527	13	O90836
39	59	23.4	599	13	O9PSH2
40	59	23.4	745	4	O9P2N8
41	59	23.4	814	11	O9QVL2
42	58.5	23.2	1321	4	O95291
43	58.5	23.2	1851	11	O9ESP3
44	58	23.0	1114	11	O9JKW7
45	57.5	22.8	410	11	O63720

#### ALIGNMENTS

RESULT 1

ID O95851 PRELIMINARY; PRT; 234 AA.

AC O95851;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ON NCBI\_TaxID=9606;

RX MEDLINE=99156876; PubMed=10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor

RT necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AAD19694.1; -

DR InterPro; IPR001368; -

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 252; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 4.5e-26;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTCRHHPCPGQGVQSGKFSFGFCI 40

|||||

Db 74 CVQPEFHCGDPCCTCRHHPCPGQGVQSGKFSFGFCI 113

|||||

RESULT 2

O9Y5U5 PRELIMINARY; PRT; 241 AA.

ID O9Y5U5;

AC O9Y5U5;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)









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DR Pfam: PF01826; TIL; 1.
FT NON_TER 1 1
FT NON_TER 62 62
SQ SEQUENCE 62 AA; 6794 MW; 154CE25A375E0B2C CRC64;

Query Match 25.0%; Score 63; DB 5; Length 62;
Best Local Similarity 36.2%; Pred. No. 0.21;
Matches 17; Conservative 4; Mismatches 18; Indels 8; Gaps

QY 1 CVQPEFHCGD----PCCTTCRHH--PCPPGGQVQ--SOGKFSFGQC 39
   | | | | | | | | | | | | | | | | | | | | | |
Db 14 CTGCEMKGDPENTPCLMCRPRSCSPGRGMRRTNDGKICIPASQC 60
   | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
Q92956 PRELIMINARY; PRT; 283 AA.
ID Q92956
AC Q92956;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HERPESVIRUS ENTRY MEDIATOR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
CX [1]
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97053782; PubMed=8998196;
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
RL the TNF/NGF receptor family.";
RL Cell 87:427-436(1996).
DR EMBL; U70321; AAB58354.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; -; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 283 AA; 30420 MW; DFCE146E4E024F4B CRC64;

Query Match 25.0%; Score 63; DB 4; Length 283;
Best Local Similarity 25.5%; Pred. No. 0.75;
Matches 14; Conservative 3; Mismatches 22; Indels 16; Gaps

QY 1 CVQPEFHCGDPCCTTCRHH-----HPCPPGGQVQSOGKFSFGQC 39
   | : | : | | | | | | | | | | | | | | | | | |
Db 42 CKEDYFVGSECCPKCSGVRKACGELTGVCPCPGTYIAHLNGLSKLQC 96
   | : | : | | | | | | | | | | | | | | | | | |

Search completed: September 4, 2001, 16:14:33
Job time: 1220 sec

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DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.L., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR.";
RL Curr. Biol. 0:0-0(1999).
DR EMBL: AF125304; AAD22635.1; -.
DR InterPro: IPR001368; -.
DR SMART: SM00208; TNFR; 1.
DR SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 255; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-26;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCM 41
DB 33 GCGPGRLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCM 73

RESULT 3
ID Q9NYJ9 PRELIMINARY; PRT; 255 AA.
AC Q9NYJ9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GTR-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Riccardi C.;
RT "Identification of a soluble human GTR splicing (hGTR-D).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF241229; AAF63506.1; -.
DR SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 100.0%; Score 255; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCM 41
DB 33 GCGPGRLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCM 73

RESULT 4
ID Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GTR-D.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229434; AAF61568.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
DR SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;

Query Match 34.3%; Score 87.5; DB 11; Length 132;
Best Local Similarity 36.6%; Pred. No. 0.00023;
Matches 15; Conservative 9; Mismatches 10; Indels 7; Gaps 1;

QY 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCM 41
DB 28 GCGPGRLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCM 61

RESULT 5
ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229433; AAF61567.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
DR SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 34.3%; Score 87.5; DB 11; Length 222;
Best Local Similarity 36.6%; Pred. No. 0.00036;
Matches 15; Conservative 9; Mismatches 10; Indels 7; Gaps 1;

QY 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCM 41
DB 28 GCGPGRLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCM 61

RESULT 6
ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:32 ; Search time 133.1 Seconds  
(without alignments)  
40.755 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_73

Perfect score: 255

Sequence: 1 CGGGRLLLTGTTCRCRV.....TTRCCRDYVGECCSEWDCM 41

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_unclassified:\*

13: sp\_vertebrate:\*

14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	255	100.0	234	4	O95851
2	255	100.0	241	4	O9Y5U5
3	255	100.0	255	4	O9NYJ9
4	87.5	34.3	132	11	O9JKR1
5	87.5	34.3	222	11	O9JKR2
6	87.5	34.3	228	11	O9JTL2
7	87.5	34.3	294	11	O9JKR3
8	66	25.9	416	10	O04507
9	65.5	25.7	423	4	O9NZV2
10	65.5	25.7	423	4	O9NS68
11	64.5	25.3	788	5	O22631
12	63.5	24.9	164	5	O22048
13	63	24.7	152	5	O9XVX3
14	62	24.3	1056	4	O9H3R0
15	62	24.3	1100	4	O94877
16	61.5	24.1	68	13	O9PTM3
17	61.5	24.1	150	11	O9JTL2
18	61.5	24.1	188	11	O70148
19	61.5	24.1	214	11	O9JHf1

20	61.5	24.1	348	11	O9QXW7
21	61.5	24.1	416	11	O9JLL3
22	61.5	24.1	416	11	O9JH6
23	61.5	24.1	434	11	O922R8
24	61.5	24.1	559	11	O9QX30
25	61.5	24.1	1116	13	O73791
26	61	23.9	188	5	O18238
27	60.5	23.7	177	4	O07627
28	59.5	23.3	122	11	O70149
29	59.5	23.3	200	10	O9XFF4
30	59.5	23.3	200	10	O9XFF3
31	59.5	23.3	200	10	O9XFF2
32	59.5	23.3	200	10	O9SBW5
33	59	23.1	152	6	O29620
34	58.5	22.9	175	4	O07628
35	58.5	22.9	4135	6	O18977
36	58	22.7	103	10	O9SBW9
37	58	22.7	182	6	O29619
38	58	22.7	331	14	O69581
39	58	22.7	506	5	O9VVP5
40	57.5	22.5	126	10	O9S9F4
41	57.5	22.5	138	5	O96100
42	57.5	22.5	138	5	O9U8P9
43	57.5	22.5	243	5	O9NL90
44	57.5	22.5	2174	5	O9GQR0
45	57.5	22.5	2910	11	O55225

## ALIGNMENTS

RESULT 1

ID O95851 PRELIMINARY; PRT; 234 AA.

AC O95851;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99156876; PubMed=10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor

RT necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AAD19694.1; -

DR InterPro; IPR001368; -

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE. 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 255; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.7e-26;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGRLLLTGTTCRCRVHTTCCRDYVGECCSEWDCM 41

|||||

DB 33 CGGGRLLLTGTTCRCRVHTTCCRDYVGECCSEWDCM 73

RESULT 2

ID O9Y5U5 PRELIMINARY; PRT; 241 AA.

AC O9Y5U5;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

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DR Pfam: PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 423 AA; 46071 MW; BB7C9917132A4B2F CRC64;

Query Match
Best Local Similarity 39.1%; Score 65.5; DB 4; Length 423;
Matches 18; Conservative 5; Mismatches 14; Indels 9; Gaps 3;

QY 2 CGPGRLL-----LGTGTDARC--CRVHTTRCCRDYPGEECCSEWDC 40
||||| | | | | | | | | | | | | | | | | | | |
DB 52 CGPWLKSKCGFGYGDAQCACRLH--RFKDWGFKQKPCLDLC 95

RESULT 10
Q9NS68 PRELIMINARY; PRT; 423 AA.
ID Q9NS68
AC Q9NS68;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HTROY.
DE HTROY.
GN HTROY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347167; PubMed=10764796;
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RT Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
DR EMBL; AB040434; BAB03269.1; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 423 AA; 46015 MW; B5891CEA9ED45361 CRC64;

Query Match
Best Local Similarity 39.1%; Score 65.5; DB 4; Length 423;
Matches 18; Conservative 5; Mismatches 14; Indels 9; Gaps 3;

QY 2 CGPGRLL-----LGTGTDARC--CRVHTTRCCRDYPGEECCSEWDC 40
||||| | | | | | | | | | | | | | | | | | | |
DB 52 CGPWLKSKCGFGYGDAQCACRLH--RFKDWGFKQKPCLDLC 95

RESULT 11
Q22631 PRELIMINARY; PRT; 788 AA.
ID Q22631
AC Q22631;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE T21B6.3 PROTEIN.
DE T21B6.3.
GN T21B6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Cottage A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=941150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RL EMBL: Z68011; CAA92014.1; -.
DR InterPro: IPR000884; -.
DR InterPro: IPR002965; -.
DR InterPro: IPR003609; -.
DR Pfam: PF00090; tsp_1; 6.
DR PRINTS: PR01217; PRICHEXTENS.
DR SMART: SMO0473; PAN_AP; 1.
SQ SEQUENCE 788 AA; 88727 MW; BB0DD9F1D29BD961 CRC64;

Query Match 25.3%; Score 64.5; DB 5; Length 788;
Best Local Similarity 39.6%; Pred. No. 1.3;
Matches 19; Conservative 4; Mismatches 10; Indels 15; Gaps 3;

QY 2 CGPG-----RLLLG-TGTDARCCR---VHTTRCCRDYGECC--SEW 38
||||| | | | | | | | | | | | | | | | | | | |
Db 667 CGPGQRTTRCGLGPNQGEATCGPSIETTLCTLC-----EGSCCNWSEW 710

RESULT 12
Q22048 PRELIMINARY; PRT; 164 AA.
ID Q22048 AC Q22048;
AC Q22048;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DE T01B7.8 PROTEIN.
GN T01B7.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sims M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=941150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RL EMBL: Z66499; CAA91301.1; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR001007; -.
DR InterPro: IPR001271; -.
DR InterPro: IPR001450; -.
DR PROSITE: PS00198; 4FEAS_FERREDOXIN; UNKNOWN_1.
DR PROSITE: PS00269; DEFENSIN; UNKNOWN_1.

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004507
ID      004507      PRELIMINARY;      PRT;      416 AA.
AC      004507;
DT      01-JUL-1997 (TrEMBLrel. 04, Created)
DT      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT      01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE      SIMILARITY TO DIANTHUS CYSTEINE PROTEINASE.
GN      F21M12.24.
OS      Arabidopsis thaliana (Mouse-ear cross).
OC      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC      Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC      Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. COLUMBIA;
RA      Vysotskaia V.S., Osborne B.I., Toriumi M., Yu G., Oji O., Shen Y.K.
RA      Araujo R., Au M., Buehler E., Conway A.B., Conway A.R., Dewar K.,
RA      Feng J., Kim C., Kurtz D., Li Y., Shinn P.,
RA      Ecker J.R., Federspiel N.A., Theologis A.;
RL      Submitted (JUN-1997) to the EMBL/GenBank/DBDJ databases.
DR      EMBL; AC000132; AB060738.1; -.
DR      HSP; P07711; ICJL.
DR      Mendel; 15355; Arath; I1134; I5355.
DR      InterPro; IPR000118; -.
DR      InterPro; IPR000169; -.
DR      InterPro; IPR000668; -.
DR      InterPro; IPR000834; -.
DR      InterPro; IPR002086; -.
DR      Pfam; PF00112; Peptidase_C1; 1.
DR      Pfam; PF00396; granulin; 1.
DR      PRINTS; PR00705; PAPAIN.
DR      PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR      PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
DR      PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR      PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR      PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
DR      SMART; SM00277; GRAN; 1.
KW      Hydrolase; Thiol protease.
SQ      SEQUENCE      416 AA;      45684 MW;      15BC47F5430F922 CRC64;

Query Match      25.9%;      Score 66;      DB 10;      Length 416;
Best Local Similarity      35.3%;      Pred. No. 0.47;
Matches 12;      Conservative      4;      Mismatches      16;      Indels      2;      Gaps

QY      2 CGGRRLLLTGGTDARCRVHTTRCCRDYPGECC 35
      | | | | | : | | | : | | | | | | |
DB      367 CCCARELFLGFCFSWKCCIESAVCKCKD--GRHC 398

RESULT      9
Q9NZV2      PRELIMINARY;      PRT;      423 AA.
AC      Q9NZV2;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE      TAJ-ALPHA.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=20270246; PubMed=10809768;
RA      Eby M.T., Jasnin A., Kumar A., Sharma K., Chaudhary P.M.;
RT      "TAJ, a Novel Member of the Tumor Necrosis Receptor Family.
RT      Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT      Independent Cell Death.";
RL      J. Biol. Chem. 275:15336-15342(2000).
DR      EMBL; AF167555; AAF71828.1; -.
DR      InterPro; IPR001368; -.

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Search completed: September 4, 2001, 16:14:32  
Job time: 1219 sec

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RESULT 14  
Q9H3R0  
ID Q9H3R0 PRELIMINARY; PRT; 1056 AA.  
AC Q9H3R0;  
DT 01-MAR-2001 (TRENBLrel. 16, Created)

Db 756 PNAFLEEDGTSLLISCAKCCVRVHAS--CYGIPSHSICDGLWC 796

```

RESULT 2
Q9Y5U5 PRELIMINARY; PRT; 241 AA.
AC Q9Y5U5;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 0:0-0(1999);
DR EMBL; AF125304; AAD2835.1; -.
DR InterPro; IPR001368; -.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7B82CBE CRC64;

Query Match 100.0%; Score 753; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. NO. 1.2e-77;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRHH 60
DB 33 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRHH 92
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTDC 120
DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTDC 152
QY 121 CV 122
DB 153 CV 154

RESULT 3
Q9NYJ9 PRELIMINARY; PRT; 255 AA.
AC Q9NYJ9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE GITR-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Ricciardi C.;
RA "Identification of a soluble human GITR splicing (hgITR-D).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241229; AAF63506.1; -.
SQ SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 85.3%; Score 642; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. NO. 4.5e-65;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRHH 60
DB 33 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRHH 92
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTDC 102
DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTDC 134

RESULT 4
Q9JKR2 PRELIMINARY; PRT; 222 AA.
ID Q9JKR2;
AC Q9JKR2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GITR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Ricciardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 59.2%; Score 445.5; DB 11; Length 222;
Best Local Similarity 57.4%; Pred. NO. 6.9e-43;
Matches 70; Conservative 21; Mismatches 24; Indels 7; Gaps 1;

QY 1 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRHH 60
DB 28 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRHH 80
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTDC 120
DB 81 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTDC 140
QY 121 CV 122
DB 141 CV 142

RESULT 5
Q35714 PRELIMINARY; PRT; 228 AA.
ID Q35714;
AC Q35714;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GITR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RX MEDLINE=97322352; PubMed=9177197;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Ricciardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis.";

```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:31 ; Search time 133.1 Seconds  
(without alignments)  
121.271 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_154

Perfect score: 753

Sequence: 1 GCGPGRLLLTGTDCRCRV.....TQFGFLTVPGNKTHNAVCV 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_unclassified.\*
- 13: sp\_vertebrate.\*
- 14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	234	4	O95851
2	753	100.0	241	4	Q9Y5U5
3	642	85.3	255	4	Q9NYJ9
4	445.5	59.2	222	11	Q9JKR2
5	445.5	59.2	228	11	O35714
6	445.5	59.2	294	11	Q9JKR3
7	332.5	44.2	132	11	Q9JKR1
8	152.5	20.3	267	6	O02764
9	145	19.3	300	4	O95407
10	140	18.6	401	11	O08727
11	139	18.5	276	13	Q9DD22
12	139	18.5	401	11	O08712
13	133	17.7	372	4	Q9UHP4
14	133	17.7	401	4	O00300
15	128.5	17.1	655	4	O75509
16	122.5	16.3	655	11	Q9EPK5
17	122	16.2	107	11	Q9JKE0
18	121	16.1	616	4	Q9Y6Q6
19	121	16.1	625	11	O35305

20	116.5	15.5	302	13	O9PUS0
21	112	14.9	152	5	Q9XVX3
22	111	14.7	439	4	O16042
23	108.5	14.4	2906	11	Q9WUH9
24	107	14.2	164	5	O22048
25	104.5	13.9	459	11	O62327
26	104.5	13.9	482	11	O88734
27	103.5	13.7	126	10	O9S9F4
28	103.5	13.7	1574	11	O88281
29	103.5	13.7	4601	5	O9V383
30	103	13.7	1963	6	O28019
31	102.5	13.6	188	5	O18238
32	102	13.5	1371	11	O9QVW4
33	100.5	13.3	1308	5	O9GPM8
34	100.5	13.3	1833	11	O08999
35	99	13.1	1764	11	O35806
36	99	13.1	2319	11	O9R172
37	98.5	13.1	351	14	O57117
38	98.5	13.1	1537	5	O9VAI2
39	98.5	13.1	1637	6	O9XSV8
40	98	13.0	1522	5	O22685
41	97	12.9	1821	4	O14767
42	96.5	12.8	410	11	O63720
43	96.5	12.8	469	11	O63721
44	96	12.7	283	6	O9XS28
45	95.5	12.7	1792	13	O57484

## ALIGNMENTS

RESULT 1

ID O95851 PRELIMINARY; PRT; 234 AA.

AC O95851;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99156876; PubMed=10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor

RT necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AAD19694.1; -

DR InterPro; IPR001368; -

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 753; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.1e-77;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDCRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGPCCTTCRRH 60

|||||

33 GCGPGRLLLTGTDCRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGPCCTTCRRH 92

QY 61 PCPPGQVQSGKFSFGFCIDCASGTFSGGHEGHCXRPWTCTQFGFLTVPGNKTHNAV 120

|||||

93 PCPPGQVQSGKFSFGFCIDCASGTFSGGHEGHCXRPWTCTQFGFLTVPGNKTHNAV 152

121 CV 122

153 CV 154

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FT SIGNAL <1 18 POTENTIAL.
FT CHAIN 19 267 OX40.
SQ SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64; 6;

Query Match 20.38; Score 152.5; DB 6; Length 267;
Best Local Similarity 32.8%; Pred. No. 1.2e-09;
Matches 43; Conservative 10; Mismatches 57; Indels 21; Gaps

QY 2 CGPGRLLLTGTDARCCRVHTRCCRDYPG--EECCSEWDCM-CVQ-----PEFHCG 50
Db 40 COP-----GYGMVSRCHNRSDTICHPCPEGYNEAVNYQACKPCTQCNRSGSPQOECT 94
QY 51 DPCCCTTCHRHPCPGQGVQSGKSFQFCIDCASGTFSGGHEGCHKPWTCTQFGFLTV 110
Db 95 HTRDTVCR---CRP--GTQPLNGYKHGVDCAPCPQGHFEGEENNRACRPWTNCTLAGKRTL 149
QY 111 FPGNKTHNAV 121
Db 150 QPASSISDAVC 160

RESULT 9
O95407 PRELIMINARY; PRT; 300 AA.
ID O95407 AC O95407;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE DCOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).
GN DCR3 OR TR6 OR TNFRSF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=99087326; PubMed=9872321;
RA Patti R.M., Masters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=BLOOD;
RC MEDLINE=89253915; PubMed=10318773;
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
SEQUENCE FROM N.A.
RP TISSUE=PANCREAS;
RC MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
SEQUENCE FROM N.A.
RA Matthews L.;
RP Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF104419; AAO3056.1; -
DR EMBL; AF134240; AAD29688.1; -
DR EMBL; AF217796; AAF35244.1; -
DR EMBL; AF217793; AAF33685.1; -
DR EMBL; AF217794; AAF33686.1; -
DR EMBL; AL121845; CAC03668.1; -
DR

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Db      81  PCPQGVQVSGDIVFGFRCVACAMGTFSAGRDGHGCLWTNCSQFGLTFMFPGNKTHNAV 140
Qy      121  CV 122
Db      141  CI 142

RESULT 7
Q9JKR1 ID Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1 ID Q9JKR1-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-D.
GN TNFRsf18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR. ";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61568.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;

Query Match 44.2%; Score 332.5; DB 11; Length 132;
Best Local Similarity 52.0%; Pred. No. 2.7e-30;
Matches 52; Conservative 17; Mismatches 24; Indels 7; Gaps

Qy 1 CGCGPELLLGTGDARCCRVHTTRCCRDYDPECECSWDCMCVQPEFHCGDPCCTTCRHH 60
Db 28 CGCGFKVQVSGNTRCCLSYA-----FGKEDCPKRCICVTPEYHCGDPOCKICKHY 80
Qy 61 PCPQGVQVSGKFSFGQCIDCASGTFSGHGHCCKPWT 100
Db 81 PCPQGVQVSGDIVFGFRCVACAMGTFSAGRDGHGCLWT 120

RESULT 8
Q02764 ID Q02764 PRELIMINARY; PRT; 267 AA.
AC Q02764;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHBB;HM;
RA Isono T., Seto A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PSS00050; TNFR_NGFR_2; 2.
DR SMART; SM00208; TNFR; 1.
DR KWT Signal.
RW NON_TER 1 1

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DR SMART: SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT DOMAIN 23 201
FT REPEAT 23 63
FT REPEAT 23 63
FT REPEAT 64 106
FT REPEAT 107 143
FT REPEAT 144 201
FT DOMAIN 306 365
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 118 142
FT DISULFID 145 160
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT VARIANT 138 138
FT VARIANT 161 161
FT VARIANT 161 161
FT VARIANT 165 165
FT VARIANT 288 288
FT VARIANT 296 296
FT VARIANT 296 296
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 18.5%; Score 139; DB 11; Length 401;
Best Local Similarity 26.4%; Pred. No. 5.6e-08;
Matches 39; Conservative 10; Mismatches 65; Indels 34; Gaps 5;

QY 2 CGPGRLLGTTGTDARCCRVHTTRCCRDYPGEECCSEW-----DCMCVQP-----EPHC 49
DB 44 CAPGTYL-----KHQTVRRKTLVCPDHSYTDWHTSDCYVCSVPCKELQSVKQEC 97
QY 50 GDCPCCTTC-----RHHPCCPGQGVQSGKFSFGFCIDCASCTFSG--GHE 93
DB 98 NRTHNRYCEGEGRYLEIEFCLKHKRSCPPGGVQAGTPERTNTVCKKCPDGFSSNETSS 157
QY 94 GHCKPWTDCQFGFLTVPPGKNTNNAVC 121
DB 158 APCIKHTNCSTFGLLLIQKGNATHDNC 185

RESULT 13
QYUHP4 PRELIMINARY; PRT; 372 AA.
AC QYUHP4
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA He 2.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL: AF134187; AAF20168.1;
DR HSSP: P25942; 1CDF.
DR InterPro: IPR000486;
DR InterPro: IPR001368;

QY 21 HTTRCCRDYPG-----ECCSEWDCMCV-----QPEFHCGRPCC--CT----- 55
DB 16 HOLLCDKCPGTYLKQHKTKWKTCAPCDPHYTDWHTSDCYVCSVPCKELQYVKQE 75
QY 56 -----TC-----RHHPCCPGQGVQSGKFSFGFCIDCASCTFSG--GH 92
DB 76 CNRTNRYCEGEGRYLEIEFCLKHKRSCPPGGVQAGTPERTNTVCKKCPDGFSSNETSS 135
QY 93 EGHCKPWTDCQFGFLTVPPGKNTNNAVC 121
DB 136 KAPCRKHTNCSTFGLLLIQKGNATHDNC 164

RESULT 14
QYUHP4 PRELIMINARY; PRT; 401 AA.
AC QYUHP4
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Farpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RX MEDLINE=98151033; Pubmed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=98351569; Pubmed=9668283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC CC
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
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DR Pfam: PF00020; TNFR_C6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS0050; TNFR_NGFR_2; 2.
DR SMART: SM00005; DEATH; 1.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 17.7%; Score 133; DB 4; Length 372;
Best Local Similarity 24.2%; Pred. No. 2.5e-07;
Matches 36; Conservative 14; Mismatches 51; Indels 48; Gaps 6;

QY 21 HTTRCCRDYPG-----ECCSEWDCMCV-----QPEFHCGRPCC--CT----- 55
DB 16 HOLLCDKCPGTYLKQHKTKWKTCAPCDPHYTDWHTSDCYVCSVPCKELQYVKQE 75
QY 56 -----TC-----RHHPCCPGQGVQSGKFSFGFCIDCASCTFSG--GH 92
DB 76 CNRTNRYCEGEGRYLEIEFCLKHKRSCPPGGVQAGTPERTNTVCKKCPDGFSSNETSS 135
QY 93 EGHCKPWTDCQFGFLTVPPGKNTNNAVC 121
DB 136 KAPCRKHTNCSTFGLLLIQKGNATHDNC 164

RESULT 14
QYUHP4 PRELIMINARY; PRT; 401 AA.
AC QYUHP4
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=97262071; Pubmed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Farpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RX MEDLINE=98151033; Pubmed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=98351569; Pubmed=9668283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC CC
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
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DR SMART; SMO0005; DEATH; 1.  
KW Glycoprotein; Repeat; Cytokine; Signal.  
FT SIGNAL 1 21 BY SIMILARITY.  
FT CHAIN 22 401 OSTEOPROTEGERIN.  
FT DOMAIN 23 201 4 X TNFR-CYS.  
FT REPEAT 23 63 TNFR-CYS 1.  
FT REPEAT 64 106 TNFR-CYS 2.  
FT REPEAT 107 143 TNFR-CYS 3.  
FT REPEAT 144 201 TNFR-CYS 4.  
FT DOMAIN 306 365 DEATH DOMAIN.  
FT DISULFID 41 54 BY SIMILARITY.  
FT DISULFID 44 62 BY SIMILARITY.  
FT DISULFID 65 80 BY SIMILARITY.  
FT DISULFID 83 97 BY SIMILARITY.  
FT DISULFID 87 105 BY SIMILARITY.  
FT DISULFID 118 142 BY SIMILARITY.  
FT DISULFID 145 160 BY SIMILARITY.  
FT CARBOHYD 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 401 AA; 46192 MW; FEC6A31F1D4E573A CRC64;

Query Match 18.6%; Score 140; DB 11; Length 401;  
Best Local Similarity 28.0%; Pred. No. 4.3e-08;  
Matches 42; Conservative 11; Mismatches 59; Indels 38; Gaps 7;

Qy 2 CGPGRLLGTGDARCCRVHTTRC--CRDY-----PGEEC-----CSEWD----- 39  
Db 44 CAPGYTL-----KHCTVRKRLCLVPCPYSYTDSWHTSDECVYCSVPVKELQTVKQECN 98  
Qy 40 -----CMCVQPEHFHGDPCCTTCRHHPGPPGGVQSGQKFSFGFCIDCASGTFSG--G 91  
Db 99 RTHNRVCECEERYLELFC---LKHRSPPGLGLVLAQTPERTVCKRCPDGFSGSETS 155

Qy 92 HGHCKPMTDCTQFGFLTVFPNGKTHNAVY 121  
Db 156 SKAPCRKHTNCSSGLLLQKGNATHDNVC 185

RESULT 11  
ID Q9DDD2 PRELIMINARY; PRT; 276 AA.  
AC Q9DDD2;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE HUMAN CD40-HOMOLOGUE.  
GN TNFSF5.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RL Tregaskes C.A.;  
RL Thesis (2001); University of Reading, Reading, UNITED KINGDOM.  
SR EMBL; AJ293700; CAC20218.1; -.  
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

Query Match 18.5%; Score 139; DB 13; Length 276;  
Best Local Similarity 26.1%; Pred. No. 4.1e-08;  
Matches 46; Conservative 10; Mismatches 58; Indels 62; Gaps 9;

Qy 7 LLIGTGT--DARCCR---VHTTRCC-RDYPGEECCSE-----WD 39  
Db 13 LLIGCGPGDAVNCSDKQYEHKGRCCNRCQPKKLASECNDTSDSVCTPCENGQYQHSWT 72  
Qy 40 -----CMCVQPEHFHGDPCCTTC-RHHPCPPGQG-- 67

Db 73 KERHCTPHEICEDNAGLIVKRHGNATHNTVCQC-RAGMHCSDASCQTCVNEPCQKQGRGF 131  
Qy 68 VQSQKFSFGFCIDCASGTFPS--GGHGHCKPMTDCTQFGFLTVFPNGKTHNAVY 121  
Db 132 VAAMAEARMTSPCEPCAEGTFSNVSSKTEPCHFWTSCEKGLVVKVKGKTNTSDVIC 187

RESULT 12  
ID O08712 PRELIMINARY; PRT; 401 AA.  
AC O08712; 070202;  
DT 01-JUL-1997 (Tremblrel. 04, Created)  
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).  
GN TNFRSF11B OR OPG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=KIDNEY;  
RX MEDLINE=97262071; PubMed=9108485;  
RA Simonet W.S.; Lacey D.L.; Dunstan C.R.; Kelley M.; Chang M.-S.;  
RA Luehthy R.; Nguyen H.Q.; Woodson S.; Bennett L.; Boone T.; Shimamoto G.;  
RA Darose M.; Elliott R.; Colombero A.; Tan H.-L.; Trail G.; Sullivan J.;  
RA Davy E.; Bucay N.; Renshaw-Gegg L.; Hughes T.M.; Hill D.; Pattison W.;  
RA Campbell S.; Sander S.; Van G.; Tarpley J.; Derby P.; Lee R.;  
RA Suggs S.; Boyle W.J.;  
RT "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";  
RL Cell 89:309-319(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/OLA, AND NIH SWISS;  
RX MEDLINE=98382527; PubMed=9714833;  
RA Mizuno A.; Murakami A.; Nakagawa N.; Yasuda H.; Tsuda E.; Morinaga T.;  
RA Higashio K.;  
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";  
RL Gene 215:339-343(1998).  
CC -I- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
CC -I- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).  
CC -I- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -I- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG, BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND PLACENTA. NOT DETECTED IN SPLEEN.  
CC -I- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY 15 TO DAY 17.  
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; U94331; AAB53708.1; -.  
DR EMBL; AB013898; BAA28269.1; -.  
DR EMBL; AB013903; BAA33388.1; -.  
DR EMBL; AB013899; BAA33388.1; JOINED.  
DR EMBL; AB013900; BAA33388.1; JOINED.  
DR EMBL; AB013901; BAA33388.1; JOINED.  
DR EMBL; AB013902; BAA33388.1; JOINED.  
DR HSSP; P25942; 1CDF.  
DR MGD; MGI:109587; Tnfrsf11b.  
DR InterPro; IPR000488; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR ProDom; PD000771; -; 1.  
DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.





```

ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.
AC Q9Y5U5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR.";
RL Curr. Biol. 0:0-0(1999).
DR EMBL: AF125304; AAD22635.1; -.
DR InterPro: IPR001368; -.
DR SMART: SM00208; TNFR: 1.
DR SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 737; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGK 60
DB 46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGK 105

QY 61 FSGFQCIDCASGTFSGGHEGHCXPTDCTQFGELTVFPGNKTNAVCPGSPPAEPLG 119
DB 106 FSGFQCIDCASGTFSGGHEGHCXPTDCTQFGELTVFPGNKTNAVCPGSPPAEPLG 164

RESULT 3
Q9NYJ9 PRELIMINARY; PRT; 255 AA.
ID Q9NYJ9;
AC Q9NYJ9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE GTR-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Riccardi C.;
RT "Identification of a soluble human GTR splicing (hGTR-D).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF241229; AAF63506.1; -.
DR SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 77.7%; Score 573; DB 4; Length 255;
Best Local Similarity 67.4%; Pred. No. 6.2e-56;
Matches 97; Conservative 2; Mismatches 9; Indels 36; Gaps 2;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGK 60
DB 46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGK 105

QY 61 FSGFQCIDCASGTFSGGHEGHCXPTDCTQFGELTVFPGNKTNAVCPGSPPAEPLG 119
DB 106 FSGFQCIDCASGTFSGGHEGHCXPTDCTQFGELTVFPGNKTNAVCPGSPPAEPLG 165
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QY 94 FLTVPFGNKTNAVCPGSPPAEP 117
DB 166 WET-----CGCEPGRPPGPP 180

RESULT 4
Q9JKR2 PRELIMINARY; PRT; 222 AA.
ID Q9JKR2;
AC Q9JKR2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229433; AAF61567.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF: 1.
DR SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 57.7%; Score 425.5; DB 11; Length 222;
Best Local Similarity 61.1%; Pred. No. 1.2e-39;
Matches 69; Conservative 16; Mismatches 27; Indels 1; Gaps 1;

QY 8 HTTRCCRDY-PGEECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGKFSFGQ 66
DB 40 NNTRCCSLYAPGKDCPKERCICVTPEYHCGDPQCKHYPCQGRVESQGDIVGFR 99

QY 67 CIDCASGTFSGGHEGHCXPTDCTQFGELTVFPGNKTNAVCPGSPPAEPLG 119
DB 100 CVACAMGTFESAGRDGHCRLTWNCSEFGFLTMFPGNKTNAVCIPEPLPTEQVG 152

RESULT 5
Q35714 PRELIMINARY; PRT; 228 AA.
ID Q35714;
AC Q35714;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RX MEDLINE=97322352; PubMed=9177197;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Riccardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA Migliorati G., Riccardi C.;
RT "Gene structure and chromosomal assignment of GTR, a mouse member of
RT the tumor necrosis factor/nerve growth factor receptor family.";
```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:31 ; Search time 133.1 Seconds  
(without alignments)  
118.289 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DARCCRVHTTRCCRDYPGEE.....GNKTHNAVCPGSPAEPLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_unclassified.\*

13: sp\_vertebrate.\*

14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737	100.0	234	4	Q95851
2	737	100.0	241	4	Q9Y5U5
3	573	77.7	255	4	Q9NYJ9
4	425.5	57.7	222	11	Q9JKR2
5	425.5	57.7	228	11	Q95714
6	425.5	57.7	294	11	Q9JKR3
7	295.5	40.1	132	11	Q9JKR1
8	147.5	20.0	267	6	O02764
9	145	19.7	300	4	Q95407
10	137	18.6	372	4	Q90HP4
11	137	18.6	401	4	O00300
12	131	17.8	401	11	O08712
13	131	17.8	616	4	Q9Y6Q6
14	130.5	17.7	401	11	O08727
15	130	17.6	276	13	Q9DD22
16	128	17.4	655	4	O75509
17	123	16.7	625	11	O35305
18	122	16.6	107	11	Q9JKE0
19	120.5	16.4	459	11	Q62327

20	120.5	16.4	482	11	O88734
21	120	16.3	655	11	Q9EP05
22	117	15.9	439	4	Q16042
23	116	15.7	302	13	Q9PUS0
24	110	14.9	1371	11	Q9QVW4
25	108	14.7	1574	11	O88281
26	107	14.5	4601	5	Q9V383
27	101.5	13.8	1537	5	Q9VAI2
28	100.5	13.6	126	10	Q9S9F4
29	99	13.4	1764	11	O35806
30	99	13.4	1833	11	O08999
31	98.5	13.4	351	14	O57117
32	97.5	13.2	176	14	O68396
33	97.5	13.2	176	14	O9PZQ7
34	97.5	13.2	176	14	Q9PX59
35	97.5	13.2	176	14	Q9PX08
36	97	13.2	1637	6	Q9XSU8
37	97	13.2	2319	11	Q9R172
38	96.5	13.1	176	14	Q9PZR9
39	96.5	13.1	176	14	Q9PZR8
40	96.5	13.1	176	14	Q9PWK6
41	96.5	13.1	757	5	Q9VZF2
42	96	13.0	1308	5	Q9GPM8
43	96	13.0	1792	13	O57484
44	95.5	13.0	814	11	O9QYL2
45	95.5	13.0	851	13	O42507

## ALIGNMENTS

RESULT 1

ID Q95851 PRELIMINARY; PRT; 234 AA.

AC Q95851;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-99156876; PubMed-10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor

RT necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AAD19694.1; -

DR InterPro; IPR001368; -

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 737; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 3.9e-74;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCSDPCCCTTRHHPCPGQVQSGK 60

|||||

Db 46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCSDPCCCTTRHHPCPGQVQSGK 105

|||||

QY 61 FSGFQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVPFGNKTNAVCPGSPAEPLG 119

|||||

Db 106 FSGFQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVPFGNKTNAVCPGSPAEPLG 164

RESULT 2

Q9Y5U5



GN TNFRSF18.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RQ SEQUENCE FROM N.A.

RA TISSUE=THYMUS;

RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,

RA Miclerini G., Riccardi C.;

RT "Identification of three novel mRNA splice variants of GITR.";

RL Cell Death Differ. 0:0-0(2000).

DR EMBL; AF229434; AAFe1568.1; -;

DR InterPro; IPR000561; -;

DR SMART; SM00181; EGF; 1.

SQ SEQUENCE 132 AA; 14106 MW; F586A5404BDFEDE CRC64;

Query Match 40.1%; Score 295.5; DB 11; Length 132;  
Best Local Similarity 58.0%; Pred. No. 1.9e-25;  
Matches 47; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

Yy 8 HTTCCRDRY-PGECCSEWDCMCVQPEHCGDPCCTTCRHHPCPPPGCVSQKFSFGFQ 66  
: ||| : | : | : ||||| : | : | : ||||| : | : | : ||||| : | :

Dd 40 NTNRCSLYAPGKGDKPKERCICITPTVEHCDDPOCKICKHYPCQPQGQRVESQGDIVFEGR 99  
: ||| : | : | : ||||| : | : | : ||||| : | : | : ||||| : | :

Oy . 67 CIDCASGTFSGGHGCHCKPWT 87  
: | : ||||| : | : | : ||||| : | : | : ||||| : | :

Dd 100 CVACAMGTFSAGRDGHCLWT 120  
: | : ||||| : | : | : ||||| : | : | : ||||| : | :

RESULT 8

OO2764 PRELIMINARY; PRT; 267 AA.

AC OO2764

DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE OX40 PRECURSOR (FRAGMENT).

OS Oryctolagus cuniculus (Rabbit).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RQ SEQUENCE FROM N.A.

RA SPRAIN-CHEBB.HM;

RA Isoo T., Seto A.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB003911; BAA20059.1; -;

HSSP; P19438; 1EXT.

DR InterPro; IPR001368; -;

DR Pfam; PF00020; TNFR\_c6; 3.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS00652; TNFR\_NGFR\_2; 2.

DR SMART; SM00208; TNFR; 1.

KW Signal.

FT NON\_TER 1 1

FT SIGNAL <1 18 POTENTIAL.

FT CHAIN 19 267 OX40.

SQ SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;

Query Match 20.0%; Score 147.5; DB 6; Length 267;  
Best Local Similarity 25.8%; Pred. No. 8.7e-09;  
Matches 41; Conservative 11; Mismatches 48; Indels 59; Gaps 6;

Oy 12 CCRR-YPGECCESEWDCMCVQPER-----HCGDPCCTTCRHHPCPPG----- 52  
: ||| : | : | : ||||| : | : | : ||||| : | : | : ||||| : | :

Dd 25 CVGDTYGDDR-----CLECPGVGMVSRNCRSQDTTC--HPCEPGFYNEAVNQACKPC 78  
: ||| : | : | : ||||| : | : | : ||||| : | : | : ||||| : | :

Oy 53 -----OGVDSQSKFSFGFCIDCASTFGSGHGCHKPW 86  
: | : ||||| : | : | : ||||| : | : | : ||||| : | : | : ||||| : | :

b 79 TCNNRSGSPEOBFCTHTRTVCRCRGTOPLVNGYKHGVDCAPCPGCFHFSEGNNRACPWP 138  
: | : ||||| : | : | : ||||| : | : | : ||||| : | : | : ||||| : | :







Qy	74	TFSGGHEG--HCKPWTDCDTQFGFLVFQPKNTHNAV---	VPG-SPDPNP	117
Db	158	YFSDAFSTDKCRPWTNCTFLGKRVEHHGTEKSDAVCSSSLPARKPPNP	207	

  

RESULT	14			
008727		PRELIMINARY;	PRT;	401 AA.
AC	008727;			
DT	01-JUL-1997 (TrEMBLrel. 04, Created)			
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)			
DE	OSTEOPTEREGIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).			
DE	GN	TNFRSF11b OR OPG.		
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
ON	NCBI_TaxID=10116;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=INTESTINE;			
RX	MEDLINE=97362071; PubMed=9108485;			
RA	Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,			
RA	Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,			
RA	Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,			
RA	Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,			
RA	Campbell P., Sander S., Van G., Farpley J., Derby P., Lee R.,			
RA	Suggs S., Boyle W.J.;			
RT	'Osteoprotegerin: a novel secreted protein involved in the regulation			
RT	of bone density."			
RL	Cell 89:309-319(1997).			
CC	-1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES			
CC	OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY			
CC	SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO			
CC	OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN			
CC	STROMAL CELLS AND OSTEOCLAST PROGENITORS.			
CC	-1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY			
CC	SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: EXTRACELLULAR.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
DR	EMBL: U94330; AA853707.1; -			
DR	HSSP: P25942; ICDP.			
DR	InterPro: IPR000488; -			
DR	InterPro: IPR001368; -			
DR	Pfam: PF00020; TNFR_c6; 4.			
DR	ProDom: PD000771; -; 1.			
DR	PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.			
DR	PROSITE: PS00500; TNFR_NGFR_2; 2.			
DR	SMART: SM00005; DEATH: 1.			
KW	Glycoprotein; Repeat; Cytokine; Signal.			
FT	SIGNAL	1	21	BY SIMILARITY.
FT	CHAIN	22	401	OSTEOPTEREGIN.
FT	DOMAIN	23	201	4 X TNFR-CYS.
FT	REPEAT	23	63	TNFR-CYS 1.
FT	REPEAT	64	106	TNFR-CYS 2.
FT	REPEAT	107	143	TNFR-CYS 3.
FT	REPEAT	144	201	TNFR-CYS 4.
FT	DOMAIN	306	365	DEATH DOMAIN.
FT	DISULFID	41	54	BY SIMILARITY.
FT	DISULFID	44	62	BY SIMILARITY.
FT	DISULFID	65	80	BY SIMILARITY.
FT	DISULFID	83	97	BY SIMILARITY.
FT	DISULFID	87	105	BY SIMILARITY.
FT	DISULFID	118	142	BY SIMILARITY.
FT	DISULFID	145	160	BY SIMILARITY.
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	155	165	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	289	289	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	401 AA;	46192 MW;	FEC6A31FD4E573A CRC64:

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RESULT 2
Q9Y5U5 PRELIMINARY; PRT; 241 AA.
AC Q9Y5U5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR.";
RL Curr. Biol. 6:0-0(1999).
DR EMBL; AF125304; AAD22635.1; -.
DR InterPro; IPR001368; -.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 979; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOHGAMGAFRALCGLALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60
Db 1 MAOHGAMGAFRALCGLALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGQGVQSGKFSFGQCIDCASGTF 120
Db 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGQGVQSGKFSFGQCIDCASGTF 120

QY 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKNHNAVCVPSPAPPLG 164
Db 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKNHNAVCVPSPAPPLG 164

QY 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKNHNAVCVPSPAPPLG 164
Db 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKNHNAVCVPSPAPPLG 164

RESULT 3
Q9NYJ9 PRELIMINARY; PRT; 255 AA.
AC Q9NYJ9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE GTR-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Mastrodicasa E., Riccardi C.;
RT "Identification of a soluble human GTR splicing (hGTR-D).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241229; AAF63506.1; -.
SQ SEQUENCE 255 AA; 26827 MW; C98652AC97AF2CC CRC64;

Query Match 83.2%; Score 815; DB 4; Length 255;
Best Local Similarity 75.1%; Pred. No. 5e-78;
Matches 142; Conservative 2; Mismatches 9; Indels 36; Gaps 2;

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QY 1 MAOHGAMGAFRALCGLALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60
Db 1 MAOHGAMGAFRALCGLALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGQGVQSGKFSFGQCIDCASGTF 120
Db 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGQGVQSGKFSFGQCIDCASGTF 120

QY 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKNHNAVCVPSPAPPLG 164
Db 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKNHNAVCVPSPAPPLG 164

QY 154 VPGSPAPPEP 162
Db 172 EPGRPFGPP 180

RESULT 4
Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 52.1%; Score 510; DB 11; Length 222;
Best Local Similarity 54.1%; Pred. No. 4.7e-46;
Matches 86; Conservative 25; Mismatches 40; Indels 8; Gaps 2;

QY 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPEG 65
Db 1 MGAWAMLYGVSMCLVDLDLQPSVVEEPGCGPKGVQSGNTRCCSLYA-----PGKE 53

QY 66 CCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGQGVQSGKFSFGQCIDCASGTFSGCHE 125
Db 54 DCKERCICVTPEYHCGDPQCKICKHYPCQGVQSGDIVFGFRCVACAMGTFSGAGRD 113

QY 126 GHCKPMTDCTQFGFLTVPFGNKNHNAVCVPSPAPPLG 164
Db 114 GHCLRLTNCQSGFLTWFPGNKNHNAVCIPLEPLTEQYG 152

RESULT 5
Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:33 ; Search time 133.1 Seconds  
(without alignments)  
163.020 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_164

Perfect score: 979

Sequence: 1 MAQHGMAMFALCALGALLC.....GNKTHNAVCPGSPPAEPLG 164

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	979	100.0	234	4	O95851 homo sapien
2	979	100.0	241	4	O9Y5U5 homo sapien
3	815	83.2	255	4	Q9NYJ9 homo sapien
4	510	52.1	222	11	Q9JKR2 mus musculu
5	510	52.1	228	11	O35714 mus musculu
6	510	52.1	294	11	Q9JKR3 mus musculu
7	380	38.8	132	11	O9JKR1 mus musculu
8	171.5	17.5	267	6	O02764 oryctolagus
9	154.5	15.8	276	13	Q9DD02 gallus gall
10	153	15.6	300	4	O95407 homo sapien
11	141.5	14.5	401	11	O08727 rattus norv
12	139.5	14.2	401	11	O08712 mus musculu
13	138.5	14.1	616	4	Q9Y6Q6 homo sapien
14	137	14.0	372	4	Q9UHP4 homo sapien
15	137	14.0	401	4	O00300 homo sapien
16	129.5	13.2	655	4	O75509 homo sapien
17	125	12.8	655	11	Q9EP05 mus musculu
18	123	12.6	625	11	O35305 mus musculu
19	122	12.5	107	11	Q9JKE0 rattus norv

20 121 12.4 302 13 Q9PUS0  
21 120.5 12.3 459 11 Q62327  
22 120.5 12.3 482 11 O88734  
23 119 12.2 439 4 Q16042  
24 117.5 12.0 1587 4 O00508  
25 116.5 11.9 1511 4 O75412  
26 115.5 11.8 1371 11 Q9QW4  
27 114.5 11.7 2906 11 Q9WUH9  
28 112 11.4 152 5 Q9XVX3  
29 112 11.4 1637 6 Q9XSV8  
30 111.5 11.4 1764 11 O35806  
31 111 11.3 1111 5 Q9XWD6  
32 111 11.3 1792 13 O57484  
33 110.5 11.3 1687 11 Q61204  
34 110 11.2 1522 5 Q22685  
35 110 11.2 1698 5 Q94438  
36 109.5 11.2 164 5 Q22048  
37 109.5 11.2 4601 5 Q9V383  
38 109 11.1 1574 11 O88281  
39 107.5 11.0 1833 11 O08999  
40 107 10.9 1308 5 Q9GPM8  
41 107 10.9 3680 5 Q9VR08  
42 106.5 10.9 870 6 O02660  
43 105 10.7 188 5 Q18238  
44 105 10.7 2009 5 Q9VXMO  
45 105 10.7 2319 11 Q9R172

## ALIGNMENTS

RESULT 1

O95851  
ID O95851 PRELIMINARY; PRT; 234 AA.  
AC O95851;  
DT 01-MAY-1999 (TREMREL. 10, Created)  
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99156876; PubMed=10037686;  
RA KWON B., YU K.Y., NI J., YU G.L., JANG I.K., KIM Y.J., XING L.,  
RA LIU D., WANG S.X., KWON B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor  
RT necrosis factor receptor superfamily and its ligand."  
RL J. Biol. Chem. 274:6056-6061(1999).  
DR EMBL; AF117297; AAD19694.1; -  
DR InterPro; IPR001368; -  
DR SMART; SM00208; TNFR; 1.  
KW Receptor.  
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 979; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 2.8e-95;

Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAMFALCALGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTCCRD 60  
DB 1 MAQHGMAMFALCALGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTCCRD 60  
QY 61 YGEECCSEWDCMCVQPEPFHCPGDPCCCTTCRHPPCPGQVQSGQKFSFGQICDASGTF 120  
DB 61 YGEECCSEWDCMCVQPEPFHCPGDPCCCTTCRHPPCPGQVQSGQKFSFGQICDASGTF 120  
QY 121 SGGHGHCKPWTDCYQFGFLTVPFGNKNTHNAVCPGSPPAEPLG 164  
DB 121 SGGHGHCKPWTDCYQFGFLTVPFGNKNTHNAVCPGSPPAEPLG 164





CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -|- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
CC BRAIN, HEART, KIDNEY, STOMACH, INTESINE, SKIN, CALVARIA AND  
CC PLACENTA. NOT DETECTED IN SPLEEN.  
CC -|- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
CC 15 TO DAY 17.  
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; U94331; AB53708.1; -.  
DR EMBL; AB013898; BAA28269.1; -.  
DR EMBL; AB013903; BAA33388.1; -.  
DR EMBL; AB013899; BAA33388.1; JOINED.  
DR EMBL; AB013900; BAA33388.1; JOINED.  
DR EMBL; AB013901; BAA33388.1; JOINED.  
DR EMBL; AB013902; BAA33388.1; JOINED.  
DR HSP; P25942; ICDF.  
DR MGD; MGI:109587; Tnfrsf11b.  
DR InterPro; IPR000488; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_C6; 3.  
DR ProDom; PD00071; -; 1.  
DR ProSite; PS50017; DEATH\_DOMAIN; 1.  
DR ProSite; PS00652; TNFR\_NGFR\_1; 1.  
DR ProSite; PS50050; TNFR\_NGFR\_2; 2.  
DR SMART; SM00005; DEATH; 1.  
KW Glycoprotein; Repeat; Cytokine; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 401 OSTEOPROTEGERIN.  
FT DOMAIN 23 201 4 X TNFR-CYS.  
FT REPEAT 23 63 TNFR-CYS 1.  
FT REPEAT 64 106 TNFR-CYS 2.  
FT REPEAT 107 143 TNFR-CYS 3.  
FT REPEAT 144 201 TNFR-CYS 4.  
FT DOMAIN 306 365 DEATH DOMAIN.  
FT DISULFID 41 54 BY SIMILARITY.  
FT DISULFID 44 62 BY SIMILARITY.  
FT DISULFID 65 80 BY SIMILARITY.  
FT DISULFID 83 97 BY SIMILARITY.  
FT DISULFID 87 105 BY SIMILARITY.  
FT DISULFID 118 142 BY SIMILARITY.  
FT DISULFID 145 160 BY SIMILARITY.  
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH  
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH  
FT VARIANT 165 165 SWISS).  
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH  
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH  
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH  
FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRG64;

Query Match 14.28; Score 139.5; DB 11; Length 401;  
Best Local Similarity 25.7%; Pred. No. 6.5e-07;  
Matches 43; Conservative 10; Mismatches 69; Indels 45; Gaps 6;  
QY 15 GLALLCALSILGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGECCESEW--- 70  
DB 36 GHQLLC-----DKCAGTYL-----KQCTVVRKTLVCPDHSYDTSNHTSD 78  
QY 71 DCMCVQP-----EFHCQDPCCTTC-----RHHPCPPGQGVQSQCKFSF 108  
DB 79 ECVGSPVKELQSVKQCNRTNHRVCECEBGRYLEIFCLKHKRSCPPGSGVVQAGTPR 138  
QY 109 GFQCIDCAGTSG--GHEGCHKPWTDCQTFQFLTFPPGNKTHNAV 153  
DB 139 NTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185

RESULT 13  
QY606 PRELIMINARY; PRT; 616 AA.  
AC Q9Y606;  
DT 01-NOV-1999 (TEMBLrel. 12, Created)  
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)  
DE 01-MAR-2001 (TEMBLrel. 16, Last annotation update)  
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-  
DE INDUCED CYTOKINE RECEPTOR) (RANK).  
GN TNFRSF11A OR RANK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,  
RA Galibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
RT and dendritic-cell function";  
RL Nature 390:175-179(1997).  
CC -|- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.  
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).  
CC -|- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN  
CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL  
CC GLAND.  
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; AF018253; AAB86809.1; -.  
DR HSP; P25942; ICDF.  
DR MIM; 603499; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_C6; 4.  
DR ProSite; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR ProSite; PS50050; TNFR\_NGFR\_2; 1.  
DR SMART; SM0208; TNFR; 1.  
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 616 RECEPTOR ACTIVATOR OF NF-KAPPA-B.  
FT DOMAIN 24 212 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 213 233 POTENTIAL.  
FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 33 195 4 X TNFR-CYS.  
FT REPEAT 33 69 TNFR-CYS 1.  
FT REPEAT 70 112 TNFR-CYS 2.  
FT REPEAT 113 152 TNFR-CYS 3.  
FT REPEAT 153 195 TNFR-CYS 4.  
FT DISULFID 34 46 BY SIMILARITY.  
FT DISULFID 47 60 BY SIMILARITY.  
FT DISULFID 50 68 BY SIMILARITY.  
FT DISULFID 71 86 BY SIMILARITY.  
FT DISULFID 92 112 BY SIMILARITY.  
FT DISULFID 114 124 BY SIMILARITY.  
FT DISULFID 126 133 BY SIMILARITY.  
FT DISULFID 127 151 BY SIMILARITY.  
FT DISULFID 154 169 BY SIMILARITY.  
FT DISULFID 175 194 BY SIMILARITY.  
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRG64;

Query Match 14.18; Score 138.5; DB 4; Length 616;  
Best Local Similarity 24.1%; Pred. No. 1.2e-06;  
Matches 52; Conservative 14; Mismatches 69; Indels 81; Gaps 10;  
QY 11 RALCGLALLCALSILGQRTGPGCGPGRLLLTGTGDARCCR---VHTTRCCR-----DY 61  
DB 9 RPLFALLLLCALL-----ARLQVALQIAPPCTSEKHVHGLRCNCNCEPKY 55

FT	DISULFID	41	54	BY SIMILARITY.
FT	DISULFID	44	62	BY SIMILARITY.
FT	DISULFID	65	80	BY SIMILARITY.
FT	DISULFID	83	97	BY SIMILARITY.
FT	DISULFID	87	105	BY SIMILARITY.
FT	DISULFID	118	142	BY SIMILARITY.
FT	DISULFID	145	160	BY SIMILARITY.
FT	CARBOHYD	98		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	165		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	178		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	289		N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	401 AA;	46192 MW; FECSA31FIDAE573A CRC64;	

Query Match 14.5%; Score 141.5; DB 11; Length 401;  
Best Local Similarity 27.2%; Pred. No. 4e-07;  
Matches 46; Conservative 11; Mismatches 63; Indels 49; Gaps

Qy	15	GLALLCALSLGQRTGGGCGPGRLLGTGTDARCCRVHTTRC	-----PGE5 65
			:
Db	36	GROLLC-----DKAPGTYL-----KQCTVRRKTLCPGCPDYSYDTSWHTSDE	79
Qy	66	C-----CSEWD-----CMCQVPEPHCGDPCCCTTCRHHPCPGQVQSGKF	106
			:
Db	80	CVYCSVPYCKELQTVKQBCNRTHNRVCEEGRYLELEFC---LKHSRCPGLGVLAQGT	136
Qy	107	SFGFOCIDCAGSTFG--GHEGCHKPWDTQCFGLTVFPNGKTHNAV	153
			:
Db	137	ERNIVCKRCPDGFSGETSSKAPCRKHTNCSSIGLLLIQKGNATHDNC	185

RESULT 12

008712 PRELIMINARY; PRT; 401 AA.

AC	008712	PRELIMINARY; PRT; 401 AA.
AC	008712;	070202;
DT	01-JUL-1997	(TREMBLrel. 04, Created)
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)
DE	OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)	
DE	(OCIF).	
DE	GN	THRSF11B OR OPG.
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BALB/C; TISSUE=KIDNEY;	
RC	MEDLINE=37262071; PubMed=9108485;	
RA	Li monet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,	
RA	Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.	
RA	Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.	
RA	Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.	
RA	Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,	
RA	Suggs S., Boyle W.J.;	
RT	"Osteoprotegerin: a novel secreted protein involved in the regulation	
RT	of bone density."	
RL	Cell 89:309-319(1997).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=129/OLA, AND NIH SWISS;	
RC	MEDLINE=98382537; PubMed=9714833;	
RA	Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.	
RA	Higashio K.;	
RT	"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)	
RT	gene and its expression in embryogenesis."	
RL	Gene 215:339-343(1998).	
CC	-1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE	
CC	OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY	
CC	SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO	
CC	OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN	
CC	STROMAL CELLS AND OSTEOCLAST PROGENITORS.	
CC	-1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).	

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FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRG64;

Query Match 14.0%; Score 137; DB 4; Length 401;
Best Local Similarity 23.8%; Pred. No. 1.2e-06;
Matches 38; Conservative 15; Mismatches 59; Indels 48; Gaps 6;

Qy 53 HTTRCRDYPG-----EECCSEWDCMCV-----QPEFHCGDPC--CT----- 87
Db 37 HOLLCDKCPGTYLKQHCYAKWKTCVACPCPDHYTDSWHTSDECLYCSPVKELQYVQE 96

Qy 88 -----TC-----RHHPCPPGQGVQSGKFSFGFCIDCASGTFSG--GH 124
Db 97 CNRTHRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNTVCKRCPDGFFSNETSS 156

Qy 125 EGHCKPWTCTQFGFUTVFPGNKTHNAVCPGSPPAEPLG 164
Db 157 KAPCRKHTNCVSFGLLLTQGNATHDNICSGNSESTQKCG 196
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Search completed: September 4, 2001, 16:14:34  
Job time: 1221 sec

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QY 62 PGECCSEWDCMVQPEHCG-----DPC----- 85
Db 56 MSSCKTTSDSVCLP-----CGPDEYLDWSNEDKCLLHKVCDTGKALVAVVAGNSTTPRR 111
QY 86 -----CCTCRHH-PCPPGQVQSQGKFGQCIDCAGTSGGHEG--HCKP 130
Db 112 CACTAGYHWSODCECCRNTECAPGLGAHQHPLQLNKDVCKPCLAGYFSDAFSSDTDKCRP 171
QY 131 WTDCTQGFGLVFPNGKTHNAV-----VPG-SPAPB 162
Db 172 WTNCTFLGKRVHEHGTGKSDAVCSSSLPARKPPNEP 207

RESULT 14
Q9UHP4 PRELIMINARY; PRT; 372 AA.
AC Q9UHP4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL; AF134187; AAP20168.1; -.
DR HSSP; P25942; 1CDF.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 14.0%; Score 137; DB 4; Length 372;
Best Local Similarity 23.8%; Pred. No. 1.le-06;
Matches 38; Conservative 15; Mismatches 59; Indels 48; Gaps 6;

QY 53 HTTRCDYPG-----EECCSEWDCMV-----QPEFHGDPG--CT----- 87
Db 16 HQLLCDRPPGTYLKQHCATAKWTVCAPCPDHYTDSWHTSDECLYCSVPCKELQYVQKE 75
QY 88 -----TC-----RHHCPGQVQSQGKFGFCIDCAGTSG--GH 124
Db 76 CNRTHNRVCECKEGRYLEIEFLCHRSPPGPGVVGQAQTPERTVCKRCPDGFSSNETSS 135
QY 125 EGCHKPWTCTQFGFLTVFPNGKTHNAVCPGSPAPBPLG 164
Db 136 KAPCRKHTNCSVFGLLLTQKNATHDNCNSGSESTQKCG 175

RESULT 15
O00300 PRELIMINARY; PRT; 401 AA.
AC O00300; 060236;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin; a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AB002146; BAA25910.1; -.
DR EMBL; AB008822; BAA32076.1; -.
DR EMBL; AB008821; BAA32076.1; JOINED.
DR EMBL; U94332; AAB53709.1; -.
DR HSSP; P25942; 1CDF.
DR MIM; 602643; -.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRODOM; PD000771; -.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT DOMAIN 23 183
FT REPEAT 23 63
FT REPEAT 64 106
FT REPEAT 107 143
FT REPEAT 144 201
FT DOMAIN 306 365
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
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RESULT 2
Q9Y5U5 ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.
AC Q9Y5U5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 0:0-0(1999).
DR EMBL; AF125304; AAD22635.1; -.
DR InterPro; IPR001368; -.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7EB2CBE CRC64;

Query Match 100.0%; Score 841; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-83;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORPTGGCGGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
DB 26 ORPTGGCGGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 85

QY 61 CTTCTRHHPCCPGQVQSGKFSFGFCIDCASGTFSGGHEGCKPWTDC----- 109
DB 86 CTTCTRHHPCCPGQVQSGKFSFGFCIDCASGTFSGGHEGCKPWTDC----- 145

QY 110 -----TQFGFLTVPFGNKNTHNAVCPGSPPAEP 137
DB 146 EAASSPRKSGASDRQRRRGGWET-----CGCEPGRPPGPP 180

RESULT 4
Q9JKR2 ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GITR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Ricciardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 55.4%; Score 465.5; DB 11; Length 222;
Best Local Similarity 56.9%; Pred. No. 6.2e-43;
Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;

QY 7 PCGPGGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTCRH 66
DB 27 PCGPGGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTCRH 79

QY 67 HPCPPGQVQSGKFSFGFCIDCASGTFSGGHEGCKPWTDC----- 126
DB 80 YPCQPGQVQSGKFSFGFCIDCASGTFSGGHEGCKPWTDC----- 139

QY 127 VCVPGSPPAE 136
DB 140 VCIPEPLPTE 149

RESULT 5
Q35714 ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GITR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RX MEDLINE=97322352; PubMed=9177197;

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Query Match 81.7%; Score 687; DB 4; Length 255;
Best Local Similarity 71.3%; Pred. No. 7e-67;
Matches 117; Conservative 2; Mismatches 9; Indels 36; Gaps 2;

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GenCore version 4.5

Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:30 ; Search time 133.1 Seconds  
(without alignments)  
136.182 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162

Perfect score: 841

Sequence: 1 QRPFGGCGGPRLLLTGT.....PFGKTHNAVCPGSPPAEP 137

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_unclassified.\*

13: sp\_vertebrate.\*

14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	841	100.0	234	4 Q95851	Q95851 homo sapien
2	841	100.0	241	4 Q9V5U5	Q9V5U5 homo sapien
3	687	81.7	255	4 Q9NVJ9	Q9NVJ9 homo sapien
4	465.5	55.4	222	11 Q3JKR2	Q3JKR2 mus musculus
5	465.5	55.4	228	11 Q35714	Q35714 mus musculus
6	465.5	55.4	294	11 Q3JKR3	Q3JKR3 mus musculus
7	339.5	40.4	132	11 Q3JKR1	Q3JKR1 mus musculus
8	154.5	18.4	267	6 O02764	O02764 oryctolagus
9	150.5	17.9	300	4 Q95407	Q95407 homo sapien
10	140	16.6	401	11 Q08727	Q08727 rattus norv
11	139	16.5	276	13 Q9DD02	Q9DD02 gallus gall
12	139	16.5	401	11 Q08712	Q08712 mus musculus
13	133	15.8	372	4 Q9UHP4	Q9UHP4 homo sapien
14	133	15.8	401	4 Q00300	Q00300 homo sapien
15	131	15.6	616	4 Q9Y6Q6	Q9Y6Q6 homo sapien
16	129.5	15.4	655	4 Q75509	Q75509 homo sapien
17	123	14.6	625	11 Q35305	Q35305 mus musculus
18	122.5	14.6	655	11 Q9EP05	Q9EP05 mus musculus
19	122	14.5	107	11 Q9JKE0	Q9JKE0 rattus norv

20	120.5	14.3	459	11 Q62327	Q62327 mus musculu
21	120.5	14.3	482	11 Q88734	Q88734 mus musculu
22	119	14.1	439	4 Q16042	Q16042 homo sapien
23	116.5	13.9	302	13 Q9PUS0	Q9PUS0 salvelinus
24	112	13.3	152	5 Q9XVX3	Q9XVX3 caenorhabdi
25	112	13.3	1637	6 Q9XSV8	Q9XSV8 bos taurus
26	111	13.2	1371	11 Q9QVW4	Q9QVW4 rattus sp.
27	109.5	13.0	4601	5 Q9V383	Q9V383 drosophila
28	109	13.0	1574	11 Q88281	Q88281 rattus norv
29	109	13.0	2906	11 Q9WUH9	Q9WUH9 rattus norv
30	107	12.7	164	5 Q22048	Q22048 caenorhabdi
31	107	12.7	1308	5 Q9GPM8	Q9GPM8 caenorhabdi
32	106.5	12.7	1698	5 Q94438	Q94438 chironomus
33	104.5	12.4	1587	4 Q00508	Q00508 homo sapien
34	104	12.4	1522	5 Q22685	Q22685 caenorhabdi
35	103.5	12.3	126	10 Q9S9F4	Q9S9F4 phytolacca
36	103.5	12.3	1511	4 Q75412	Q75412 homo sapien
37	103	12.2	1242	4 Q9NS15	Q9NS15 homo sapien
38	103	12.2	1382	4 Q9H7K2	Q9H7K2 homo sapien
39	103	12.2	1764	11 Q35806	Q35806 rattus norv
40	103	12.2	1833	11 Q08999	Q08999 mus musculu
41	103	12.2	1963	6 Q28019	Q28019 bos taurus
42	102.5	12.2	188	5 Q18238	Q18238 caenorhabdi
43	102.5	12.2	283	6 Q9XS28	Q9XS28 cercopithec
44	102.5	12.2	870	6 Q02660	Q02660 bos taurus
45	102.5	12.2	1792	13 Q57484	Q57484 gallus gall

## ALIGNMENTS

RESULT 1

ID Q95851 PRELIMINARY; PRT; 234 AA.  
AC Q95851;  
DT 01-MAY-1999 (TREMREL. 10, Created)  
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE FROM N.A.  
RX MEDLINE-99156876; Pubmed=10037686;  
RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,  
RA Liu D., Wang S.X., Kwon B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor  
RT necrosis factor receptor superfamily and its ligand.";  
RL J. Biol. Chem. 274:6056-6061(1999).  
DR EMBL; AF117297; AAD19694.1; -;  
DR InterPro; IPR001368; -;  
DR SMART; SM00208; TNFR; 1.  
KW Receptor.  
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 841; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.4e-83;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QRPFGGCGGPRLLLTGTGTTCRCRDYPCGECCECCSDWCMVPEFHCGRP	60
Db	26	QRPFGGCGGPRLLLTGTGTTCRCRDYPCGECCECCSDWCMVPEFHCGRP	85
QY	61	CTTCRRHPCPPGQVQSGQKFSFGFCIDCASGTFSGSGHEGCKPWTDTCTQFGFLTVP	120
Db	86	CTTCRRHPCPPGQVQSGQKFSFGFCIDCASGTFSGSGHEGCKPWTDTCTQFGFLTVP	145
QY	121	NKTHNAVCPGSPPAEP	137
Db	146	NKTHNAVCPGSPPAEP	162

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DR PROSITE; PS50050; TNFR_NGFR_2; 2.  
DR SMART; SMO0208; TNFR; 1.  
KW Signal.  
FT NON_TER <1 1  
FT SIGNAL 18 POTENTIAL.  
FT CHAIN 19 267 OX40.  
FT SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;  
  
Query Match 18.4%; Score 154.5; DB 6; Length 267;  
Best Local Similarity 31.1%; Pred. No. 3.6e-09;  
Matches 46; Conservative 11; Mismatches 62; Indels 29; Gaps 7;  
  
QY 9 CGPGRLLGTGDARCCRVHTRCCRDPG--EECCSEWDCM-CVQ-----PEFHCG 57  
| | : | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 40 CQP-----GYGMVSRCNRNSQDTICHPCEPGFEAVNYQACKPCTQCNRRSRGSBPQOECT 94  
| | : | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 58 DPCCTTCRRHHPCPGQGVQSOGKSFQFCIDCASGFPSGGHEGHCKRPWTCTQGFLTV 117  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 95 HTRDVTVC---CRP--GTQPLNGYKHGVDCAPCPQGHFSEGNACRPWTNCTLAGKRRL 149  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 118 FPGNKTHNAV-----VPGSPPAEP 137  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 150 QPASSISDAVCEDRSSLATQPWETPSAP 177  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
  
RESULT 9  
Q95407 PRELIMINARY; PRT; 300 AA.  
ID AC Q95407;  
AD 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).  
GN DCR3 OR TR6 OR TNFRSF6B.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI_TaxId=9606;  
RN [1]  
RP MEDLINE-99087326; PubMed-9877321;  
RX Platt R.M., Masters S.A., Lawrence D.A., Roy M., Kischkel F.C.,  
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,  
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,  
RA Goddard A.D., Rotstein D., Ashkenazi A.;  
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and  
RT colon cancer.";  
RL Nature 396:699-703(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE-BLOOD;  
RC MEDLINE-99253915; PubMed-10318773;  
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;  
RT "A newly identified member of tumor necrosis factor receptor  
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";  
J. Biol. Chem. 274:13733-13736(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX TISSUE-PANCREAS;  
RC MEDLINE-20122600; PubMed-10655513;  
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,  
RA Sodeman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;  
RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors  
RT independent of gene amplification and its location in a four-gene  
RT cluster.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Matthews L.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF104419; AAD03056.1; -;  
DR EMBL; AF134240; AAD29688.1; -;
```

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RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Riccardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C;
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA Migliorati G., Riccardi C.;
RT "Gene structure and chromosomal assignment of GTR, a mouse member of
RT the tumor necrosis factor/nerve growth factor receptor family.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U82534; AAB81243.1; -.
DR MGD; AF109216; AAF14231.1; -.
DR MGD; MGI:894675; Tnfrsf18.
DR InterPro: IPR000561; -.
DR SMART; SM00181; EGF; 1.
KW Signal; Receptor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY
FT FT RELATED PROTEIN.
SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 55.4%; Score 465.5; DB 11; Length 228;
Best Local Similarity 56.9%; Pred. No. 6.3e-43;
Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;

QY 7 PGCGRLLLGTTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66
DB 27 PGCGRLLLGTTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66
QY 67 HPCPPGGVQSGKFGFGQIDCASGTFSGGHEGCKPWTDCQFGFLTVPFGNKTHNA 126
DB 80 YPCQPGQGVESQGDIVFGRCVACAMGTFSAGRDGCHRLWNTCSQFGFLTVPFGNKTHNA 139

QY 127 VCVPGSPPAE 136
DB 140 VCIPEPLPTE 149

Query Match 55.4%; Score 465.5; DB 11; Length 294;
Best Local Similarity 56.9%; Pred. No. 7.9e-43;
Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;

QY 7 PGCGRLLLGTTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66
DB 27 PGCGRLLLGTTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66
QY 67 HPCPPGGVQSGKFGFGQIDCASGTFSGGHEGCKPWTDCQFGFLTVPFGNKTHNA 126
DB 80 YPCQPGQGVESQGDIVFGRCVACAMGTFSAGRDGCHRLWNTCSQFGFLTVPFGNKTHNA 139

QY 127 VCVPGSPPAE 136
DB 140 VCIPEPLPTE 149

Query Match 55.4%; Score 465.5; DB 11; Length 294;
Best Local Similarity 56.9%; Pred. No. 7.9e-43;
Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;

QY 7 PGCGRLLLGTTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66
DB 27 PGCGRLLLGTTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66
QY 67 HPCPPGGVQSGKFGFGQIDCASGTFSGGHEGCKPWTDCQFGFLTVPFGNKTHNA 126
DB 80 YPCQPGQGVESQGDIVFGRCVACAMGTFSAGRDGCHRLWNTCSQFGFLTVPFGNKTHNA 139

QY 127 VCVPGSPPAE 136
DB 140 VCIPEPLPTE 149

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DB 27 PGCGRLLLGTTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 79
QY 67 HPCPPGGVQSGKFGFGQIDCASGTFSGGHEGCKPWTDCQFGFLTVPFGNKTHNA 126
DB 80 YPCQPGQGVESQGDIVFGRCVACAMGTFSAGRDGCHRLWNTCSQFGFLTVPFGNKTHNA 139

QY 127 VCVPGSPPAE 136
DB 140 VCIPEPLPTE 149

RESULT 7
Q9JKR1 ID Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61566.1; -.
DR InterPro: IPR000561; -.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5404BIDFEDE CRC64;

Query Match 40.4%; Score 339.5; DB 11; Length 132;
Best Local Similarity 52.5%; Pred. No. 1.8e-29;
Matches 53; Conservative 17; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGRLLLGTTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66
DB 27 PGCGRLLLGTTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66
QY 67 HPCPPGGVQSGKFGFGQIDCASGTFSGGHEGCKPWT 107
DB 80 YPCQPGQGVESQGDIVFGRCVACAMGTFSAGRDGCHRLWT 120

RESULT 8
O02764 ID O02764 PRELIMINARY; PRT; 267 AA.
AC O02764;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHB;HM;
RA Isono T., Seto A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro: IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.

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DR PRODOM: PD000771; -. 1.
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
DR PROSITE; PSS00652; TNFR_NGFR_1; 1.
DR PROSITE; PSS0050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401 OSTEOPROTEGERIN.
FT DOMAIN 23 201 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 16.5%; Score 139; DB 11; Length 401;
Best Local Similarity 26.4%; Pred. No. 2.4e-07;
Matches 39; Conservative 10; Mismatches 65; Indels 34; Gaps 5;

QY 9 CGGRLLLGTGTCARCRVHTTCRRDYPGECCSEW-----RHHPCPGGVQSGKSFQFCIDCAGTFSG--CHE 100
DB 44 CAPGTYL-----KHQCTVRARKTLCPDHSYTDWHTSDCYVCSPVKELQSVKQEC 97
QY 57 GDPCTTC-----RHHPCPGGVQSGKSFQFCIDCAGTFSG--CHE 100
DB 98 NRTHNRVCECEEGRYLEIEFCLKHRSCTPPGSGVQAGTPERTNTVCKKCPDGFSGTSSK 157
QY 101 GHCKPWTDCQTFQGLTVFPNGKTHNAV 128
DB 158 APCIKHTNCTFGLLLTQKGNATHDNIC 185

RESULT 13
Q9UHP4 PRELIMINARY; PRT; 372 AA.
AC Q9UHP4
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX He 2.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Huahue Yu Sheng Wu Li Huaueh pao 31:680-684(1999).
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DR EMBL; AF134187; AAF20168.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PSS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PSS0050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
FT NON_TER 1 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 15.8%; Score 133; DB 4; Length 372;
Best Local Similarity 24.2%; Pred. No. 1e-06;
Matches 36; Conservative 14; Mismatches 51; Indels 48; Gaps 6;

QY 28 HTTRCCRDYPG-----EECCSEWDCMCV-----QPERHCGDPC--CT----- 62
DB 16 HQLLCDKCPGPGYLYKQHCYAKWTKVCACPDHYHYDWSHTSDCYVCSPVKELQYVKQE 75
QY 63 -----TC-----RHHPCPGGVQSGKSFQFCIDCAGTFSG--GH 99
DB 76 CNRTHNRVCEKEGRYLEIEFCLKHRSCTPPGSGVQAGTPERTNTVCKKCPDGFSGTSS 135
QY 100 EGHCKPWTDCQTFQGLTVFPNGKTHNAV 128
DB 136 KAPCRKHTNCSVFGLLLTQKGNATHDNIC 164

RESULT 14
O00300 PRELIMINARY; PRT; 401 AA.
AC O00300; O60236;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
DE GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.-Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
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Db 158 YFSDAFSSTDKCRPWTNCTFLGKRVEHHGTEKSDAVCSSLPARKPNP 207

Search completed: September 4, 2001, 16:14:30  
Job time: 1217 sec



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RESULT 2
Q9Y5U5 PRELIMINARY; PRT; 241 AA.
AC Q9Y5U5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR.";
RL Curr. Biol. 0:0-0(1999).
DR EMBL; AF125304; AAD22635.1; -.
DR InterPro; IPR001368; -.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 969; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.6e-94;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCALSLGORTGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60
DB 1 MAQHGAMGAFRALCALSLGORTGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQPFHCGDCPCTTCRHHPCPPGQVQSGKFSFGQICDASGTF 120
DB 61 YPGECCSEWDCMCVQPFHCGDCPCTTCRHHPCPPGQVQSGKFSFGQICDASGTF 120

QY 121 SGGHEGCHKPWTDC-----TQFGFLTVFPGNKTHNAVC 153
DB 121 SGGHEGCHKPWTDC-----TQFGFLTVFPGNKTHNAVC 153

QY 154 VPGSPPAEP 162
DB 172 EPGRPVPP 180

RESULT 4
Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 52.2%; Score 506; DB 11; Length 222;
Best Local Similarity 54.5%; Pred. No. 8.6e-46;
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

QY 7 MGAFRALCALSLGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVLDLQGPSVVEEPGCGPGKVGQSGNNTCCSLYA-----PGKE 53

QY 66 CCSEWDCMCVQPFHCGDCPCTTCRHHPCPPGQVQSGKFSFGQICDASGTFSGGHE 125
DB 54 DCPKERCICVTEYHCGDPCCKICKHYPCQPGQORVESQGDIVFGRCVACAMGTFSGAGRD 113

QY 126 GHCKPMTDCTQFGFLTVFPGNKTHNAVCVPGSPPAE 161
DB 114 GHCLWTNCSQFGFLTFMFGNKTHNAVCPEPLPTE 149

RESULT 5
Q95714 PRELIMINARY; PRT; 228 AA.
AC Q95714;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:30 ; Search time 133.1 Seconds  
(without alignments)  
161.032 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_162

Perfect score: 969

Sequence: 1 MAQHGAMGAFRALCGLALLC.....FPGNKTNAVCPGSPPAEP 162

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rhodent.\*

12: sp\_unclassified.\*

13: sp\_vertebrate.\*

14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	969	100.0	234	4	Q95851
2	969	100.0	241	4	Q9V5U5
3	815	84.1	255	4	Q9NVJ9
4	506	52.2	222	11	Q9JKR2
5	506	52.2	228	11	Q35714
6	506	52.2	294	11	Q9JKR3
7	380	39.2	132	11	Q9JKR1
8	171.5	17.7	267	6	O02764
9	154.5	15.9	276	13	Q9DD22
10	153	15.8	300	4	Q93407
11	141.5	14.6	401	11	O08727
12	139.5	14.4	401	11	O08712
13	138.5	14.3	616	4	Q9V6Q6
14	133	13.7	372	4	Q9UHP4
15	133	13.7	401	4	O00300
16	129.5	13.4	655	4	O75509
17	125	12.9	655	11	Q9EP05
18	123	12.7	625	11	O35305
19	122	12.6	107	11	Q9JKE0

20	121	12.5	302	13	Q9PUS0
21	120.5	12.4	459	11	O62327
22	120.5	12.4	482	11	O88734
23	119	12.3	439	4	Q16042
24	115.5	11.9	1371	11	Q9QVW4
25	114.5	11.8	1587	4	O00508
26	114.5	11.8	2906	11	Q9WUH9
27	113.5	11.7	1511	4	O75412
28	112	11.6	152	5	Q9XVX3
29	112	11.6	1637	6	Q9XSV8
30	111.5	11.5	1764	11	O35806
31	111	11.5	1111	5	Q9XWD6
32	111	11.5	1792	13	O57484
33	110.5	11.4	1687	11	O61204
34	110	11.4	1522	5	O22685
35	110	11.4	1698	5	O94438
36	109.5	11.3	164	5	O22048
37	109.5	11.3	4601	5	Q9V383
38	109	11.2	1574	11	O88281
39	107.5	11.1	1833	11	O08999
40	107	11.0	1308	5	O9GPN8
41	107	11.0	3680	5	O9VR08
42	106.5	11.0	870	6	O02660
43	105	10.8	188	5	Q18238
44	105	10.8	2009	5	Q9VXM0
45	105	10.8	2319	11	Q9R172

## ALIGNMENTS

RESULT 1

ID Q95851 PRELIMINARY; PRT; 234 AA.

AC Q95851;

DT 01-MAY-1999 (TRENBLrel. 10, Created)

DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)

DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-99156876; Pubmed-10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor

RT necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AAD19694.1; -

DR InterPro; IPR001368; -

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match

Best Local Similarity 100.0%; Score 969; DB 4; Length 234;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALLCALSIGQRTGGPGGPGRLLLGTGTDARCCRVHTRCCRD 60

|||||

DB 1 MAQHGAMGAFRALCGLALLCALSIGQRTGGPGGPGRLLLGTGTDARCCRVHTRCCRD 60

|||||

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHPCPGGVQSGKFSFGFCIDCASGTF 120

|||||

DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHPCPGGVQSGKFSFGFCIDCASGTF 120

|||||

QY 121 SGGHEGCKPWTDCDTQFGFLTVPFGNKTNAVCPGSPPAEP 162

|||||

DB 121 SGGHEGCKPWTDCDTQFGFLTVPFGNKTNAVCPGSPPAEP 162

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RC STRAIN-CHBB-HM;
RA Isono T., Seto A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00208; TNFR; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 267
FT CHAIN OX40.
SQ SEQUENCE 267 AA; 28489 MW; ABB4CD3173C9500B CRC64;

Query Match 17.7%; Score 171.5; DB 6; Length 267;
Best Local Similarity 32.6%; Pred. No. 1.7e-08;
Matches 59; Conservative 11; Mismatches 74; Indels 37; Gaps 10;

QY 12 ALCGLA-LLCALSLGQRTPGPGC-----GPRLL-----GTGTDARCCRVHTTRCCRD 60
DB 4 AALGLALLLLGLLGAEP--PDCVGDTPGDRCLCQPGYGVNSRNSQDTICHP 61
QY 61 YPG--EECCSEWDCM-CVQ-----PEFHCGDPCCTTCRHHPCPPGQVQSQGKFSFG 109
DB 62 EPGFVNEAVNYOACKPCTQCNRSSGSEPOQECTHTRDTVCR---CRP--GTQPLNGYKKG 116
QY 110 QCIDCASGTFSGHEGCKPWTCTQCGFLTVFGNTHNAV-----VPCSPAE 161
DB 117 VDCAPCPQGHFSEGNRACRPWTNCTLAGKRTLPASSIDAVCEDRSLSLATQPWETPSA 176
QY 162 P 162
DB 177 P 177

RESULT 9
Q9DDD2 PRELIMINARY; PRT; 276 AA.
AC Q9DDD2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE HUMAN CD40-HOMOLOGUE.
GN TNFSF5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tregaskes C.A.;
RL Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
DR EMBL; AJ293700; CAC20218.1; -.
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB8245AE CRC64;

Query Match 15.9%; Score 154.5; DB 13; Length 276;
Best Local Similarity 26.8%; Pred. No. 1.1e-08;
Matches 53; Conservative 10; Mismatches 58; Indels 77; Gaps 11;

QY 16 LALLCALSLGQRTPGPGCG-PGRLLLTGTGDARCC-----VHTTRCC-RDYPGECCSE 69
DB 7 LGLLCALL-----GCGPG-----DAVNCSDKQVEHKRCRCRCPGKKLASE 50
QY 70 -----ND-----CMCVQPEF 79
DB 51 CNDTDSVCTPCNGQVQHSHTKHCPTHEICEDNAGLIVKRHGNATHNTVCQC-RAGM 109
QY 80 HCGDPCCTTC-RHNPCCPPGQC-VOSQGKFSFGFQCIDCASGTFSS--GGHEGCKPWTDTCT 135
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Db 110 HCSDDSCQTCVENEPCKQGFVAAAEARMTSPCEPCAEGTFNSVSSKTEPCHFWTSCB 169
QY 136 QFGFLTVFPNGKTHNAV 153
DB 170 EKGLVVVKVKGTTNTSDVIC 187

RESULT 10
Q95407 PRELIMINARY; PRT; 300 AA.
AC Q95407;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).
GN DCR3 OR TR6 OR TNFRSF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Bolstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD.
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREAS;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104419; AAD03056.1; -.
DR EMBL; AF134240; AAD29688.1; -.
DR EMBL; AF217796; AAF35244.1; -.
DR EMBL; AF217793; AAF33685.1; -.
DR EMBL; AF217794; AAF33686.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR000561; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; -.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AEB33718449AF CRC64;
```

Query Match 15.8%; Score 153; DB 4; Length 300;  
Best Local Similarity 26.3%; Pred. No. 1.7e-08;

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C3H/HEN;
RX  MEDLINE=97322352; PubMed=9177197;
RA  Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RT  Moraca R., Migliorati G., Riccardi C.;
RT  "A new member of the tumor necrosis factor/nerve growth factor
RT  receptor family inhibits T cell receptor-induced apoptosis.";
RL  Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/C;
RA  Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RT  Migliorati G., Riccardi C.;
RT  "Gene structure and chromosomal assignment of GTR, a mouse member of
RT  the tumor necrosis factor/nerve growth factor receptor family.";
RL  Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U82534; AAB81243.1; -.
DR  EMBL; AF109216; AAF14231.1; -.
DR  MGD; MGI:894675; Tnfrsf18.
DR  SMART; IPR000561; -.
DR  SMART; SM00181; EGF; 1.
KW  Signal; Receptor.
FT  SIGNAL 1 19 POTENTIAL.
FT  CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY
FT  RELATED PROTEIN.
SQ  SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 52.2%; Score 506; DB 11; Length 228;
Best Local Similarity 54.5%; Pred. No. 8.8e-46;
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

QY 7 MGAFRALCGALLCALSLGQ-RPTGGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVLDLQGPSVVEEPCGPGKVGQSGNNTGCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCCTTCRHHPGPGQVQSGKFSFGQCIDCASGTFSGGHE 125
DB 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVQSGDIVFGFRVCACAMGTFSGARD 113
QY 126 GHCKPWTCTQFGFLTVFPNGKTHNAVCPGSPPAE 161
DB 114 GHCLWNTCSQFGFLTFMPGKTHNAVCIPEPLPTE 149

RESULT 6
QYJRK3 ID Q9JKR3 PRELIMINARY; PRT; 294 AA.
AC Q9JKR3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RT Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229432; AAF61566.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 52.2%; Score 506; DB 11; Length 294;
Best Local Similarity 54.5%; Pred. No. 8.8e-46;
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

QY 7 MGAFRALCGALLCALSLGQ-RPTGGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVLDLQGPSVVEEPCGPGKVGQSGNNTGCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCCTTCRHHPGPGQVQSGKFSFGQCIDCASGTFSGGHE 125
DB 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVQSGDIVFGFRVCACAMGTFSGARD 113
QY 126 GHCKPWTCTQFGFLTVFPNGKTHNAVCPGSPPAE 161
DB 114 GHCLWNTCSQFGFLTFMPGKTHNAVCIPEPLPTE 149

RESULT 6
QYJRK3 ID Q9JKR3 PRELIMINARY; PRT; 294 AA.
AC Q9JKR3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RT Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229432; AAF61566.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 52.2%; Score 506; DB 11; Length 294;
Best Local Similarity 54.5%; Pred. No. 8.8e-46;
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

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Best Local Similarity 54.5%; Pred. No. 1.1e-45;
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

QY 7 MGAFRALCGALLCALSLGQ-RPTGGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVLDLQGPSVVEEPCGPGKVGQSGNNTGCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCCTTCRHHPGPGQVQSGKFSFGQCIDCASGTFSGGHE 125
DB 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVQSGDIVFGFRVCACAMGTFSGARD 113
QY 126 GHCKPWTCTQFGFLTVFPNGKTHNAVCPGSPPAE 161
DB 114 GHCLWNTCSQFGFLTFMPGKTHNAVCIPEPLPTE 149

RESULT 7
QYJRK1 ID Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE GTR-D.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RT Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61568.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5404BIDFEDE CRC64;

Query Match 39.2%; Score 380; DB 11; Length 132;
Best Local Similarity 50.4%; Pred. No. 1e-32;
Matches 64; Conservative 21; Mismatches 34; Indels 8; Gaps 2;

QY 7 MGAFRALCGALLCALSLGQ-RPTGGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVLDLQGPSVVEEPCGPGKVGQSGNNTGCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCCTTCRHHPGPGQVQSGKFSFGQCIDCASGTFSGGHE 125
DB 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVQSGDIVFGFRVCACAMGTFSGARD 113
QY 126 GHCKPWT 132
DB 114 GHCLWNT 120

RESULT 8
QYJRK1 ID Q02764 PRELIMINARY; PRT; 267 AA.
AC Q02764;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.

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CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
CC PLACENTA. NOT DETECTED IN SPLEEN.
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
CC 15 TO DAY 17.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; U94331; AAB53708.1; -.
DR EMBL; AB013898; BAA28269.1; -.
DR EMBL; AB013903; BAA33388.1; -.
DR EMBL; AB013899; BAA33388.1; JOINED.
DR EMBL; AB013900; BAA33388.1; JOINED.
DR EMBL; AB013901; BAA33388.1; JOINED.
DR EMBL; AB013902; BAA33388.1; JOINED.
DR HSSP; P25942; ICDF.
DR MGD; MG1:109587; Tnfsl1b.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; -.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
DR Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401 OSTEOPROTEGERIN.
FT DOMAIN 23 201. 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).
FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
Query Match 14.48; Score 139.5; DB 11; Length 401;
Best Local Similarity 25.78; Pred. No. 5.8e-07;
Matches 43; Conservative 10; Mismatches 69; Indels 45; Gaps 6;
QY 15 GLALLCALSLGORTGGCGPGRLLLTGTGDARCRVHTTRCCRDYPCGECSSW---- 70
DB 36 CHQLLC-----DKCAPGTYL-----KQCTVRRKTLVCPDPSYDSWHFSD 78
QY 71 DCMCVQP-----EFHCGDPCCPTC-----RHHPCPPEGQVQSGKFSF 108
DB 79 ECVYCSPVCKELQSVKQCNRTNHRVCEEGRYLEIEFLKHKRSCPPGSGVVQAGTPDR 138
QY 109 GFQCIDCASCTFSG--GHEGCHCKPMTDCTQFGFLVFFGNKTHNVC 153
DB 139 NTVCKKCPDGFSGFTSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
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RESULT 13
QY9Y606
ID QY9Y606; PRELIMINARY; PRT; 616 AA.
AC QY9Y606;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
DE INDUCED CYTOKINE RECEPTOR) (RANK).
GN TNFRSF11A OR RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98032977; PubMed-9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
CC GLAND.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC EMBL; AF018253; AAB86809.1; -.
DR HSSP; P25942; ICDF.
DR MIM; 603499; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
DR SMART; SM00208; TNFR; 1.
DR Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 616 RECEPTOR ACTIVATOR OF NF-KAPPA-B.
FT DOMAIN 24 212 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 213 233 POTENTIAL.
FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 195 4 X TNFR-CYS.
FT REPEAT 33 69 TNFR-CYS 1.
FT REPEAT 70 112 TNFR-CYS 2.
FT REPEAT 113 152 TNFR-CYS 3.
FT REPEAT 153 195 TNFR-CYS 4.
FT DISULFID 34 46 BY SIMILARITY.
FT DISULFID 47 60 BY SIMILARITY.
FT DISULFID 50 68 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 92 112 BY SIMILARITY.
FT DISULFID 114 124 BY SIMILARITY.
FT DISULFID 126 133 BY SIMILARITY.
FT DISULFID 127 151 BY SIMILARITY.
FT DISULFID 154 169 BY SIMILARITY.
FT DISULFID 175 194 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;
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Query Match 14.38; Score 138.5; DB 4; Length 616;
Best Local Similarity 24.18; Pred. No. 1.1e-06;
Matches 52; Conservative 14; Mismatches 69; Indels 81; Gaps 10;
QY 11 RALCGLLALCALSLGORTGGCGPGRLLLTGTGDARCCR-----VHTTRCCR-----DY 61
DB 9 RPLFALLLLCALL-----ARLQVALQIAPPCTSEKHVHGLGCCNCKECPGKY 55
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FT	DISULFID	41	54		BY SIMILARITY.
FT	DISULFID	44	62		BY SIMILARITY.
FT	DISULFID	65	80		BY SIMILARITY.
FT	DISULFID	83	97		BY SIMILARITY.
FT	DISULFID	87	105		BY SIMILARITY.
FT	DISULFID	118	142		BY SIMILARITY.
FT	DISULFID	145	160		BY SIMILARITY.
FT	CARBOHYD	98	98		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	165	165		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	178	178		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	289	289		N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	401 AA;	46192 MW; FECSA31FD4E573A CRC64;		

  

Query Match      14.6%    Score 141.5; DB 11; Length 401;  
Best Local Similarity 27.2%; Pred. No. 3.6e-07;  
Matches 46; Conservative 11; Mismatches 63; Indels 49; Gaps

  

Qy	15	GLALLCALSLGORTGGPGCGPGRLLGTGDARCVRHTRC--CRDY-----PCGE 65				:
Db	36	GROLIC-----DKCAPGYL-----KQHCTVRRKTLCVPDPDYSYTDTSWHTSDE 79				:
Qy	66	C-----CSEWD-----CMQVPEFHCGDPCCCTCRHHPPCPGQVSOGKF 106				:
Db	80	CVYCSPVKELQTIVKEQNTHNRVCCEERYLELFEC---LAHRSCPPLGVLAGTP 130				:
Qy	107	SFGQCIDCASGFSG--GHGHCKPWTCDTQCFGLTFVFPGNKTHNVAVC 153		:   :	:   :	
Db	137	ERNIVCKRCPDGFFSGETSSKAPCKRHTNCSSLGILLIKGNATHDNVC 185		:   :	:   :	

  

RESULT 12

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O08712 PRELIMINARY; PRT; 401 AA.
AC O08712: 070202;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DI 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DD OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
(DCIF).
OS MUS musculus OR OPS.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=KIDNEY;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Ra Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W
RA Campbell B., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density."
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/OLA, AND NIH SWISS;
RX MEDLINE=98382527; PubMed=9714833;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
gene and its expression in embryogenesis".
RL Gene 215:339-343(1998).
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
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FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;

Query Match 13.7%; Score 133; DB 4; Length 401;
Best Local Similarity 24.2%; Pred. No. 2.8e-06;
Matches 36; Conservative 14; Mismatches 51; Indels 48; Gaps 6;

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Db 37 HQLLCDKCPPTYLKQHCTAKWTVCACPDPHYTDSWHTSDECLYCSVPCKELQYVQKE 96

Qy 88 -----TC-----RHHPCPPGGVQSQKSFSGFQCIDCAGTFSG--GH 124
Db 97 CNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERTVCKRCPDGGFFSNETSS 156

Qy 125 ECHCKPHTDCTQFGFLTVFPCKNTHNAV 153
Db 157 KAPCRKHTNCSVFGLLLTQKGNATHDNIC 185
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Search completed: September 4, 2001, 16:14:30  
Job time: 1217 sec

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QY 62 PGEECCSEWDCMCVQPEFHCG-----DPC----- 85
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QY 86 -----CTTGRHH-PCPPGQGVQSGKFSGFCQIDCASGTFSGHEG--HCKP 130
Db 112 CACTAGYHNSQDCECCRRNTECAPGLGAQHPLQNLKNDTVCKPCLAGYFSAFSTDKCRP 171
QY 131 WTDCTQFGELTVFPGNKTHNAV-----VPG-SPPAEP 162
Db 172 WTNCFGLGRVHHGTEKSDAVCSSLPARKPPNEP 207

RESULT 14
Q9UHP4
ID Q9UHP4 PRELIMINARY; PRT; 372 AA.
AC Q9UHP4;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA He 2.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL; AF134187; AAF20168.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR000488; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH_1.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 13.7%; Score 133; DB 4; Length 372;
Best Local Similarity 24.2%; Pred. No. 2.6e-06;
Matches 36; Conservative 14; Mismatches 51; Indels 48; Gaps 6;

QY 53 HTRCCRDYPG-----BECCSEWDCMCV-----QPEFHCGDPC--CT----- 87
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QY 88 -----TC-----RHHPCPPGQGVQSGKFSGFCQIDCASGTFSG--GH 124
Db 76 CNRTHNRVCECKRGYLEIEFCLKHSRCPGPGVGQAGTPERNTVCKRCPDGFFSNETSS 135
QY 125 ECHCAKPTDCTQFGELTVFPGNKTHNAV 153
Db 136 KAPCRHNTCSVFGLLLTOKGNATHDNIC 164

RESULT 15
Q00300
ID Q00300 PRELIMINARY; PRT; 401 AA.
AC Q00300; O60236;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPB OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AB021446; BAA25910.1; -
DR EMBL; AB008822; BAA32076.1; -
DR EMBL; AB008821; BAA32076.1; JOINED.
DR EMBL; U94332; AAB53709.1; -
DR HSSP; P25942; ICDF.
DR MIM; 602643; -
DR InterPro; IPR000488; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_C6; 3.
DR PRODOM; PD000771; -; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH_1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 401 OSTEOPROTEGERIN.
FT DOMAIN 23 183 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID -83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:14 ; Search time 12.35 Seconds  
(without alignments)  
390.133 Million cell updates/sec

Title: US-09-512-363-2

Perfect score: 234

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- Issued\_Patents\_AA:\*
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  - 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pap:\*
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  - 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pap:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	193	82.5	241	3	US-08-911-423-4
3	187	79.9	311	3	US-08-911-423-8
4	99	42.3	232	3	US-08-911-423-7
5	11	4.7	228	3	US-08-911-423-2
6	8	3.4	782	1	US-07-725-083-2
7	8	3.4	782	4	US-08-669-286-10
8	8	3.4	782	4	US-09-469-253-10
9	7	3.0	335	2	US-08-289-699A-4
10	7	3.0	335	1	US-08-878-283-4
11	7	3.0	603	4	US-09-097-889-23
12	7	3.0	713	1	US-08-188-228-62
13	7	3.0	713	1	US-08-332-643-56
14	7	3.0	713	1	US-08-332-638-62
15	7	3.0	751	4	US-09-036-987A-24
16	7	3.0	1010	4	US-08-882-046-7
17	7	3.0	1218	2	US-08-400-159-6
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19	7	3.0	1218	4	US-08-882-046-2
20	7	3.0	1219	4	US-08-882-046-5
21	6	2.6	15	4	US-09-077-354B-6
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23	6	2.6	16	3	US-08-793-426A-4
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25	6	2.6	29	1	US-08-376-362A-18
26	6	2.6	34	1	US-08-190-802A-165
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Patent No. 5489533  
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Sequence 3, Appli  
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Sequence 1, Appli  
Sequence 52, Appli  
Sequence 360, App

28 6 2.6 89 4 US-09-188-930-191  
29 6 2.6 93 1 US-08-480-449-2  
30 6 2.6 93 2 US-08-660-542-2  
31 6 2.6 93 2 US-08-660-542-25  
32 6 2.6 93 4 US-09-232-878-6  
33 6 2.6 93 5 PCT-US95-07294-2  
34 6 2.6 134 3 US-09-191-647-12  
35 6 2.6 163 1 US-08-469-667-11  
36 6 2.6 163 5 PCT-US95-07289-11  
37 6 2.6 179 1 US-08-665-966-8  
38 6 2.6 179 3 US-09-041-780-8  
39 6 2.6 185 6 5489533-4  
40 6 2.6 202 1 US-08-048-700-2  
41 6 2.6 202 2 US-08-855-261A-3  
42 6 2.6 202 3 US-08-839-711-3  
43 6 2.6 223 2 US-08-928-612-1  
44 6 2.6 252 3 US-08-513-974B-52  
45 6 2.6 252 3 US-08-513-974B-360

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
;; STREET: 1100 New York Avenue, Suite 600  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/725,083  
;; FILING DATE: 03-JUL-1991  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/353,432  
;; FILING DATE: 18-MAY-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldstein, Jorge A.  
;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0609.2170001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 782 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-07-725-083-2

Query Match 3.4%; Score 8; DB 1; Length 782;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ALLCALS 24  
Db 9 ALLCALS 16

RESULT 7  
US-08-669-286-10  
; Sequence 10, Application US/08669286  
; Patent No. 6130060  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, SEIJI  
; APPLICANT: NAKURAI, TAKASHI  
; APPLICANT: NEZU, JUNI-ICHI  
; TITLE OF INVENTION: GENE ENCODING ADSEVERIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/669,286  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977

;; REFERENCE/DOCKET NUMBER: 230-110P  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 205-8000  
;; TELEFAX: (703) 205-8050  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 782 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-669-286-10

Query Match 3.4%; Score 8; DB 4; Length 782;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ALLCALS 24  
Db 9 ALLCALS 16

RESULT 8  
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; Sequence 10, Application US/09469253  
; Patent No. 6184352  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, SEIJI  
; APPLICANT: SAKURAI, TAKASHI  
; APPLICANT: NEZU, JUNI-ICHI  
; TITLE OF INVENTION: GENE ENCODING ADSEVERIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/469,253  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/669,286  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 230-110P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 782 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-469-253-10

Query Match 3.4%; Score 8; DB 4; Length 782;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MGAFRALCGLLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSQGKFSFGFQIDCASGTFSGGHEG 126  
Db 61 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSQGKFSFGFQIDCASGTFSGGHEG 120  
QY 127 HCKPWTCTQGFGLTVFPGNKTNNVAVCPGPPAPBPLGWLTVVLLAVAAVLLLSAQLG 186  
Db 121 HCKPWTCTQGFGLTVFPGNKTNNVAVCPGPPAPBPLGWLTVVLLAVAAVLLLSAQLG 180  
QY 187 LHIWQLR 193  
Db 181 LHIWQLR 187

RESULT 4  
US-08-911-423-7  
; Sequence 7, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-7

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Best Local Similarity 100.0%; Pred. No. 3.7e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSQGK 99  
RESULT 5  
US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-2

Query Match 4.7%; Score 11; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 0.0045;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 FPGNKTNNVAVC 153  
Db 131 FPGNKTNNVAVC 141

RESULT 6  
US-07-725-083-2  
; Sequence 2, Application US/07725083  
; Patent No. 5407821  
; GENERAL INFORMATION:  
; APPLICANT: Breakfield, Xandra O.  
; APPLICANT: Ozellus, Laurie J.  
; TITLE OF INVENTION: Genetic Diagnosis of Torsion Dystonia  
; NUMBER OF SEQUENCES: 2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-097-889-23

Query Match 3.0%; Score 7; DB 4; Length 603;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 SAQLGLH 188  
Db 224 SAQLGLH 230

RESULT 12  
US-08-188-228-62  
; Sequence 62, Application US/08188228  
; Patent No. 5597725  
; GENERAL INFORMATION:  
; APPLICANT: Suzuki, Shintaro  
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/188,228  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/049,460  
; FILING DATE: 19 APR 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,643  
; FILING DATE: 17 APR 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NO. 5597725and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31340  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 713 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-188-228-62

Query Match 3.0%; Score 7; DB 1; Length 713;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 VLLTSA 183  
Db 16 VLLTSA 22  
RESULT 13  
US-08-332-643-56  
; Sequence 56, Application US/08332643  
; Patent No. 5639634  
; GENERAL INFORMATION:  
; APPLICANT: Suzuki, Shintaro  
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/332,643  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/872,643  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NO. 5639634and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30795  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 713 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-332-643-56

Query Match 3.0%; Score 7; DB 1; Length 713;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 VLLTSA 183  
Db 16 VLLTSA 22

RESULT 14  
US-08-332-638-62  
; Sequence 62, Application US/08332638  
; Patent No. 5646250  
; GENERAL INFORMATION:  
; APPLICANT: Suzuki, Shintaro  
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago

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QY 17 ALLCALS 24
      |||||
Db 9 ALLCALS 16

RESULT 9
US-08-289-699A-4
; Sequence 4, Application US/08289699A
; Patent No. 5695993
; GENERAL INFORMATION:
; APPLICANT: Fukudome, Kenji
; APPLICANT: Esmon, Charles T.
; TITLE OF INVENTION: Cloning and Regulation of an Endothelial
; TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30306-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,699A
; FILING DATE: 12-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
; TELEFAX: (404)873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-289-699A-4

Query Match 3.0%; Score 7; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 GPGRLLL 41
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Db 216 GPGRLLL 222

RESULT 10
US-08-878-283-4
; Sequence 4, Application US/08878283
; Patent No. 5852171
; GENERAL INFORMATION:
; APPLICANT: Fukudome, Kenji
; APPLICANT: Esmon, Charles T.
; TITLE OF INVENTION: Cloning and Regulation of an Endothelial
; TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; STREET: Street
; CITY: Atlanta

Query Match 3.0%; Score 7; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 GPGRLLL 41
      |||||
Db 216 GPGRLLL 222

RESULT 11
US-09-097-889-23
; Sequence 23, Application US/09097889
; Patent No. 6218117
; GENERAL INFORMATION:
; APPLICANT: Heirnsstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT QUANTITATIVELY ALTER DETECTABLE
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,889
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.417
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, FILING DATE: 09-MAR-1998
, CLASSIFICATION: 435
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Stuart, Donald R.
, REGISTRATION NUMBER: 28,479
, REFERENCE/DOCKET NUMBER: 50,608
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (317)337-4816
, TELEFAX: (317)337-4847
, INFORMATION FOR SEQ ID NO: 24:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 751 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: protein
US-09-036-987A-24

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Query Match 3.0%; Score 7; DB 4; Length 751;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels

QY 29 TGGPGCG 35  
Db 364 TGGPGCG 370

Search completed: September 5, 2001, 09:46:36  
Job time: 22 sec

Query Match 3.0%; Score 7; DB 1; Length 713;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 VLLTSA 183  
Db 16 VLLTSA 22

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RESULT 15
US-09-036-987A-24
; Sequence 24, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences LLC Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036.987A

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Qy 181 TSAQLGLHIWQLRKTOLLLEVPSTEDARSCOFFPEERGERSAEKRGRLGLWV 234  
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Db 181 TSAQLGLHIWQLRKTOLLLEVPSTEDARSCOFFPEERGERSAEKRGRLGLWV 234

RESULT 2  
QY505 PRELIMINARY; PRT; 241 AA.  
AC QY505;  
DT 01-NOV-1999 (TremBLrel. 12, Created)  
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)  
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.  
GN TNFRSF18.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,  
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,  
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.,  
RT "Identification of a new member of the tumor necrosis factor family  
and its receptor, a human ortholog of mouse GITR.";  
RL Curr. Biol. 0:0-0(1999).  
DR EMBL; AF125304; AAD22635.1; -.  
DR InterPro; IPR001368; -.  
DR SMART; SM00208; TNFR; 1.  
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 82.5%; Score 193; DB 4; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-184;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQHGMAGAFRALCGLALLCALSGLGQRTGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
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Db 1 MAQHGMAGAFRALCGLALLCALSGLGQRTGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
Qy 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120  
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Db 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120  
Qy 121 SGGHEGCHKPWTDC 193  
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Db 121 SGGHEGCHKPWTDC 193

RESULT 3  
QY9J9 PRELIMINARY; PRT; 255 AA.  
AC QY9J9;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)  
DE GITR-D.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=THYMUS;  
RA Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Riccardi C.,  
RT "Identification of a soluble human GITR splicing (hGITR-D).";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF241229; AAF63506.1; -.  
SQ SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;  
Query Match 57.3%; Score 134; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 1.1e-125;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAQHGMAGAFRALCGLALLCALSGLGQRTGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
|||||  
Db 1 MAQHGMAGAFRALCGLALLCALSGLGQRTGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
Qy 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120  
|||||  
Db 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120  
Qy 121 SGGHEGCHKPWTDC 134  
|||||  
Db 121 SGGHEGCHKPWTDC 134

RESULT 4  
Q9JKR2 PRELIMINARY; PRT; 222 AA.  
AC Q9JKR2;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)  
DE GITR-C.  
GN TNFRSF18.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=THYMUS;  
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
RA Migliorati G., Riccardi C.,  
RT "Identification of three novel mRNA splice variants of GITR.";  
RL Cell Death Differ. 0:0-0(2000).  
DR EMBL; AF229433; AAF61567.1; -.  
DR InterPro; IPR000561; -.  
DR SMART; SM00181; EGF; 1.  
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 4.7%; Score 11; DB 11; Length 222;  
Best Local Similarity 100.0%; Pred. No. 0.007;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 FPGNKTHNAV 153  
|||||  
Db 131 FPGNKTHNAV 141

RESULT 5  
O35714 PRELIMINARY; PRT; 228 AA.  
AC O35714;  
DT 01-JAN-1998 (TremBLrel. 05, Created)  
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)  
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.  
GN TNFRSF18 OR GITR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/HEN;  
RX MEDLINE=97322352; PubMed=9177197;



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:19 ; Search time 22.44 Seconds  
(without alignments)  
1379.651 Million cell updates/sec

Title: us-09-512-363-2

Perfect score: 234

Sequence: 1 MAQHGMAMGAFRALCGLLALC.....EEERGSRAEKGRLGLMW 234

Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 425026 segs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_16.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_unclassified.\*  
13: sp\_vertebrate.\*  
14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	100.0	234	4	Q95851 homo sapien
2	193	82.5	241	4	Q9Y5U5 homo sapien
3	134	57.3	255	4	Q9NYJ9 homo sapien
4	11	4.7	222	11	Q9JKR2 mus musculus
5	11	4.7	228	11	Q35714 mus musculus
6	11	4.7	294	11	Q9JKR3 mus musculus
7	8	3.4	215	5	Q9T2D2 caenorhabdi
8	8	3.4	241	2	O67793 aquifex aeo
9	8	3.4	245	4	O14596
10	8	3.4	260	2	Q9L2D4
11	8	3.4	422	10	Q9LPM8
12	8	3.4	438	14	O39493
13	8	3.4	504	4	O75850
14	8	3.4	509	2	O05457
15	8	3.4	548	2	Q9EWY9
16	8	3.4	829	4	Q9Y5D4
17	8	3.4	932	4	Q9Y5H0
18	7	3.0	69	2	Q9HUV7
19	7	3.0	79	4	Q9Y2Q7 homo sapien

20	7	3.0	93	4	Q9UMM3	Q9umm3 homo sapien
21	7	3.0	106	5	Q9VG89	Q9vg89 drosophila
22	7	3.0	120	2	Q53783	Q53783 streptomyce
23	7	3.0	124	2	Q9FC37	Q9fc37 streptomyce
24	7	3.0	133	1	O58336	O58336 pyrococcus
25	7	3.0	133	1	Q9UYT8	Q9uyt8 pyrococcus
26	7	3.0	144	2	Q91146	Q91146 pseudomonas
27	7	3.0	148	8	Q9G9S8	Q9g9s8 metridia lu
28	7	3.0	172	2	O54470	O54470 serratia ma
29	7	3.0	200	2	Q9I7A2	Q9i7a2 pseudomonas
30	7	3.0	204	2	O9X6Q0	O9x6q0 leptospira
31	7	3.0	213	2	O9PSD5	O9psd5 deinococcus
32	7	3.0	222	4	O14569	O14569 homo sapien
33	7	3.0	222	11	Q9WUE3	Q9wue3 mus musculu
34	7	3.0	233	3	Q9HFL8	Q9hfl8 metarhizium
35	7	3.0	242	10	O9LDY4	O9ldy4 oryza sativ
36	7	3.0	256	2	O31618	O31618 bacillus su
37	7	3.0	261	2	Q9LOW0	Q9low0 streptomyce
38	7	3.0	272	2	Q9RS38	Q9rs38 deinococcus
39	7	3.0	287	8	Q9XLV8	Q9xlv8 dipionema p
40	7	3.0	288	2	O9RYI1	O9ryi1 deinococcus
41	7	3.0	296	10	O9FWE7	O9fwe7 oryza sativ
42	7	3.0	306	6	O9GKE3	O9gke3 oryctolagus
43	7	3.0	315	5	Q9V738	Q9v738 drosophila
44	7	3.0	320	2	Q9ZBX6	Q9zbx6 streptomyce
45	7	3.0	320	2	Q9X7P6	Q9x7p6 streptomyce

#### ALIGNMENTS

RESULT 1

ID O95851 PRELIMINARY; PRT; 234 AA.

AC O95851;

DT 01-MAY-1999 (TREMREL. 10, Created)

DT 01-MAY-1999 (TREMREL. 10, Last sequence update)

DE 01-MAR-2001 (TREMREL. 16, Last annotation update)

DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99156876; PubMed=10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor

RT necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AAD19694.1; -.

DR InterPro; IPR001368; -.

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE 234 AA; 25110 MW; 55D593CD0B1DB45 CRC64;

Query Match 100.0%; Score 234; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.4e-225;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAMGAFRALCGLLALCALSGLQRPYGGCGGPRLLLTGTGTDARCCRVHTTCCRD 60

Db 1 MAQHGMAMGAFRALCGLLALCALSGLQRPYGGCGGPRLLLTGTGTDARCCRVHTTCCRD 60

QY 61 YPEECCSMDCMQVPEFHCGDPCCTTCRHHPCCPGQVQSGKSFQCIDCASGTF 120

Db 61 YPEECCSMDCMQVPEFHCGDPCCTTCRHHPCCPGQVQSGKSFQCIDCASGTF 120

QY 121 SGHEHCHCKPWTDCQTFGLTVFPGNKNVAVCPGSPPAEPLGWLTVVLLAAVACVLL 180

Db 121 SGHEHCHCKPWTDCQTFGLTVFPGNKNVAVCPGSPPAEPLGWLTVVLLAAVACVLL 180

KW Hypothetical protein.  
SQ SEQUENCE 241 AA; 27514 MW; B9432671E3308A77 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 241;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 ALLCALSL 24  
| | | | | | | |  
Db 38 ALLCALSL 45

RESULT 9  
O14596 PRELIMINARY; PRT; 245 AA.  
AC O14596;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
DE FOLATE BINDING PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SALIVARY GLAND;  
RA Verma R.S., Elwood P.C.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF000380; AAB91937.1; -;  
SQ SEQUENCE 245 AA; 26268 MW; BA36B7DB95FC0E20 CRC64;

Query Match 3.4%; Score 8; DB 4; Length 245;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 LTSQQLGL 187  
| | | | | | | |  
Db 177 LTSQQLGL 184

RESULT 10  
Q9L2D4 PRELIMINARY; PRT; 260 AA.  
AC Q9L2D4;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 26.0 KDA PROTEIN.  
GN SC7A8.24C  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Oliver K., Harris D.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
DR EMBL; AL137187; CAB69773.1; -;  
DR InterPro: IPR002781; -;  
DR Pfam: PF01925; DUF81; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 260 AA; 25996 MW; DA0F43E1197BACE1 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 260;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 VLLAVAA 175  
| | | | | | | |  
Db 112 VLLAVAA 119

RESULT 11  
Q9LFM8 PRELIMINARY; PRT; 422 AA.  
AC Q9LFM8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE HYPOTHETICAL 48.6 KDA PROTEIN.  
GN F2I11.180.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,  
RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL360314; CAB96664.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 422 AA; 48570 MW; 31D1BC828F40BC39 CRC64;

Query Match 3.4%; Score 8; DB 10; Length 422;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 VAACVLL 180  
| | | | | | | |  
Db 402 VAACVLL 409

RESULT 12  
O39493 PRELIMINARY; PRT; 438 AA.  
AC O39493;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE GLYCOPROTEIN M.  
GN UL10.  
OS Bovine herpesvirus 1.  
OC Viruses; GSDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_TaxID=10320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-JURA;  
RX MEDLINE=95313343; PubMed=7793062;  
RA Vlcek C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,

RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,  
 RA Moraca R., Migliorati G., Riccardi C.;  
 RT "A new member of the tumor necrosis factor/nerve growth factor  
 RT receptor family inhibits T cell receptor-induced apoptosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,  
 RA Migliorati G., Riccardi C.;  
 RT "Gene structure and chromosomal assignment of GTR, a mouse member of  
 RT the tumor necrosis factor/nerve growth factor receptor family.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U82534; AAB81243.1; -;  
 DR EMBL; AF109216; AAF14231.1; -;  
 DR MGD; MGI:894675; Tnfrsf18.  
 DR InterPro: IPR000561; -;  
 DR SMART; SM00181; EGF; 1.  
 KW SIGNAL 1 19 POTENTIAL.  
 FT SIGNAL 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY  
 FT CHAIN 20 228 RELATED PROTEIN.  
 FT  
 FT  
 SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 4.7%; Score 11; DB 11; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 0.0072;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 FPGNKTTHNAVC 153  
 Db 131 FPGNKTTHNAVC 141  
 |||||

RESULT 6  
 Q9JKR3 PRELIMINARY; PRT; 294 AA.  
 AC Q9JKR3;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE GTR-B.  
 GN TNFRSF18.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
 RA Migliorati G., Riccardi C.;  
 RT "Identification of three novel mRNA splice variants of GTR.";  
 RL Cell Death Differ. 0:0-0(2000).  
 DR EMBL; AF229432; AAF61566.1; -;  
 DR InterPro: IPR000561; -;  
 DR SMART; SM00181; EGF; 1.  
 SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 4.7%; Score 11; DB 11; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 0.0088;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 FPGNKTTHNAVC 153  
 Db 131 FPGNKTTHNAVC 141  
 |||||

RESULT 7  
 Q9T2D2 PRELIMINARY; PRT; 215 AA.  
 AC Q9T2D2;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE R160.6 PROTEIN.  
 GN R160.6  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,  
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RN Nature 368:32-38(1994).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Nelson J., Gattung S.;  
 RT "The sequence of C. elegans cosmid R160.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF099001; AAC68733.1; -;  
 SQ SEQUENCE 215 AA; 24502 MW; 0AAC4FFF7914F65 CRC64;

Query Match 3.4%; Score 8; DB 5; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 VLLAVAAC 176  
 Db 24 VLLAVAAC 31  
 |||||

RESULT 8  
 O67793 PRELIMINARY; PRT; 241 AA.  
 ID O67793;  
 AC O67793;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE HYPOTHETICAL 27.5 KDA PROTEIN.  
 GN AQ\_1986.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VF5;  
 RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus.";  
 RL Nature 392:353-358(1998).  
 DR EMBL; AE000766; AAC07762.1; -;

RT "A set of ordered cosmids and a detailed genetic and physical map for  
RL the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
DR EMBL; AL445503; CAC13089.1; -  
KW Kinase.  
SQ SEQUENCE 548 AA; 58276 MW; 72F37F817FD5D8E9 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 548;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 VLLAVAA 175  
| | | | |  
Db 24 VLLAVAA 31

Search completed: September 5, 2001, 09:47:57  
Job time: 98 sec

RA Letchworth G.J., Schwyzler M.;  
 RT "Nucleotide sequence analysis of a 30-kb region of the bovine  
 RT herpesvirus 1 genome which exhibits a colinear gene arrangement with  
 RT the UL21 to UL4 genes of herpes simplex virus.";

RL Virology 210:100-108(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-JURA;  
 RA Schwyzler M., Paces V., Letchworth G.J., Misra V., Buhk H.J.,  
 RA Lowery D.E., Simard C., Bello L.J., Thiry E., Vilek C.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ004801; CAA06124.1; -;  
 DR InterPro: IPR000785; -;  
 DR Pfam: PF01528; Herpes\_glycop. 1.  
 DR PRINTS: PR00333; HSVINTEGLMP.  
 DR SEQUENCE 438 AA; 45517 MW; 4E7C7FA64FAAEFC7 CRC64;

Query Match 3.4%; Score 8; DB 14; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLLAVAA 175  
 Db 93 VLLAVAA 100  
 |||||

RESULT 13  
 OT5850  
 ID 075850 PRELIMINARY; PRT; 504 AA.  
 AC 075850;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE WUGSC:HJD0751H13.3 PROTEIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Leonard S., Graves T., Strommatt C.;  
 RT "The sequence of Homo sapiens PAC clone DJ0751H13.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.H.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 DR EMBL: AC004877; AAC36300.1; -;  
 DR HSP: P08047; 1SP2.  
 DR InterPro: IPR000822; -;  
 DR Pfam: PF00096; zf-C2H2; 12.  
 DR PRINTS: PR00048; ZINC\_FINGER.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 12.  
 DR SMART: SM00355; ZnF\_C2H2; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.  
 SQ SEQUENCE 504 AA; 55490 MW; F9308169B56DA27B CRC64;

Query Match 3.4%; Score 8; DB 4; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GPGCGPG 37  
 Db 317 GPGCGPG 324  
 |||||

RESULT 14  
 O05457  
 ID 005457 PRELIMINARY; PRT; 509 AA.  
 AC 005457;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE HYPOTHETICAL 53.2 KDA PROTEIN.  
 GN RV3887C OR WTCY15F10.25  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feldwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,  
 RA Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 DR EMBL: Z94121; CAB08087.1; -;  
 DR TuberculList; RV3887c; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 509 AA; 53278 MW; 00F961EAF1C4B1B9 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLLAVAA 175  
 Db 205 VLLAVAA 212  
 |||||

RESULT 15  
 Q9EWY9  
 ID Q9EWY9 PRELIMINARY; PRT; 548 AA.  
 AC Q9EWY9;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE PUTATIVE TWO COMPONENT SYSTEM HISTIDINE KINASE.  
 GN 28CG38.30C.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Saunders D.C., Harris D.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RX MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;

FT Domain 107..113 /note= "conserved domain CD-IV"  
 FT Domain 128..134 /note= "conserved domain CD-V"  
 FT Domain 153..160 /note= "conserved domain CD-VI"  
 FT Domain 176..186 /note= "conserved domain CD-VII"  
 FT Domain 204..209 /note= "conserved domain CD-IX"  
 FT Domain 224..233 /note= "conserved domain CD-X"  
 FT Region 27..36 /note= "epitope-bearing region"  
 FT Region 43..51 /note= "epitope-bearing region"  
 FT Region 59..67 /note= "epitope-bearing region"  
 FT Region 56..64 /note= "epitope-bearing region"  
 FT Region 66..71 /note= "epitope-bearing region"  
 FT Region 99..107 /note= "epitope-bearing region"  
 FT Region 125..133 /note= "epitope-bearing region"  
 FT Region 143..151 /note= "epitope-bearing region"  
 FT Region 156..164 /note= "epitope-bearing region"  
 FT Region 203..211 /note= "epitope-bearing region"  
 FT Region 222..230 /note= "epitope-bearing region"  
 XX WO200050459-A1.  
 XX 31-AUG-2000.  
 XX 23-FEB-2000; 2000WO-US04572.  
 XX 24-FEB-1999; 98US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX Ruben SM, NI J;  
 XX WPI; 2000-572072/53.  
 DR N-PSDB; AAA50304.  
 XX  
 PT Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -  
 PS  
 PS Claim 14(c); Fig 1A-B; 278pp; English.

XX The present sequence is that of human tumor necrosis factor  
 CC receptor-like protein Tril1, a novel 25 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
 CC Tril1 activated NF-kappaB through a TRAF2-mediated mechanism.  
 CC Expression is activation-inducible. The Tril1 ligand is constitutively  
 CC expressed in an endothelial cell line. This suggests that Tril1 and  
 CC its ligand may be involved in activated T-cell trafficking.  
 CC The invention provides Tril1, Tril1SV1 and Tril1SV2 nucleic acids  
 CC (see AAA50304-06) and highly conserved encoded proteins (see  
 CC AAY95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. Tril1, Tril1SV1 and/or Tril1SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an

CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. Tril1, Tril1SV1 and/or Tril1SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognose  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 SQ Sequence 234 AA;  
 Query Match 100.0%; Score 234; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-214;  
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAQHGMGAFRALCGLALLCALSLGQRPTGGPGCGRLILGTGTARCCRVHTTRCRD 60  
 DB 1 maqhgmgafralcgiallcalslgqrptggpgcgrrllgtgtardcrrvhttrcrd 60  
 QY 61 YPGEECCSEWDCMCVQPEFHCGDPCCCTTCRRHPCPPGQGVQSGKFSFGQICDASGTF 120  
 DB 61 ypgeeccsewdcmcvqpefhcgdpcccttcrrhpcppgqgvsgqkfsfgqicdasgtf 120  
 QY 121 SGGHEGHCKPWTDOCTQGFILTFVPGNKTHNAVCPGSPPAEPLGLWTLVLLAAACVLLL 180  
 DB 121 sggheghckpwtddctqgfiltfvpgnkhnavcpgsppaepglwltvllavaacvlll 180  
 QY 181 TSAQLGLHIWOLRKTOLLLEVPPTSDARSCORPEEERGERSAEEKRLGDLW 234  
 DB 181 tsaqlglhiwqlrktolllevpptsdarscqfpeergerersaekrgldlw 234  
 RESULT 2  
 AAY52158  
 ID AAY52158 standard; Protein; 234 AA.  
 XX AC AAY52158;  
 XX DT 01-FEB-2000 (first entry)  
 XX DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.  
 XX KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;  
 KW GTR; growth; differentiation; cell death; immune deficiency disorder;  
 KW Dilgeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
 KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW inflammatory condition.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..25 /label= Signal\_peptide  
 FT Protein 26..234 /label= TR11  
 FT Domain 26..162 /note= "Extracellular domain"  
 FT Domain 163..179 /note= "Transmembrane domain"  
 FT Domain 180..234 /note= "Intracellular domain"  
 XX WO9920758-A1.  
 XX 29-APR-1999.  
 XX 21-OCT-1998; 98WO-US22085.  
 PF

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:14 ; Search time 20.66 Seconds  
(without alignments)  
686.641 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 234  
Sequence: 1 MAQHGMGAFRALGGLALLC.....EEDRGRSAEEKGRGLDLWV 234

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_0601:\*

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- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:\*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT:\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT:\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT:\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT:\*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT:\*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT:\*
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- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT:\*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT:\*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT:\*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT:\*
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- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT:\*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT:\*
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- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT:\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	234	100.0	234	Human tumour necro
2	234	100.0	234	Tumour necrosis fa
3	228	97.4	228	Truncated human 31
4	193	82.5	241	Amino acid sequenc
5	193	82.5	241	Human TNF receptor
6	193	82.5	241	Human protein PRO3
7	193	82.5	241	Human PRO364 prote
8	193	82.5	241	Human tumour necro
9	193	82.5	241	Human PRO364 prote
10	193	82.5	241	Human PRO364 prote
11	193	82.5	241	Human immunostimul

12	193	82.5	241	22	AAB47054	Human PRO364. Hom
13	193	82.5	241	22	AAB50910	Human PRO364 prote
14	193	82.5	241	22	AAB50982	Human angiotensin
15	193	82.5	241	22	AAB53090	Human molecule ass
16	187	79.9	235	21	AAV44825	Human 312C2 protei
17	187	79.9	311	19	AAW37842	Human tumour necro
18	173	73.9	240	21	AAV5881	TRILSV2 amino acid
19	173	73.9	240	21	AAV52160	PRO364-related EST
20	139	59.4	317	22	AAV06645	polypeptide encode
21	138	59.0	316	22	AAB47055	Human tumour necro
22	132	56.4	241	21	AAV95880	TRILSV1 amino acid
23	132	56.4	241	21	AAV52159	Human 312C2 protei
24	99	42.3	232	19	AAW37841	Mouse glucocortic
25	11	4.7	222	19	AAW49018	Mouse glucocortic
26	11	4.7	228	19	AAW49016	Amino acid sequenc
27	11	4.7	228	19	AAW37838	Mouse glucocortic
28	11	4.7	294	19	AAW49017	Amino acid sequenc
29	7	3.0	50	20	AAV11945	Human 5' EST secre
30	7	3.0	61	21	AAV65057	Human 5' EST relat
31	7	3.0	79	19	AAW70320	Secreted protein B
32	7	3.0	79	20	AAV59687	Secreted protein 1
33	7	3.0	79	20	AAV59706	Secreted protein 4
34	7	3.0	120	21	AAB41195	Human ORFX ORF959
35	7	3.0	138	13	AAW26820	CA455 protein. Ze
36	7	3.0	242	21	AAB00040	Human COMP/TSP-1 c
37	7	3.0	297	20	AAV07078	Renal cancer assoc
38	7	3.0	299	22	AAB61485	Murine TANGO 300 e
39	7	3.0	300	21	AAB00041	Human COMP/TSP-2 c
40	7	3.0	307	21	AAG44824	Zea mays protein f
41	7	3.0	312	21	AAG44823	Zea mays protein f
42	7	3.0	341	22	AAB61462	TANGO 300 signal p
43	7	3.0	355	22	AAB50055	Murine Dendritic C
44	7	3.0	361	21	AAB23618	Human secreted pro
45	7	3.0	361	22	AAB61421	Human TANGO 300 pr

#### ALIGNMENTS

RESULT 1  
AAV95879  
ID AAV95879 standard; Protein; 234 AA.  
XX  
AC AAV95879;  
XX  
DT 20-NOV-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-like protein TR11.  
XX  
KW TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antineumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT Protein 26..234 /label= Signal\_peptide  
FT Domain 26..162 /label= Mature\_protein  
FT Domain 163..179 /label= Extracellular\_domain  
FT Domain 180..234 /label= Transmembrane\_domain  
FT Modified-site 146 /label= Intracellular domain  
FT Domain 72..81 /note= "N-glycosylated"  
FT Domain 84..93 /note= "conserved domain CD-II"  
FT Domain 94..99 /note= "conserved domain CD-III"

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RESULT 4
AAW37839
ID AAW37839 standard; Protein; 241 AA.
XX
AC AAW37839;
XX
DT 28-JUL-1998 (first entry)
XX
DE Amino acid sequence of the human 312C2 T cell protein.
XX
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
KW antigen-specific T cell proliferation; cytokine production by T-cell;
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;
KW autoimmune disorders.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..726
FT /*tag= a
FT /product= "human 312C2 protein"
XX
PN WO9806842-A1.
XX
PD 19-FEB-1998.
XX
PF 14-AUG-1997; 97WO-US13931.
XX
PR 07-OCT-1996; 96US-0027901.
PR 16-AUG-1996; 96US-0689943.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Gorman DM, Randall TD, Zlotnik A;
XX
DR WPI; 1998-159534/14.
DR N-PSDB; AAV19153.
XX
PT Isolated 312C2 T cell gene - used to develop products for treating,
PT e.g. cancers, auto-immune disorders, transplantation rejection and
PT other T cell disorders
XX
PS Claim 2; Pages 59-60; 71pp; English.
XX
CC This is the amino acid sequence encoding the human 312C2 T cell
CC protein. The 312C2 proteins are expressed in thymus cells and are
CC induced on T cells and spleen cells following activation. Engagement
CC of 312C2 stimulates proliferation of T cell clones, antigen-specific
CC proliferation and cytokine production by T-cells, and potentiates T
CC cell expansion or apoptosis. The products can be used in the
CC treatment of conditions associated with abnormal physiology or
CC development, including abnormal proliferation, e.g. cancerous
CC conditions or degenerative conditions. They can be used in the
CC regulation or development of haematopoietic cells, e.g. lymphoid cells
CC which affect immunological responses, e.g. autoimmune disorders.
XX
SQ Sequence 241 AA;

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```

Db 121 sggheghckpwtcdtqflltcfpgnktbnacvpgspgpaepglwtvllavaacvlll 180
Qy 181 TSAQLGLHIWQLR 193
Db 181 tsagqlghiwqlr 193
RESULT 5
AAW06605
ID AAY06605 standard; Protein; 241 AA.
XX
AC AAY06605;
XX
DT 26-OCT-1999 (first entry)
XX
DE Human TNF receptor homologue PRO364.
XX
KW PRO364; tumour necrosis factor receptor; human; apoptosis;
KW inflammation; antiinflammatory; NF-KB activation;
KW autoimmune disease; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /note= "signal peptide"
FT Protein 26..241
FT /note= "mature protein"
FT Modified-site 146
FT /note= "N-glycosylated"
FT Domain 162..180
FT /note= "transmembrane domain"
XX
PN WO9940196-A1.
XX
PD 12-AUG-1999.
XX
PF 09-FEB-1999; 99WO-US026642.
XX
PR 09-FEB-1998; 98US-0024087.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;
PI Pitti RM, Wood WI;
XX
DR WPI; 1999-494296/41.
DR N-PSDB; AAX87670.
XX
PT Tumour necrosis factor receptor homologue - useful for, e.g.
PT modulating apoptosis and NF-KB activation and proinflammatory or
PT autoimmune responses
XX
PS Claim 17; Fig 2A; 104pp; English.
XX
CC The present sequence represents human PRO364, a novel member of the
CC tumour necrosis factor receptor family. The sequence was deduced
CC from a bone marrow cDNA clone (see AAX87670). Methods for the
CC recombinant production of PRO364 polypeptides, e.g. in CHO,
CC Escherichia coli or yeast host cells, are provided. Claimed
CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the
CC mature protein) and 26-X of the present sequence, where X is any
CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides
CC are useful for modulating apoptosis, NF-KB activation and
CC proinflammatory or autoimmune responses in mammalian cells
CC (claimed). Chimeric molecules comprising a PRO364 polypeptide
CC fused to a heterologous sequence such as epitope tag or
CC immunoglobulin Fc region are also claimed. PRO364 can be used in
CC assays to identify other proteins or molecules involved in binding
CC interactions. This is useful for identifying inhibitors or
CC agonists of receptor/ligand binding. The PRO364 polypeptides may
CC also be combined with an agent that is cytotoxic, chemotherapeutic

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XX PR 21-OCT-1997; 97US-0063212.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI N1 J, Ruben SM;  
XX DR WPI; 2000-061922/05.  
XX DR N-PSDB; AAZ37762.  
XX PT New tumour necrosis factor receptor-like polypeptides used to, e.g.  
XX PT treat Digeorge syndrome -  
XX PS Claim 14; Fig 1; 167pp; English.  
XX  
CC This is the amino acid sequence of the human tumour necrosis factor  
CC receptor-like protein (TRL1 receptor). The invention relates to TRL1 and  
CC two splice variants TRL1SV1 and TRL1SV2. The nucleotide sequences were  
CC determined by sequencing cloned cDNAs AAZ37765-237766. The TRL1 receptor  
CC and its splice variants show homology to the murine glucocorticoid  
CC induced tumour necrosis factor receptor family-related gene (GIFR).  
CC TRL1, TRL1SV1 and TRL1SV2 polypeptides may be involved in the regulation  
CC of cell-type specific receptor-mediated cell growth, differentiation,  
CC and ultimately, cell death. They can be used for screening for  
CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
CC used for treating a disease state associated with aberrant cell  
CC survival. They can be used for treating immune deficiency disorders,  
CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
CC platelet disorders or wounds resulting from trauma or surgery. They can  
CC also be used to treat heart attacks, strokes, Addison's disease,  
CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
CC hypersensitivity to an antigenic molecule, organ rejection or graft  
CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
CC disease, hyperproliferative disorders, or infections. They can also be  
CC used to repair, replace, or protect tissue damaged by congenital  
CC defects, trauma, age, disease, surgery, including cosmetic plastic  
CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
CC detection, diagnosis and prognosis.  
XX  
SQ Sequence 234 AA;

Query Match 100.0%; Score 234; DB 21; Length 234;  
Best Local Similarity 100.0%; Pred. No. 5.8e-214;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGAMGAFRALCGALLCALSLCQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 maqhgamgafRALCGALLCALSLCQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
QY 61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGGQVSGQKFSFGFCIDCASGTF 120  
DB 61 ypgeeccsewDCMCVQPEFHCGDPCCTTCRRHPCPPGGQVSGQKFSFGFCIDCASGTF 120  
QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTNAVCPVGPSPAPPLGWLTVVLLAAVACVLL 180  
DB 121 sgghegchkpWTCTQFGFLTVFPGNKTNAVCPVGPSPAPPLGWLTVVLLAAVACVLL 180  
QY 181 TSAQLGHIWOLRKLTQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLWV 234  
DB 181 tsaqLgHIWOLRKLTQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLWV 234

RESULT 3

AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX  
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX  
OS Homo sapiens.  
XX  
PN WO9806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 14-AUG-1997; 97WO-US13931.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX (SCHE ) SCHERING CORP.  
XX Gorman DM, Randall TD, Zioltnik A;  
XX WPI; 1998-159534/14.  
XX N-PSDB; AAV19154.  
XX Isolated 312C2 T cell gene - used to develop products for treating,  
XX e.g. cancers, auto-immune disorders, transplantation rejection and  
XX other T cell disorders  
XX  
PS Disclosure; Pages 61-62; 71pp; English.  
XX  
CC This is the amino acid sequence of the truncated human 312C2 T cell  
CC protein from clone\_A8. The 312C2 proteins are expressed in thymus  
CC cells and are induced on T cells and spleen cells following activation.  
CC Engagement of 312C2 stimulates proliferation of T cell clones,  
CC antigen-specific proliferation and cytokine production by T-cells, and  
CC potentiates T cell expansion or apoptosis. The products can be used  
CC in the treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX  
SQ Sequence 228 AA;

Query Match 97.4%; Score 228; DB 19; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.8e-208;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 MGAFRALCGALLCALSLCQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYGEEC 66  
DB 1 mgafralcgALLCALSLCQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYGEEC 66  
QY 67 CSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGGQVSGQKFSFGFCIDCASGTFSGHEG 126  
DB 61 csewDCMCVQPEFHCGDPCCTTCRRHPCPPGGQVSGQKFSFGFCIDCASGTFSGHEG 126  
QY 127 HCKPWTCTQFGFLTVFPGNKTNAVCPVGPSPAPPLGWLTVVLLAAVACVLLTSAQLG 186  
DB 121 hckpWTCTQFGFLTVFPGNKTNAVCPVGPSPAPPLGWLTVVLLAAVACVLLTSAQLG 186  
QY 187 LHWOLRKLTQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLWV 234  
DB 181 lhwOLRKLTQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLWV 228

PD 14-SEP-2000.  
XX PF 02-MAR-2000; 2000WO-US05841.  
XX PR 08-MAR-1999; 99WO-US05028.  
XX PR 10-MAR-1999; 99US-0123618.  
PR 12-MAR-1999; 99US-0123957.  
PR 23-MAR-1999; 99US-0125775.  
PR 12-APR-1999; 99US-0128849.  
PR 20-APR-1999; 99WO-US08615.  
PR 28-APR-1999; 99US-0131445.  
PR 04-MAY-1999; 99US-0132371.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 26-JUL-1999; 99US-014758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
XX  
DR WPI: 2000-572271/53.  
DR N-PSDB; AAC58596.  
XX  
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
XX  
PS Claim 33: Fig 36; 309pp; English.  
XX  
XX The present invention describes sixty four human PRO proteins which can  
CC be used in the treatment of immune related diseases. The human PRO  
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
CC treating and diagnosing immune related disorders. The disorders are  
CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
CC autoimmune or immune-mediated skin diseases, allergic diseases,  
CC immunological diseases of the lung, and transplantation associated

CC diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 241 AA;  
  
Query Match 82.5%; Score 193; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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|||||  
Db 1 maqhgamafralcgiallcalslgqrptggpgcgrllltgttdarcrcrvhtrccrd 60  
|||||  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTCRHHPGPPGGVQSQKFGQFCIDCASGTF 120  
|||||  
Db 61 ypgeccsewdcmcvqpefhcgdpccctcrhpcppggvqsgkfsfgqfcidcasgtf 120  
|||||  
QY 121 SGGHEGHCKEWTDCTQFGFLTVPFGNKTNAVCVPGSPPAEPLGWLTVLLAVAACVLLL 180  
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Db 121 sggheghckpwtcdctqfgfltvfpngkthnavcvpgspgaepigwltvllavaacvlll 180  
|||||  
QY 181 TSAQLGLHIWQLR 193  
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Db 181 tsaqglghlwqlr 193  
|||||  
  
RESULT 8  
AA95895  
ID AAY95895 standard; Protein; 241 AA.  
XX AC AAY95895;  
XX DT 20-NOV-2000 (first entry)  
XX DE Human tumour necrosis factor receptor-like protein TR11 mutein.  
XX KW TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
KW mutant.  
XX OS Homo sapiens.  
XX PN WO200050459-A1.  
XX PD 31-AUG-2000.  
XX PF 23-FEB-2000; 2000WO-US04572.  
XX PR 24-FEB-1999; 99US-0121648.  
PR 13-MAY-1999; 99US-0134172.  
PR 16-JUL-1999; 99US-0144076.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Ni J;  
XX WPI: 2000-572072/53.  
XX Human tumor necrosis factor receptor-like proteins useful for  
PT diagnosis, prevention and treatment of disease states associated with  
PT aberrant cell survival such as autoimmune disease and rheumatoid  
PT arthritis -  
XX Disclosure; 294-295; 278pp; English.  
XX The present sequence is that of human tumour necrosis factor  
CC receptor-like protein TR11 (see also AAY95879), a novel protein



XX Human PRO364 protein.  
 DE  
 KW PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;  
 KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
 KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
 KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;  
 KW tumour necrosis factor receptor; GTR protein homologue.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Location/Qualifiers  
 FH Key 1..25  
 FT Peptide /label= Signal\_peptide  
 FT Modified-site 5..11  
 FT /note= "N-myristoylation site"  
 FT Modified-site 8..14  
 FT /note= "N-myristoylation site"  
 FT Modified-site 25..31  
 FT /note= "N-myristoylation site"  
 FT Protein 26..241  
 FT /label= Mature\_PRO364\_protein  
 FT Modified-site 30..36  
 FT /note= "N-myristoylation site"  
 FT Modified-site 33..39  
 FT /note= "N-myristoylation site"  
 FT Modified-site 118..124  
 FT /note= "N-myristoylation site"  
 FT Modified-site 122..128  
 FT /note= "N-myristoylation site"  
 FT Modified-site 146..150  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 156..162  
 FT /note= "N-myristoylation site"  
 FT Domain 163..183  
 FT /label= Transmembrane\_domain  
 FT Binding-site 166..177  
 FT /note= "Prokaryotic membrane lipoprotein lipid attachment site"  
 FT Region 171..193  
 FT /note= "Leucine zipper pattern"  
 XX  
 PN WO200032778-A2.  
 XX  
 XX 08-JUN-2000.  
 XX  
 XX 30-NOV-1999; 99WO-US28409.  
 XX  
 XX 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 22-DEC-1998; 98US-0113296.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
 XX WPI: 2000-412325/35.  
 DR N-PSDB; AAD01240.  
 XX  
 XX New composition useful for inhibiting neoplastic cell growth and for  
 PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
 PT their antagonists  
 XX  
 XX Claim 31; Fig 4; 108pp; English.  
 XX  
 XX The present sequence is the human PRO364 protein, encoded by the cDNA  
 CC clone, designated as DNA47365-1206. It is isolated from human small  
 CC intestine tissue cDNA library, identified using probes based on the  
 CC consensus sequence DNA4825, relative to the Incyte expressed sequence  
 CC tag (EST) 3003460. This EST has homology to tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows

CC homology to members of the TNFR family and mouse GTR protein.  
 CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as  
 CC a neoplastic cell growth inhibitor and is used for treating tumours,  
 CC using an effective amount of PRO655, PRO364 and PRO344. This composition  
 CC is especially useful for treatment of human cancers such as breast,  
 CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.  
 XX  
 XX Sequence 241 AA;  
 XX  
 Query Match 82.5%; Score 193; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAQHAGAFRALCGLALCALSLGQRTGGPGCGPRLLLGTCDARCCRVHTCCRD 60  
 DB 1 maqhgangafralcgiallcalalslgrptggpgcgrflllgtdarccrvhtccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTCRHHPCCPGQGVQSGKFSFGQCIDCASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpccctcrhpcppgvgvsgkfsfgqcidcasgtf 120  
 QY 121 SGGHEGHCKPWTCTQFGFLTVFPNGKTHNAVCPGSPPAEPGLWTLVLLAVACVLL 180  
 DB 121 sggheghckpwtcdctgftvfpngkthnavcvpgspapiepigtvllavacvll 180  
 QY 181 TSAQLGLHIWQLR 193  
 DB 181 tsaqlglhiwqlr 193  
 RESULT 11  
 AAB20115  
 ID AAB20115 standard; Protein; 241 AA.  
 XX  
 AC AAB20115;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Human immunostimulant PRO364.  
 XX  
 KW PRO364; UNQ319; human; immune disease; autoimmune disease;  
 KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
 KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
 KW hepatotropic; virucide; dermatological; antipsoriatic;  
 KW antiasthmatic; antiallergic; immunostimulant.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Location/Qualifiers  
 FH Key 1..25  
 FT Peptide /label= Signal\_peptide  
 FT Protein 26..241  
 FT Domain 163..183  
 FT /note= "Transmembrane domain"  
 FT Modified-site 5..11  
 FT /note= "N-myristoylation site"  
 FT Modified-site 8..14  
 FT /note= "N-myristoylation site"  
 FT Modified-site 25..31  
 FT /note= "N-myristoylation site"  
 FT Modified-site 30..36  
 FT /note= "N-myristoylation site"  
 FT Modified-site 33..39  
 FT /note= "N-myristoylation site"  
 FT Modified-site 118..124  
 FT /note= "N-myristoylation site"  
 FT Modified-site 122..128  
 FT /note= "N-myristoylation site"  
 FT Modified-site 156..162  
 FT /note= "N-myristoylation site"  
 FT Modified-site 146..150

CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved Tril1, TrilSV1 and TrilSV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. Tril1, TrilSV1 and/or TrilSV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. Tril1, TrilSV1 and/or TrilSV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGPGCGPGRLLLTGTGTDARCCRVHTTRCCRD 60  
 |||||  
 Db 1 maqhgamafralcgallcalcslsigrptggpgcgprlllgtgttdarccrvhttrccrd 60  
 |||||

QY 61 YPGEECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGGVGSQGFSGFCIDCASGTF 120  
 |||||  
 Db 61 ypgeccsewdcmcvqpefhcgdpccctcrhhpcppggvgvsgqkfsfgfcidcasgtf 120  
 |||||

QY 121 SGGHEGCHKPWTDCDTQFGFLTVFPGNKTHNAVCPGSPPAEPLGWLTVLLAVACVLL 180  
 |||||  
 Db 121 sggheghckpwtcdctqfgfltvfpgnkthnavcvpgspppaeplgwltvllavaacvll 180  
 |||||

QY 181 TSAQLGLHIWQLR 193  
 |||||  
 Db 181 tsqqlglhiwqlr 193  
 |||||

RESULT 9  
 AAB24409  
 ID AAB24409 standard; Protein; 241 AA.  
 XX  
 AC AAB24409;  
 XX  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO364 protein sequence SEQ ID NO:117.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX WPI; 2000-412154/35.  
 DR N-PSDB; AAA77604.  
 DR  
 XX  
 PT Nucleic acids encoding PRO polypeptides useful for preventing,  
 PT diagnosing and treating diagnosing a cardiovascular, endothelial or  
 PT angiogenic disorders in mammals -  
 XX  
 PS Claim 72; Fig 44; 315pp; English.  
 XX  
 CC The present invention describes nucleic acids encoding PRO polypeptides  
 CC useful for preventing, diagnosing and treating diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder in mammals by  
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
 CC and for identifying agonists and antagonists of these processes. The  
 CC nucleic acids and the proteins they encode may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PRO expression such as cardiovascular, endothelial or  
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and  
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors  
 CC containing them and the PRO polypeptide may be used to treat disorders  
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
 CC the exemplification of the present invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGPGCGPGRLLLTGTGTDARCCRVHTTRCCRD 60  
 |||||  
 Db 1 maqhgamafralcgallcalcslsigrptggpgcgprlllgtgttdarccrvhttrccrd 60  
 |||||

QY 61 YPGEECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGGVGSQGFSGFCIDCASGTF 120  
 |||||  
 Db 61 ypgeccsewdcmcvqpefhcgdpccctcrhhpcppggvgvsgqkfsfgfcidcasgtf 120  
 |||||

QY 121 SGGHEGCHKPWTDCDTQFGFLTVFPGNKTHNAVCPGSPPAEPLGWLTVLLAVACVLL 180  
 |||||  
 Db 121 sggheghckpwtcdctqfgfltvfpgnkthnavcvpgspppaeplgwltvllavaacvll 180  
 |||||

QY 181 TSAQLGLHIWQLR 193  
 |||||  
 Db 181 tsqqlglhiwqlr 193  
 |||||

RESULT 10  
 AAY71467  
 ID AAY71467 standard; Protein; 241 AA.  
 XX  
 AC AAY71467;  
 XX  
 DT 08-NOV-2000 (first entry)

CC cardiovascular, endothelial, angiogenic or angiostatic disorder. The  
CC PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)  
CC database as having homology to members of the tumour necrosis factor  
CC receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
CC isolated from a library of cDNA fragments derived from human umbilical  
CC vein endothelial cells (HUVEC). Administering an effective amount of  
CC PRO364 or PRO175 or their antagonists is useful for treating cardiac  
CC hypertrophy (which is initiated by myocardial infarction and  
CC trauma, a cancer, or age-related macular degeneration in a human).  
CC Administering a therapeutically effective amount of an antibody that  
CC binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
CC by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
CC disorder. PRO364 or PRO175, or their antagonists, are useful for the  
CC vascular-related drug targeting or as therapeutic targets for the  
CC treatment or prevention of atherosclerosis, hypertension, inflammatory  
CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
CC and treatment of lung or liver fibrosis, periodontal diseases,  
CC attraction of bone-forming cells, central and peripheral nervous  
CC system disease and neuropathies and rheumatoid arthritis.  
XX  
SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLLALCALSLGQRPFGCGGGRLLLTGTGTCARCRVHTTCRCD 60  
DB 1 maqhgmgafraicgllalcalcslgrptggpgcgprlllgtgdarcrcvhttrcd 60

QY 61 YPGEECCSEWDCMVCQPEFHGCDPCCTTCRHHPCPGQGVQSGKSFQPCIDCASGTF 120  
DB 61 ypgееccsewdcmvcqpєfhgсdpccttcrrhhpcpgqgvqsgkfsfqіcdcasgtf 120

QY 121 SGHGHGCKPWTDCQTQGFLLTFPPGNKTHNAVCPGSPPAEPLGWLTVLLAVAAACVLL 180  
DB 121 sghghgckpwtcdqtfqfltfppgnkthnavcvpgsppeaplgwltvllavaacvll 180

QY 181 TSAQGLLHTWQLR 193  
DB 181 tsaqglhlwqlr 193

RESULT 13  
ID AAB50910 standard; Protein; 241 AA.  
XX AAB50910;  
XX 21-MAR-2001 (first entry)  
XX Human PRO364 protein.  
XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
KW antidiabetic; nontropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antiasthmatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy.  
XX  
OS Homo sapiens.  
XX  
XX WO200073452-A2.  
XX 07-DEC-2000.  
XX  
XX 02-JUN-2000; 2000WO-US15264.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144732.  
PR 20-JUL-1999; 99US-0144758.

PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 09-DEC-1999; 99US-0170262.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
XX WPI; 2001-025253/03.  
XX N-PSDB; AAC91469.  
XX  
XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
PT in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -  
XX  
XX Claim 58; Fig 18; 218pp; English.  
XX  
XX The present sequence is one of thirty three novel PRO polypeptides.  
CC The PRO polypeptides, anti-PRO antibodies, agonists and  
CC antagonists are useful for treating and diagnosing immune related  
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.  
XX  
XX Sequence 241 AA;

Query Match 82.5%; Score 193; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLLALCALSLGQRPFGCGGGRLLLTGTGTCARCRVHTTCRCD 60  
DB 1 maqhgmgafraicgllalcalcslgrptggpgcgprlllgtgdarcrcvhttrcd 60

FT Peptide /note= "Asn is N-glycosylated"  
FT 166..177 /note= "prokaryotic membrane lipoprotein lipid  
FT attachment site"  
FT Peptide 171..193  
FT /note= "leucine zipper pattern"  
FN W0200105972-A1.  
XX  
XX  
XX 25-JAN-2001.  
XX  
XX 15-MAR-2000; 2000WO-US06884.  
XX  
XX 20-JUL-1999; 99US-0144758.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
XX Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
XX Wood WI;  
XX WPI: 2001-103149/11.  
XX N-PSDB; AAF30057.  
XX  
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
XX diagnosing and treating immune-related disorders, such as multiple  
XX sclerosis, rheumatoid arthritis and diabetes -  
XX  
XX Claim 20; Fig 16; 127pp; English.  
XX  
XX The present sequence is that of novel human immunomodulator PRO364  
XX (UNQ319), as deduced from cDNA (see AAF30057) isolated from a  
XX small intestine library. PRO364 (26 kDa, pI 6.34) shows sequence  
XX homology to mouse GITR protein and may be its human counterpart.  
XX The invention provides polynucleotides (see AAF30050-62) encoding  
XX novel human PRO proteins (see AAF30050-62) including PRO364.  
XX Claimed compositions comprising these proteins or their agonists  
XX are useful for increasing infiltration of inflammatory cells into  
XX a tissue of a mammal, stimulating or enhancing an immune  
XX response, or increasing the proliferation of T-lymphocytes in a  
XX mammal in response to an antigen. Claimed compositions comprising  
XX a PRO polypeptide or its antagonist have the opposite effect. A  
XX claimed method for treating an immune related disorder, such as a T  
XX cell disorder, involves administering a PRO polypeptide, an agonist  
XX antibody or an antagonist antibody. The disorder is selected from  
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
XX juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
XX thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated  
XX renal disease, demyelinated diseases (such as multiple sclerosis),  
XX autoimmune chronic active hepatitis, primary biliary cirrhosis,  
XX granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
XX disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
XX enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
XX (such as bullous skin disease, erythema multiforme and psoriasis),  
XX allergic diseases (such as asthma, allergic rhinitis, atopic  
XX dermatitis, food hypersensitivity and urticaria), immunologic  
XX diseases of the lung and transplantation associated diseases (such  
XX as graft rejection and graft-versus-host disease) (all claimed).  
XX Claimed methods of diagnosing these disorders comprise detecting  
XX the level of expression of the PRO gene. Also claimed are a method  
XX of identifying a compound capable of inhibiting the expression or  
XX activity of the PRO polypeptide, vectors, host cells, antibodies,  
XX and a method of stimulating the proliferation of T lymphocytes  
XX using PRO364.  
SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGIALCALSLGQRTGGCGGPRLLLLGTGTDAACRVHTTRCCRD 60  
DB 1 maqhgmgafralcglialcalslgrptggpgcpgprlllgtgtdarccrvhttrccrd 60  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCCPPGQGVQSGQKFSFGQCIDCASGTF 120  
DB 61 ypgeccsewdcmcvqpefhcgdpcccttcrrhnpccppggvgvgqgkfsfgfcidcasgtf 120  
QY 121 SGGHEGCHKPWTDCQTQFGFLTVFPGNKTHNAVCPGSPPAEPLGWLTVLLAVAAACVLLL 180  
DB 121 sghegchkpwtcdtqfgfltvfpngkthnavcvsppaepglwltvllavaacvlll 180  
QY 181 TSAQLGLHIWQLR 193  
DB 181 tsaqglhiwqlr 193  
RESULT 12  
AAB47054  
ID AAB47054 standard; Protein; 241 AA.  
XX  
XX AC AAB47054;  
XX  
XX DT 08-MAY-2001 (first entry)  
XX  
XX DE Human PRO364.  
XX  
XX KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
KW hGIRL; ligand; hGIRL; PRO175; tumor necrosis factor receptor; TNFR;  
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
KW myocardial infarction; PCF-2alpha; trauma; cancer; angiogenesis;  
KW age-related macular degeneration; antibody; periodontal disease;  
KW vascular-related drug targeting; atherosclerosis; hypertension;  
KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.  
XX  
XX OS Homo sapiens.  
XX  
XX FH Key Location/Qualifiers  
FT Peptide 1..26 /note= "Potential signal peptide"  
FT Modified-site 146 /note= "N-glycosylated"  
FT Domain 162..180 /note= "Potential transmembrane domain"  
XX  
XX WO200103720-A2.  
XX  
XX PD 18-JAN-2001.  
XX  
XX PF 11-JUL-2000; 2000WO-US18867.  
XX  
XX PR 12-JUL-1999; 99US-0143304.  
XX  
XX PA (GETH ) GENENTECH INC.  
XX  
XX PI Williams PM, Gerritsen ME;  
XX  
XX DR WPI: 2001-138257/14.  
XX N-PSDB; AAC85433.  
XX  
XX Composition for diagnosing and treating cardiovascular, endothelial and  
XX angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -  
XX  
XX PS Claim 1; Fig 1; 76pp; English.  
XX  
XX CC This sequence represents PRO364 polypeptide, which is a human gluco-  
XX corticoid-induced tumor necrosis factor receptor (hGIRL). The  
XX corresponding ligand (hGIRL), PRO175, is given in AAB47056.  
XX PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
XX endothelial, angiogenic or angiostatic agent for the treatment of a





QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSOGKFSFGQCIDCASGTF 120  
|||||  
Db 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppggvgqgkfsfgqcidcasgtf 120  
  
QY 121 SGGHEGCHKPWTDCQFGFLTFVPGNKTNAVCVPGSPPAEPLGWLTVVLLAVAAACVLLL 180  
|||||  
Db 121 sgghegchckpwtcdtqfgfltfvpgnktnavcvpgspppaepglwltvllavaacvlll 180  
  
QY 181 TSAQLGLHIWQLR 193  
|||||  
Db 181 tsaqglhiwqlr 193  
  
RESULT 14  
AAB50982  
ID AAB50982 standard; Protein; 241 AA.  
XX  
AC AAB50982;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Human PRO364 protein.  
XX  
KW Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;  
KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
KW vulnerary; antianginal; gene therapy; cardiovascular disease;  
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
KW wound healing.  
XX  
OS Homo sapiens.  
XX  
PN WO200073445-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 17-MAY-2000; 2000WO-US13705.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gertitsen ME;  
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2001-025251/03.  
DR N-PSDB; AAC90566.  
XX  
PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
PT disorders in a mammal -  
XX  
PS Claim 71; Fig 8; 182pp; English.  
XX  
CC The present sequence is one of seventeen novel PRO polypeptides. The PRO

CC nucleic acids, polypeptides, agonists and antagonists are useful for  
CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
CC antagonists are also used to prevent tumour angiogenesis and for treating  
CC periodontal diseases. They are also used to stimulate wound healing and  
CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
XX angiogenic disorder.  
SQ Sequence 241 AA;  
  
Query Match 82.5%; Score 193; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAQHGAMGAFRALCGIALCALSLGQRPCTGGPGCGPGRLLLTGTGDARCRVHTTRCCRD 60  
|||||  
Db 1 maqhgamgafralcglallcalslgqrptggpgcprlllgtgdarccrvhttrccrd 60  
  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSOGKFSFGQCIDCASGTF 120  
|||||  
Db 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppggvgqgkfsfgqcidcasgtf 120  
  
QY 121 SGGHEGCHKPWTDCQFGFLTFVPGNKTNAVCVPGSPPAEPLGWLTVVLLAVAAACVLLL 180  
|||||  
Db 121 sgghegchckpwtcdtqfgfltfvpgnktnavcvpgspppaepglwltvllavaacvlll 180  
  
QY 181 TSAQLGLHIWQLR 193  
|||||  
Db 181 tsaqglhiwqlr 193  
  
RESULT 15  
AAB53090  
ID AAB53090 standard; Protein; 241 AA.  
XX  
AC AAB53090;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Human angiogenesis-associated protein PRO364, SEQ ID NO:142.  
XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.



---

CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof.  
 CC PRO nucleic acids, PRO proteins, or an agonist or antagonist thereof.  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to  
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
 CC animals useful for the development and screening of potential  
 CC therapeutic agents. The present sequence represents a PRO protein of the  
 CC invention.

XX  
 SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 22; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGANGAFRALCGLALCALSLGQRTGPGCGPGRLLILGTGTARCCRVHTRCCRD 60  
 DB 1 maqhgangafralcglaalcalslgqrptgpgcgprllilgtgtardccrvhtrccrd 60  
 QY 61 YPGEECCSEWDCMCVQPEFHCGDPCCCTTCRRHPPCPGQGVQSGKFSFGFCIDCASGTF 120  
 DB 61 ypgееccsewdcmcvqpefhcgdpcccttcrrhppcgpggvsgqkfsfgfcidcasgtf 120  
 QY 121 SGHGEHCKPWTCTQGFGLTVFPGNKNHNAVCPGSPAPLGLWLTVLLAVAACVLL 180  
 DB 121 sghgehckpwtctqgfgltvfpgnknhnavcpgspaplgwltvllavaacvll 180  
 QY 181 TSAQLGLHIWQL-----BKTOLLLEVPPTEDARSCQFPEEERGSAAEKGRLGLDW 233  
 DB 181 tsqqlglhiwqlsqmwpretqlillevppstedarscqfpeeeergersaeekgrlglw 240  
 QY 234 V 234  
 DB 241 V 241

RESULT 15  
 AAW37840  
 ID AAW37840 standard; Protein; 228 AA.

XX AAW37840;

XX 28-JUL-1998 (first entry)

XX Truncated human 312C2 protein from clone\_A8 amino acid sequence.

XX Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.

OS Homo sapiens.

XX W09806842-A1.

XX 19-FEB-1998.

XX 14-AUG-1997; 97WO-US13931.

XX

PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX (SCHE ) SCHERING CORP.  
 XX Gorman DM, Randall TD, Zlotnik A;  
 XX WPI; 1998-159534/14.  
 DR N-PSDB; AAV19154.  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX Disclosure; Pages 61-62; 71pp; English.  
 XX This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone\_A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.

XX SQ Sequence 228 AA;

Query Match 97.6%; Score 1308; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-98;  
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGLALCALSLGQRTGPGCGPGRLLILGTGTARCCRVHTRCCRDYPGEEC 66  
 DB 1 mgafralcglaalcalslgqrptgpgcgprllilgtgtardccrvhtrccrdypgeec 60  
 QY 67 CSEWDCMCVQPEFHCGDPCCCTTCRRHPPCPGQGVQSGKFSFGFCIDCASGTFSGGHEG 126  
 DB 61 csewdcmcvqpefhcgdpcccttcrrhppcgpggvsgqkfsfgfcidcasgtsfggheg 120  
 QY 127 HCKPWTCTQGFGLTVFPGNKNHNAVCPGSPAPLGLWLTVLLAVAACVLLLSAQIG 186  
 DB 121 hckpwtctqgfgltvfpgnknhnavcpgspaplgwltvllavaacvllltsaig 180  
 QY 187 LHIWQLRKTOLLLEVPPTEDARSCQFPEEERGSAAEKGRLGLDW 234  
 DB 181 lhiwqlrktqlillevppstedarscqfpeeeergersaeekgrlglw 228

Search completed: September 4, 2001, 15:56:21  
 Job time: 338 sec

PF 17-MAY-2000; 2000WO-US13705.  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI: 2001-025251/03.  
 DR N-PSDB; AAC90566.  
 XX  
 XX Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 PT disorders in a mammal -  
 XX  
 XX Claim 71; Fig 8; 182pp; English.  
 PS  
 CC The present sequence is one of seventeen novel PRO polypeptides. The PRO  
 CC nucleic acids, polypeptides, agonists and antagonists are useful for  
 CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
 CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
 CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
 CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
 CC antagonists are also used to prevent tumour angiogenesis and for treating  
 CC periodontal diseases. They are also used to stimulate wound healing and  
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder.  
 XX  
 SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 22; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

Qy 1 MAQHGAMGAFRALCGALLCALSLGQRTGGCGGGRLLLTGTGDARCCRVHTTRCCRD 60  
 Db 1 maqhgamafraloglallcalslgrptggpggrlllgtgdarccrvhttrccrd 60

Qy 61 YPGECCEWCMQVQPFHCGDPCCTTCRHHPCPGQVQSGKFSFGQIDCASGTF 120  
 Db 61 ypgecccewcmqvqpfhcgdpcttcrhhpcppggvgvggkfsfgqidcasgtf 120

Qy 121 SGGHEGHCKPTDCQFGFLTFPCGNKTHNVCVPGSPAPLGMVTVLLVAACVLL 180  
 Db 121 sggheghckpctdcqfgfltfvpgnktmncvcpvpgspapelpglvllvllaacvll 180

Qy 181 TSAQLGLHIWQL-----RKTQLLEVPPTSTEDARSCQFPPEERGSAEKGRLGDLW 233  
 Db 181 tsaqglghlwlrsqcmwpretklllevpptstedsarscfpeergsaeekegrlgdlw 240

QY 234 V 234  
 Db 241 V 241

RESULT 14  
 AAB53090  
 ID AAB53090 standard; Protein; 241 AA.  
 AC  
 XX AAB53090;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Human angiogenesis-associated protein PRO364, SEQ ID NO:142.  
 XX  
 KW Human: angiogenesis-associated protein; PRO: endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053753-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 05-JAN-2000; 2000WO-US00219.  
 XX  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI: 2001-090793/10.  
 DR N-PSDB; AAC97479.  
 XX  
 PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or  
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
 XX  
 PS Claim 69; Fig 54; 293pp; English.  
 CC  
 CC The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity; diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated  
 CC renal disease, demyelinated diseases (such as multiple sclerosis),  
 CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
 CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
 CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
 CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
 CC (such as bullous skin disease, erythema multiforme and psoriasis),  
 CC allergic diseases (such as asthma, allergic rhinitis, atopic  
 CC dermatitis, food hypersensitivity and urticaria), immunologic  
 CC diseases of the lung and transplantation associated diseases (such  
 CC as graft rejection and graft-versus-host disease) (all claimed).  
 CC Claimed methods of diagnosing these disorders comprise detecting  
 CC the level of expression of the PRO gene. Also claimed are a method  
 CC of identifying a compound capable of inhibiting the expression or  
 CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
 CC and a method of stimulating the proliferation of T lymphocytes  
 CC using PRO364.  
 XX

SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 22; Length 241;  
 Best Local Similarity 96.7%; Pred. NO. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMAGAFRALCALGLALCALSGORPTGGCGPGRLLLTGTDAACRVRHTRCCRD 60  
 DB 1 maqhgamaafRALCALGLALCALSGORPTGGCGPGRLLLTGTDAACRVRHTRCCRD 60  
 QY 61 YPGEECCSEWDCMCVQPFHCGDPCTCTCRHHPCPGPGVQSGKFSFGQICDASGTF 120  
 DB 61 ypgeeccsewDCMCVQPFHCGDPCTCTCRHHPCPGPGVQSGKFSFGQICDASGTF 120  
 QY 121 SGGHEGCHKPWTCTQFGFLTVFPNGKTHNAVCPGSPPAEPLGWLTVLLAVAACVLL 180  
 DB 121 sgghegchkpWTCTQFGFLTVFPNGKTHNAVCPGSPPAEPLGWLTVLLAVAACVLL 180  
 QY 181 TSAQLGLHIWOL-----RKLTQLLEVPSTEDARSCQFPEEGERSAEKGRLGDLW 233  
 DB 181 tsqLGLHIWOL-----RKLTQLLEVPSTEDARSCQFPEEGERSAEKGRLGDLW 240  
 QY 234 V 234  
 DB 241 V 241

RESULT 11  
 AAB47054  
 ID AAB47054 standard; Protein; 241 AA.

XX AAB47054;

XX 08-MAY-2001 (first entry)

XX Human PRO364.

XX PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
 KW hGTR; ligand; hGTR; PRO175; tumor necrosis factor receptor; TNFR;  
 KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
 KW myocardial infarction; PGF<sub>2</sub>alpha; trauma; cancer; angiogenesis;  
 KW age-related macular degeneration; antibody; periodontal disease;  
 KW vascular-related drug targeting; atherosclerosis; hypertension;  
 KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
 KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
 KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..26

FT /note= "Potential signal peptide"

FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 XX /note= "Potential transmembrane domain"

PN WO200103720-A2.

PD 18-JAN-2001.

XX 11-JUL-2000; 2000WO-US18867.

XX 12-JUL-1999; 99US-0143304.

XX (GETH ) GENENTECH INC.

XX Williams PM, Gerritsen ME;

XX WPI; 2001-138257/14.

DR N-PSDB; AAC85433.

XX Composition for diagnosing and treating cardiovascular, endothelial and  
 PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -

PS Claim 1; Fig 1; 76pp; English.

CC This sequence represents PRO364 polypeptide, which is a human gluco-  
 CC corticoid-induced tumor necrosis factor receptor (hGTR). The  
 CC corresponding ligand (hGTRL), PRO175, is given in AAB47056.

CC PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
 CC endothelial, angiogenic or angiotensin agent for the treatment of a  
 CC cardiovascular, endothelial, angiogenic or angiotensin disorder. The  
 CC PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)

CC database as having homology to members of the tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
 CC isolated from a library of cDNA fragments derived from human umbilical  
 CC vein endothelial cells (HUVEC). Administering an effective amount of  
 CC PRO364 or PRO175 or their antagonists is useful for treating cardiac  
 CC hypertrophy (which is initiated by myocardial infarction and

CC characterized by the presence of an elevated level of PGF<sub>2</sub>alpha),

CC trauma, a cancer, or age-related macular degeneration in a human.

CC Administering a therapeutically effective amount of an antibody that  
 CC binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
 CC by PRO364 or PRO175 in a human suffering from a tumor or a retinal

CC disorder. PRO364 or PRO175, or their antagonists, are useful for  
 CC vascular-related drug targeting or as therapeutic targets for the

CC treatment or prevention of atherosclerosis, hypertension, inflammatory  
 CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
 CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration

CC and treatment of lung or liver fibrosis, periodontal diseases,  
 CC attraction of bone-forming cells, central and peripheral nervous

CC system disease and neuropathies and rheumatoid arthritis.

XX Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 22; Length 241;

Best Local Similarity 96.7%; Pred. NO. 1e-99;

Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMAGAFRALCALGLALCALSGORPTGGCGPGRLLLTGTDAACRVRHTRCCRD 60  
 DB 1 maqhgamaafRALCALGLALCALSGORPTGGCGPGRLLLTGTDAACRVRHTRCCRD 60

QY 61 YPGEECCSEWDCMCVQPFHCGDPCTCTCRHHPCPGPGVQSGKFSFGQICDASGTF 120  
 DB 61 ypgeeccsewDCMCVQPFHCGDPCTCTCRHHPCPGPGVQSGKFSFGQICDASGTF 120

QY 121 SGGHEGCHKPWTCTQFGFLTVFPNGKTHNAVCPGSPPAEPLGWLTVLLAVAACVLL 180  
 DB 121 sgghegchkpWTCTQFGFLTVFPNGKTHNAVCPGSPPAEPLGWLTVLLAVAACVLL 180

QY 181 TSAQLGLHIWOL-----RKLTQLLEVPSTEDARSCQFPEEGERSAEKGRLGDLW 233  
 DB 181 tsqLGLHIWOL-----RKLTQLLEVPSTEDARSCQFPEEGERSAEKGRLGDLW 233

Db 181 tsaqlghlwlrsqcmwpretqlllevppstedsarcsqfpeergersaeekgrlgdlw 240  
 QY 234 V 234  
 Db 241 V 241

RESULT 12  
 AAB50910 standard; Protein; 241 AA.  
 ID AAB50910 standard; Protein; 241 AA.  
 AC AAB50910;  
 DT 21-MAR-2001 (first entry)  
 DE Human PRO364 protein.  
 KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KW antiarheumatic; cardiant; antianemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
 KW antiallergic; antialsthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy.  
 OS Homo sapiens.  
 XX  
 PN WO200073452-A2.  
 XX 07-DEC-2000.  
 XX 02-JUN-2000; 2000WO-US15264.  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 28-JUL-1999; 99US-0144758.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30811.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX  
 DR WPI: 2001-025253/03.  
 DR N-PSDB; AAC91469.  
 XX  
 XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 58; Fig 18; 218pp; English.

CC The present sequence is one of thirty three novel PRO polypeptides.  
 CC The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.  
 XX  
 SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 22; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMCAFRALCGLALLCALSLGCRPTGGPGGPRLLILGTGTDAACCRVHTTRCCRD 60  
 Db 1 maqhgamafralcgllallcalslgrptggpggrllilgtgdarccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGGVSGQKFSFGFCIDCASGTF 120  
 Db 61 ypgeccsewdcmcvqpefhcgdpcttcrrhpcppggvgvsgqkfsfgfcidcasgtf 120  
 QY 121 SGGHEGHCKPWTDCITQFGFLTVFPGNKTNAVCVPGSPAPPLGWLTVVLLAVAACVLL 180  
 Db 121 sggheghckpwtcdtqfgfltvfpgnktcnavcvpgspapelpglwtvllavaacvlll 180  
 QY 181 TSAQLGLHIWOL-----RKTQLLLEVPPTEDARSCQFPEERGERSAEKGRLGDLW 233  
 Db 181 tsaqlglhiwqlrsqcmwpretqlllevppstedsarcsqfpeergersaeekgrlgdlw 240  
 QY 234 V 234  
 Db 241 V 241

RESULT 13  
 AAB50982  
 ID AAB50982 standard; Protein; 241 AA.  
 AC AAB50982;  
 XX  
 XX 21-MAR-2001 (first entry)  
 XX  
 DE Human PRO364 protein.  
 XX  
 KW Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
 KW vasotropic; antiarheumatic; antiarthritic; antiinflammatory; cytostatic;  
 KW vulneryary; antiangular; gene therapy; cardiovascular disease;  
 KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
 KW wound healing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073445-A2.  
 XX  
 XX 07-DEC-2000.  
 XX

KW angiogetic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cyostatic; gene therapy; vaccine.

OS Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1998; 98WO-US25108.

XX 16-DEC-1998; 98US-0112850.

XX 12-JAN-1999; 99US-0115554.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-OCT-1999; 99US-0162508.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Fertara N, Gerber H, Hillan KJ, Goddard A;

PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;

PI Watanabe CK, Williams PM, Wood WI;

XX WPI; 2000-412154/35.

XX N-PSDB; AAA77604.

XX Nucleic acids encoding PRO polypeptides useful for preventing,  
 PT diagnosing and treating disorders in mammals -  
 PT angiogenic disorders in mammals -

XX Claim 72; Fig 44; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides  
 CC useful for preventing, diagnosing and treating disorders in mammals  
 CC cardiovascular, endothelial or angiogenic disorder in mammals by  
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
 CC and for identifying agonists and antagonists of these processes. The  
 CC nucleic acids and the proteins they encode may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PRO expression such as cardiovascular, endothelial or  
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and  
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors  
 CC containing them and the PRO polypeptide may be used to treat disorders  
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
 CC the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 21; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

OY 1 MAOHGAMGAFCALCALCALSLGORTPGCGPGRLLLTGTDTARCRVHTTRCCRD 60  
 |||||||

Db 1 maqhgamafralcgialcalcalcslgprlpgpccgprlllgtcdarccrvhttrccrd 60  
 |||||||

OY 61 YPGERCCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGCGVQSGKFSFGFCIDCASGTF 120  
 |||||||

Db 61 ypgeccsewdcmcvqpefhcgdpctcttrhhpcppgqgvsqgkfsfgfcidcasgtf 120  
 OY 121 SGHEGHCKPWTDTQFGFLTVFPGNKTHNAVCPGSPPAEPGLWLTVVLAVAACVLLL 180  
 |||||||  
 Db 121 sggheghckpwtctqfgfltvfpgnkthnavcvpgspapelpglwtvvlavaacvlll 180  
 |||||||  
 OY 181 TSAQLGLHIWQL-----RKQTQLLEVPPESTEDARSCQFPPEERGERSAEEKRLGDLW 233  
 |||||||  
 Db 181 tsaqglghiwlrsqcmwpretqlillevppestedarscqfpeeergergsaekgrlgdlw 240  
 |||||||  
 OY 234 V 234  
 ||  
 Db 241 V 241  
 ||  
 RESULT 9  
 AAY71467  
 ID AAY71467 standard; Protein; 241 AA.  
 XX  
 AC AAY71467;  
 XX  
 DT 08-NOV-2000 (first entry)  
 XX  
 DE Human PRO364 protein.  
 XX  
 KW PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;  
 KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
 KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
 KW CNS; leukemia; melanoma; Expressed Sequence tag; EST; TNFR homologue;  
 KW tumour necrosis factor receptor; GTR protein homologue.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FH Peptide  
 FT Location/Qualifiers  
 FT 1..25  
 FT /label= Signal\_peptide  
 FT Modified-site  
 FT 5..11  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 8..14  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 25..31  
 FT /note= "N-myristoylation site"  
 FT Protein  
 FT 26..241  
 FT /label= Mature\_PRO364\_protein  
 FT Modified-site  
 FT 30..36  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 33..39  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 118..124  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 122..128  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 146..150  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site  
 FT 156..162  
 FT /note= "N-myristoylation site"  
 FT Domain  
 FT 163..183  
 FT /label= Transmembrane\_domain  
 FT Binding-site  
 FT 166..177  
 FT /note= "Prokaryotic membrane lipoprotein lipid  
 FT attachment site"  
 FT Region  
 FT 171..193  
 FT /note= "Leucine zipper pattern"  
 XX  
 WO200032778-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28409.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 22-DEC-1998; 98US-0113296.





XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX WPI: 2000-611444/58.  
 DR N-PSDB; AAA99903.  
 XX Novel PRO polypeptides and agonists and antagonists of them, used to  
 PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
 PT .  
 XX Claim 71: Fig 6; 181pp; English.  
 PS The present invention relates to methods for stimulating or inhibiting  
 XX angiogenesis and cardiovascularization. The methods involve the use of  
 CC pharmaceutical compositions based on the following proteins, PRO179,  
 CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,  
 CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
 CC proteins were identified by isolating cDNA clones encoding secreted  
 CC proteins. The proteins of the invention may be used to diagnose and  
 CC treat cardiovascular, endothelial or angiogenic disorders. The present  
 CC sequence is one of the proteins of the invention.  
 XX Sequence 241 AA;  
 SQ

Query Match 98.7%; Score 1322.5; DB 21; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

Oy 1 MAQHGMAGAFRALGIALCALSLGPRPGCGPGRLLLGTDARCRVHTTRCCRD 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 maqhgmagafRALGIALCALSLGPRPGCGPGRLLLGTDARCRVHTTRCCRD 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 61 YPGECCSWDCMCVQPEFHCGDPDCTTCRHHPCPPGQGVQSGKFSFGQIDCASGTF 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 ypgeccswdcmcvqpefhcgdpdcttcrhhpcppgqgvqsgkfsfgqidcasgtf 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 121 SGHGHCXKPTDCTQFGELTVFPGNKTNVAVCPGSPPAEPGLWTLVLLAVAAVLLL 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 sgghegchxkptdctqfgeltvfpgnktnavcpvpsppaepglwtlvllavaacvlll 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 181 TSAQLGLHTWQL-----RKQTLLLEVPSTEDARSCQFPEERGERSAEKGRGLDLW 233  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 tsaqiglhwqlrqscmwprctqlillevpstedarscdfpeergersaeekgrigdlw 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 234 V 234  
 |  
 Db 241 V 241

RESULT 6  
 AAB33431  
 ID AAB33431 standard; Protein; 241 AA.  
 XX  
 AC AAB33431;  
 XX  
 XX 29-JAN-2001 (first entry)  
 DT  
 XX Human PRO364 protein UNQ319 SEQ ID NO:92.  
 DE  
 XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;

KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.  
 XX  
 OS Homo sapiens.  
 XX WO200053758-A2.  
 PN  
 XX 14-SEP-2000.  
 PD  
 XX  
 PF 02-MAR-2000; 2000WO-US05841.  
 XX  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 26-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 16-DEC-1999; 99WO-US28565.  
 PR 20-DEC-1999; 99WO-US30095.  
 PR 30-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 03-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 11-FEB-2000; 2000WO-US00376.  
 PR 18-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX  
 DR WPI: 2000-572271/53.  
 DR N-PSDB; AAC58596.  
 XX  
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 33; Fig 36; 309pp; English.  
 XX  
 CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are

CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC anemias, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, demyelinating diseases of the central  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 21; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
 DB 1 maqhgmagafralcglalcalslgqrtgpgcgpggrlllgtgdarccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPFHCGDPCCCTTCRHHPCPPGQVQSGKFSFGQICDASGTF 120  
 DB 61 ypgeccsewdcmcvqpfhcgdpcccttcrrhhpcppgqvgvsgqkfsfgqicdasgtf 120  
 QY 121 SGGHEGCHKPMTDCTQFGFLTFVPGNKNHNAVCPGSPPAELGLWLTVLLAVAACVLL 180  
 DB 121 sgghegchkpmtctqfgfltfvpgnknhnavcvpgspapaelglwltvllavaacvll 180  
 QY 181 TSAQLGLHWTQ-----RKTQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLW 233  
 DB 181 tsaqglhlwq-----rktqllevpstetdarscfppeerersaeekgrigdlw 240  
 QY 234 V 234  
 DB 241 v 241

RESULT 7  
 AAY95895  
 ID AAY95895 standard; Protein; 241 AA.

XX  
 AC AAY95895;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-like protein TR11 mutein.  
 XX  
 KW TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
 KW mutant.

XX Homo sapiens.

XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J;  
 XX WPI; 2000-572072/53.  
 XX  
 XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -  
 XX  
 PS Disclosure; 294-295; 278pp; English.

XX The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.

XX Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 21; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
 DB 1 maqhgmagafralcglalcalslgqrtgpgcgpggrlllgtgdarccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPFHCGDPCCCTTCRHHPCPPGQVQSGKFSFGQICDASGTF 120  
 DB 61 ypgeccsewdcmcvqpfhcgdpcccttcrrhhpcppgqvgvsgqkfsfgqicdasgtf 120  
 QY 121 SGGHEGCHKPMTDCTQFGFLTFVPGNKNHNAVCPGSPPAELGLWLTVLLAVAACVLL 180  
 DB 121 sgghegchkpmtctqfgfltfvpgnknhnavcvpgspapaelglwltvllavaacvll 180  
 QY 181 TSAQLGLHWTQ-----RKTQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLW 233  
 DB 181 tsaqglhlwq-----rktqllevpstetdarscfppeerersaeekgrigdlw 240  
 QY 234 V 234  
 DB 241 v 241

RESULT 8  
 AAB24409  
 ID AAB24409 standard; Protein; 241 AA.

XX  
 AC AAB24409;

XX 07-NOV-2000 (first entry)

XX Human PRO364 protein sequence SEQ ID NO:117.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;

Result 3

XX 21-OCT-1997; 97US-0063212.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX N1 J, Ruben SM;  
 PI WPI; 2000-061922/05.  
 DR N-PSDB; AA237762.

XX New tumour necrosis factor receptor-like polypeptides used to, e.g.  
 PT treat Digeorge syndrome -  
 XX

PS Claim 14; Fig 1; 167pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor-like protein (TR11 receptor). The invention relates to TR11 and  
 CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
 CC determined by sequencing cloned cDNAs AA37765-237766. The TR11 receptor  
 CC and its splice variants show homology to the murine glucocorticoid  
 CC induced tumour necrosis factor receptor family-related gene (GIR).  
 CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation  
 CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency,  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.

XX Sequence 234 AA;

Query Match 100.0%; Score 1340; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-101;  
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFALCGLALLCALSLGQRPCTTCRRHPCPPGQVQSGKFSFGQICDASGTF 60  
 DB 1 maqhgmagafalcgllallcalslgqrptgpggprlllgtgtardccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRRHPCPPGQVQSGKFSFGQICDASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpcttcrhpcppgqvgqgkfsfgqicdasgtf 120  
 QY 121 SGGHEGCHKPWTDCQFGFLTVFPNGKTNHNCVCPGSPPAEPLGWLTVLLAVAAVLL 180  
 DB 121 sgghegchkpwtcdctqfgfltvfpngktnhncvcpgpsppaeplgwlvtvllavaacvll 180  
 QY 181 TSAQLGLHQLWRKTLQLLEVPSTEDARSCOFFPEERGERSAEKRGLDLWV 234  
 DB 181 tsaq19lhlwlrkqlqllevpstedarscqfpeeergerseaeekrgldlwv 234

RESULT 3

AAW37839  
 XX ID AAW37839 standard; Protein; 241 AA.  
 XX AC AAW37839;  
 XX 28-JUL-1998 (first entry)  
 DT  
 XX Amino acid sequence of the human 312C2 T cell protein.  
 XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /\*tag= a  
 FT /product= "human 312C2 protein"  
 XX  
 PN WO9806842-A1.  
 XX  
 PD 19-FEB-1998.  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 XX  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Gorman DM, Randall TD, Zlotnik A;  
 XX  
 DR WPI; 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 XX  
 PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 XX  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 19; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMAGAFALCGLALLCALSLGQRPCTTCRRHPCPPGQVQSGKFSFGQICDASGTF 60  
 DB 1 maqhgmagafalcgllallcalslgqrptgpggprlllgtgtardccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRRHPCPPGQVQSGKFSFGQICDASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpcttcrhpcppgqvgqgkfsfgqicdasgtf 120  
 QY 121 SGGHEGCHKPWTDCQFGFLTVFPNGKTNHNCVCPGSPPAEPLGWLTVLLAVAAVLL 180  
 DB 121 sgghegchkpwtcdctqfgfltvfpngktnhncvcpgpsppaeplgwlvtvllavaacvll 180

QY 181 TSAQLGLHIWQL-----RKTQLLLEVPSTEDARSCQFPPEERGERSAEEKGRIGDLW 233  
 ||||||||| :|||||||||  
 Db 181 tsaqlglhiwqlrscqmwpretqlllevppstedarscqfpeegergsaeekgrigdlw 240  
 QY 234 V 234  
 |  
 Db 241 V 241

RESULT 4  
 AAY06605  
 ID AAY06605 standard; Protein; 241 AA.  
 XX  
 AC AAY06605;  
 XX  
 DT 26-OCT-1999 (first entry)  
 XX  
 DE Human TNF receptor homologue PRO364.  
 XX  
 KW PRO364; tumour necrosis factor receptor; human; apoptosis;  
 KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25 /note= "signal peptide"  
 FT Protein 26..241 /note= "mature protein"  
 FT Modified-site 146 /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "transmembrane domain"  
 XX  
 PN WO9940196-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 09-FEB-1999; 99WO-US02642.  
 XX  
 PR 09-FEB-1998; 98US-0024087.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 PI Pitti RM, Wood WI;  
 XX  
 DR WPI; 1999-494296/41.  
 DR N-PSDB; AAX87670.  
 XX  
 PT Tumour necrosis factor receptor homologue - useful for, e.g.  
 PT modulating apoptosis and NF-KB activation and proinflammatory or  
 PT autoimmune responses  
 XX  
 PS Claim 17; Fig 2A; 104pp; English.

XX The present sequence represents human PRO364, a novel member of the  
 CC tumour necrosis factor receptor family. The sequence was deduced  
 CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
 CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or

CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.

XX Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 20; Length 241;  
 Best Local Similarity 96.7%; Pred. No. le-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGANAFRALCGIALCALSLGQRTGGPGCGPGRLLLTGTDAKRCRVTTRCCRD 60  
 ||||||||| :|||||||||  
 Db 1 maqhgamgafralcglallcalslgqrgtggpgcgprlllgtgdarcrcrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGGGVQSGKFSFGFCIDCASGTF 120  
 ||||||||| :|||||||||  
 Db 61 ypgeccsewdcmcvqpefhcgdpccctcrhpcppggvgvsgkfsfgfcidcasgtf 120  
 QY 121 SGGHEGHCCKPWTDCQTQFGFLTVFPGNKTNNAYCVPGSPAPPLGLWLVVLLAVAAACVLLL 180  
 ||||||||| :|||||||||  
 Db 121 sggheghckpwtcdtqfgfltvfpgnktnnaycvpgspapplglwlvvllavaacvlll 180  
 QY 181 TSAQLGLHIWQL-----RKTQLLLEVPSTEDARSCQFPPEERGERSAEEKGRIGDLW 233  
 ||||||||| :|||||||||  
 Db 181 tsaqlglhiwqlrscqmwpretqlllevppstedarscqfpeegergsaeekgrigdlw 240  
 QY 234 V 234  
 |  
 Db 241 V 241

RESULT 5

AAB27651  
 ID AAB27651 standard; Protein; 241 AA.  
 XX  
 AC AAB27651;  
 XX  
 DT 26-JAN-2001 (first entry)  
 XX  
 DE Human protein PRO364.  
 XX  
 KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
 KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
 KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25 /label= "Signal peptide"  
 XX  
 PN WO200053757-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 24-FEB-2000; 2000WO-US05004.  
 XX  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.



Domain 107..113 /note= "conserved domain CD-IV"  
 Domain 128..134 /note= "conserved domain CD-V"  
 Domain 153..160 /note= "conserved domain CD-VI"  
 Domain 176..186 /note= "conserved domain CD-VII"  
 Domain 204..209 /note= "conserved domain CD-IX"  
 Domain 224..233 /note= "conserved domain CD-X"  
 Region 27..36 /note= "epitope-bearing region"  
 Region 43..51 /note= "epitope-bearing region"  
 Region 59..67 /note= "epitope-bearing region"  
 Region 56..64 /note= "epitope-bearing region"  
 Region 66..71 /note= "epitope-bearing region"  
 Region 99..107 /note= "epitope-bearing region"  
 Region 125..133 /note= "epitope-bearing region"  
 Region 143..151 /note= "epitope-bearing region"  
 Region 156..164 /note= "epitope-bearing region"  
 Region 203..211 /note= "epitope-bearing region"  
 Region 222..230 /note= "epitope-bearing region"

WO200050459-A1.

31-AUG-2000.

23-FEB-2000; 2000WO-US04572.

24-FEB-1999; 99US-0121648.

13-MAY-1999; 99US-0134172.

16-JUL-1999; 99US-0144076.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Ni J;

WPI; 2000-572072/53.

N-PSDB; AAA50304.

Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis -

Claim 14(c); Fig 1A-B; 278pp; English.

The present sequence is that of human tumor necrosis factor receptor-like protein TR11, a novel 25 kDa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The sequence was deduced from a cDNA clone (see AAA50304) discovered in a T-helper cell library. TR11 activated NF-kappaB through a TRAF2-mediated mechanism. Expression is activation-inducible. The TR11 ligand is constitutively expressed in an endothelial cell line. This suggests that TR11 and its ligand may be involved in activated T-cell trafficking. The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AA95879-81), as well as vectors, host cells and recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an

CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.

XX Sequence 234 AA;

Query Match 100.0%; Score 1340; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-101;  
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAQHGMGAFRALCGLALCALSLGQRTGGPGCGRLLLTGTDAACRVHTTRCCRD 60  
 DB 1 maqhgmgaftalcalgallcalslgprtgpgcgprlllgtgdarcrrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGQIDCASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpcttcrrhhpcppgqgvqsgkfsfgqidcasgtf 120  
 QY 121 SGGHEGHCKPTDCTQFGFLTVFPNGKTHNAVCPGSPAEPLGWLTVVLLAAACVLL 180  
 DB 121 sggheghckptdctqfgfltvfpngkthnavcvpgspaeplgwlvtvllaaacvlll 180  
 QY 181 TSAQLGLHIWLRKLTQLLEVPPTSDARSCQFPEERGERSAEEKGRIGDLWV 234  
 DB 181 tsaqlglhiwlrkltqllevpptsdarscqfpeeergeraeeekgrigdlwv 234

RESULT 2

AA52158

ID AA52158 standard; Protein; 234 AA.

XX AC AA52158;

XX DT 01-FEB-2000 (first entry)

XX DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.

XX KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;

KW GTR; growth; differentiation; cell death; immune deficiency disorder;

KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;

KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease;

KW inflammatory condition.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal\_peptide

FT Domain /label= TR11

FT Domain /note= "Extracellular domain"

FT Domain /note= "Transmembrane domain"

FT Domain 180..234

FT Domain /note= "Intracellular domain"

XX WO9920758-A1.

PN 29-APR-1999.

XX 21-OCT-1998; 98WO-US22085.





Search completed: September 4, 2001, 15:57:34  
Job time: 376 sec

Db 111 PRDSGKGLGVDCVPCPPGPHFSPGNNAQCKPWTNCTLSGKQTRHPASDSLDAVC----- 164  
QY 160 AEPGLWITVVLAVACVLLTSAQLGLHIW----QLRKQTLLLEVPSP-----TEDARSCQ 212  
Db 165 -EDRSLATLLWETQRTFRFTTVO-STTVMPRTSELPTTLVE-PRSCDKTHTCPCPCP 221  
QY 213 PPEEE 217  
Db 222 APEAE 226

## RESULT 15

US-08-097-827-7  
; Sequence 7, Application US/08097827  
; Patent No. 5457035  
; GENERAL INFORMATION:  
; APPLICANT: Baum, Peter  
; APPLICANT: Goodwin, Ray  
; APPLICANT: Fanslow, William  
; APPLICANT: Gayle, Richard  
; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for  
; TITLE OF INVENTION: OX40  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/097,827  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2806  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0730  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 206 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-097-827-7

Query Match 12.4%; Score 166.5; DB 1; Length 206;  
Best Local Similarity 28.7%; Pred. No. 5e-08;  
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;  
QY 26 QRTTGGCGCGPGRLLLG--TGTDAR--CCRVHT----TRCRD-YPG-----EECCSEWDC 72  
Db 6 QOPT-----ALLLGLTLGVTARRLNCVKRHTYPSGHKCCRECQPGHGMVNRCDHTRDT 58  
QY 73 MCVPQPFHCGDPC-----CCTCRHHP-----CPPGQG 99  
Db 59 LC-----HPCETGFYNEAVNTDCTQCKQCNHRSGSELKQNCPTQDTVCRCPGTQ 110  
QY 100 VQSGKSFQFCIDCASGTFSGGHEGCKPWTDCQTFGFLTVPFGNKTNAVC 153  
Db 111 PRDSGKGLGVDCVPCPPGPHFSPGNNAQCKPWTNCTLSGKQTRHPASDSLDAVC 164

[illegible]

```

RESULT 14
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

```

Query Match	13.1%	Score 175.5;	DB 1;	Length 438;
Best Local Similarity	27.3%;	Pred. No. 1.7e-08;		
Matches	67;	Conservative 17;	Mismatches 84;	Indels 77; Gaps 14;
QY	26	QRPRTGGCGGPRLLLG--TGTDA--CCRVHT-----TRCRD-YPG-----EECCSWDC	72	
Db	6	QQPT-----ALLLLGLTGTARRLNCVKHTYPSGHKKCCRCQPGMGVMNRCDHTRDT	58	
QY	73	MCVQPEFHGDPG-----CCTCRHHP-----CPTGQG	99	
Db	59	LC-----HPCBTGYNEAVNTDTCQCTQCNHRSGSELKQNCCTPTQDTVCRREGTQ	110	
QY	100	VQSQKSFQFCQIDCASGTFSGGHEGCKPWTDCQTFGELTVPPGNKHTNAVCPGSP	159	

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KW05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-03965-2

Query Match 15.0%; Score 201.5; DB 5; Length 256;  
Best Local Similarity 28.7%; Pred. No. 4.2e-11;  
Matches 62; Conservative 26; Mismatches 85; Indels 43; Gaps 10;  
QY 34 CGPGRLLLTGTDARCCRVHTRCCRDYPGEECCSEW---DCMCVQPERFHCGRPCTTC 89  
Db 47 CPSTFSSIGGPPGNCNCRV---CAGYFRKFKFCSTHNAECECIE-GPHCLGPGQTRC 101  
QY 90 RHHPCCPGGVQSGVQSGFQFCIDCASGTFSGGH-EGHCKPWTDCDTQFGFLVFPNGKT 148  
Db 102 -EKDCRPGQELTKG-----CKTCSLGTFTNDNGTGVCRPWTNCSLDGRSVLKTGTTT 153  
QY 149 HNAVCVP-----GSPAPPLGLWTVVLLAVACVLLTSAQLGLHI--W 190  
Db 154 KDVCVPPVPSFSPSTISVTPEGGGSHSLQVLTFLTALTSALLALIFITLLFSVLKW 213  
QY 191 QLKKTKOLLLEVP-----PSTEDARSCQFPPEERG 219  
Db 214 TRKKPHIFRQPKTKTGAQAEDACSCRPQEEG 249

RESULT 9  
US-08-236-918A-8  
; Sequence 8, Application US/08236918A  
; Patent No. 5674704  
; GENERAL INFORMATION:  
; APPLICANT: Alderson, Mark R.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple 7.5.3  
; SOFTWARE: Microsoft Word, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,918A  
; FILING DATE: 06-May-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,843  
; FILING DATE: 07-May-1993  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2801-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-236-918A-8  
Query Match 14.7%; Score 197; DB 1; Length 255;  
Best Local Similarity 30.2%; Pred. No. 1.1e-10;  
Matches 67; Conservative 20; Mismatches 81; Indels 54; Gaps 12;  
QY 34 CGPGRLLLTGTDARCCRVHTRCCRDYPG-----EECCS-----EWDCCMCVQPERFHCGRP 84  
Db 48 CPPNSFSAGG--ORTCDI-----CRCKGVFRTRKCSSTSNACDC---TPGFHCLGA 97  
QY 85 CCTCRHHPCCPGGVQSGVQSGFQFCIDCASGTFSGHGGHCKPWTDCDTQFGFLTVFP 144  
Db 98 GCSMC-EQDCKQGOELTKG-----CKDCCFTGNDOKRGICRPWTNCSLDGKSVLVN 149  
QY 145 GNKTHNAVCPG-----SPPA---BPLGLWTVV---LLAVACVLLTSAQLGLH 188  
Db 150 GTKERDVVCGSPADLSPGASSVTPAPAREPGHSPQIISFFLALTSTALLFLFLTLR 209  
QY 189 ---TWLRKTKOLLLEVP-----STEDARSCQFPPEERG 219  
Db 210 FSVYKRGKKLLYIFKQFMRPVQTTQEDGCSRCRFPPEERG 251  
RESULT 10  
US-08-816-605-9  
; Sequence 9, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,605  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8512  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids



Qy	7	MGAFRALCGIALLCALSLGQ--RPTGGPGCGPGRLLLTGTDAARCCRVHVTTRCCRDY	65
		:     :     :     :     :     :     :     :     :	
Db	1	MGAMWLYGVSMCLVLDLGGPSVVVEEPGCCGPQKVGSGNNTRCCSLYA-----PGKE	53
Qy	66	CCSEWDCMCVQPEHFCHDPCCTTCRRHHPCPPGOVGVSQGKFEGFCQIDCASGTFSGHE	129
		: : :     :     :     :     :     :     :     :     :     :	
Db	54	DCPKERICIVTPHYCHGDGPCKICKHPGPCPGQRVESQGDIVFGFRCVACAMGTF\$AGRD	113
Qy	126	GHCXKPWTDCITQFGLTVFPNGKNTHNVCVPGPSAPAEPLGMLTVLLVAACVLLLTSAQL	185
		:     :     :     :     :     :     :     :     :     :	
Db	114	GHCRLWNCSQFGLTWPPGNKTHNAVCIPELPTEQYGHILTVFLFYNAACIEFLTIVQL	173
Qy	186	GLHTIWLQRK-----TQLLELVPPSTEDARSCQFPEEERGESAEKBKRGDLNW	233
		:     :     :     :     :     :     :     :     :	
Db	174	GLHTIWLRLRHMCPRCTOPAEVOLSAEDACSFOFPEEBCEOT-EBKHHLGGSW	227

RESULT 5  
US-08-911-423-7  
; Sequence 7, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA

```

RESULT 4
US-08-911-423-2
; Sequence 2, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGEN
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.300
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996

```

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, BRUNNEN: 001-1230
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Ching, Edwin P.
, REGISTRATION NUMBER: 34,090
, REFERENCE/DOCKET NUMBER: DX0612K
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 650-852-9196
, TELEFAX: 650-496-1200
, INFORMATION FOR SEQ ID NO: 7:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 232 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: peptide
, DS-08-911-423-7

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Query Match	52.5%;	Score 703;	DB 3;	Length 228;	
Best Local Similarity	54.9%;	Pred. NO. 9.4e-57;			
Matches 129;	Conservative 32;	Mismatches 58;	Indels 16;	Gaps 4;	

  

Query Match	45.1%;	Score 605;	DB 3;	Length 232;	
Best Local Similarity	78.1%;	Pred. NO. 7.7e-48;			
Matches 107;	Conservative 5;	Mismatches 17;	Indels 8;	Gaps 3;	

  

Qy	7	MGAFRALCGALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEC	66

Db 1 MGAFRALCGLLALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFHCGDPCCCTTCHRHPCPPGQGVQSGKFSFGQCI-----DCASGTFSG 122  
Db 61 CSEWDCMCVQPEFHCGDPCCCTTCHRHPCPPGQGVQSGK----SWRCLWESTQARGSTRAR 117  
QY 123 GH-EGHCKPWTDCQTFG 138  
Db 118 GRAGHRCPARTCGVWG 134

RESULT 6  
US-09-188-930-191  
; Sequence 191, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; FILE REFERENCE: 11000.1011c1  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 191  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-188-930-191

Query Match 19.08; Score 255; DB 4; Length 89;  
Best Local Similarity 46.3%; Pred. No. 1.8e-16;  
Matches 44; Conservative 17; Mismatches 26; Indels 8; Gaps 2;  
QY 8 GAFRALCGLLALCALSLGQ-RPTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
Db 1 GAWAMLYGVSMCLVDLGLQPSWVEEPGCGKGVQNGSGNTRCCSLYA-----PGRED 53

QY 67 CSEWDCMCVQPEFHCGDPCCCTTCHRHPCPPGQGVQ 101  
Db 54 CPERCICVTPEYHCGDPQCKICKHYPCQPGQORVE 88

RESULT 7  
US-08-236-918A-6  
; Sequence 6, Application US/08236918A  
; Patent No. 5674704  
; GENERAL INFORMATION:  
; APPLICANT: Alderson, Mark R.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple 7.5.3  
; SOFTWARE: Microsoft Word, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,918A  
; FILING DATE: 06-May-1994

; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,843  
; FILING DATE: 07-May-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2801-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-236-918A-6

Query Match 15.0%; Score 201.5; DB 1; Length 256;  
Best Local Similarity 28.7%; Pred. No. 4.2e-11;  
Matches 62; Conservative 26; Mismatches 85; Indels 43; Gaps 10;  
QY 34 CGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEW----DCMCVQPEFHCGDPCCCTTC 89  
Db 47 CPPSTFGSIGGQPCNCRV-----CAGYFRFKKFCSSTHNAECIE-GFHCGLGPGQCTRC 101  
QY 90 RHHPCCPGQGVQSGKFSFGQCIDCASGTFSGGH-EGHCKPWTDCQTFGLTVFPGNKT 148  
Db 102 -EKDCRPGQELTKQG-----CKTCSLGTFNQDNGTGVCRPWTNCSLDGRSVLKTGTE 153  
QY 149 HNAVCV-----GSPPAEPLGWLTVLLVAACVLLLTSAQLGHI--W 190  
Db 154 KDVCVGPVVSFSPSTTISVTPGPGGSHLQVLTFLALTSALLLALIFITLLFSVLKW 213  
QY 191 QLRKTQLLEVP-----PSTEDARSCQFPPEERG 219  
Db 214 IRKKPFPHFQPPFKTKTGAAGQEDACSCRCPOEERG 249

RESULT 8  
PCT-US96-03965-2  
; Sequence 2, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuil  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-1BB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:51:18 ; Search time 65.86 Seconds  
(without alignments)  
73.157 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 1340  
Sequence: 1 MAQHGMAGFALCGLALC.....EEERGSABEKGRLGLDW 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1322.5	98.7	241	3	US-08-911-423-4
2	1308	97.6	228	3	US-08-911-423-6
3	1093	81.6	311	3	US-08-911-423-8
4	703	52.5	228	3	US-08-911-423-2
5	605	45.1	232	3	US-08-911-423-7
6	255	19.0	89	4	US-09-188-930-191
7	201.5	15.0	256	1	US-08-236-918A-6
8	201.5	15.0	256	1	PCT-US96-03965-2
9	197	14.7	255	1	US-08-236-918A-8
10	197	14.7	255	2	US-08-816-605-9
11	197	14.7	255	5	PCT-US96-03965-8
12	194	14.5	219	2	US-08-816-605-2
13	175.5	13.1	438	1	US-08-097-827-11
14	175.5	13.1	438	1	US-08-494-574-11
15	166.5	12.4	206	1	US-08-097-827-7
16	166.5	12.4	206	1	US-08-494-574-7
17	165	12.3	277	2	US-08-147-784-2
18	165	12.3	277	4	US-08-195-967-2
19	160.5	12.0	205	3	US-08-974-022-51
20	157	11.7	191	3	US-08-974-022-52
21	153	11.4	300	2	US-08-794-796-2
22	150	11.2	451	3	US-08-996-139-4
23	150	11.2	451	4	US-08-995-659-4
24	150	11.2	616	3	US-08-996-139-6
25	150	11.2	616	4	US-08-995-659-6
26	149	11.1	140	4	US-08-477-347-17
27	142.5	10.6	591	3	US-08-996-139-2

28	142.5	10.6	591	4	US-08-995-659-2	Sequence 2, Appl
29	141.5	10.6	401	3	US-08-974-022-2	Sequence 2, Appl
30	141.5	10.6	461	4	US-09-042-785A-7	Sequence 7, Appl
31	139.5	10.4	139	2	US-08-219-237B-8	Sequence 8, Appl
32	139.5	10.4	401	3	US-08-974-022-4	Sequence 4, Appl
33	139.5	10.4	401	4	US-09-042-785A-13	Sequence 13, Appl
34	139.5	10.4	461	1	US-08-385-229-2	Sequence 2, Appl
35	139.5	10.4	461	2	US-08-650-000-2	Sequence 2, Appl
36	139.5	10.4	461	4	US-08-477-347-3	Sequence 3, Appl
37	139.5	10.4	461	6	5395760-2	Patent No. 5395760
38	139	10.4	289	4	US-09-042-785A-11	Sequence 11, Appl
39	138	10.3	401	3	US-08-974-022-6	Sequence 6, Appl
40	138	10.3	401	4	US-09-042-785A-12	Sequence 12, Appl
41	135.5	10.1	197	3	US-08-974-022-49	Sequence 49, Appl
42	134.5	10.0	625	3	US-08-996-139-15	Sequence 15, Appl
43	134.5	10.0	625	4	US-08-995-659-15	Sequence 15, Appl
44	131.5	9.8	253	4	US-09-042-785A-4	Sequence 4, Appl
45	129.5	9.7	605	4	US-09-042-785A-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-911-423-4

Query Match 98.7%; Score 1322.5; DB 3; Length 241;

Best Local Similarity 96.7%; Pred. No. 4.8e-113;  
Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGAFAFALCGLALLCALSIGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 MAQHGAFAFALCGLALLCALSIGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
QY 61 YPEECSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGQVQSGKFSFGQCIDCASGTF 120  
DB 61 YPEECSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGQVQSGKFSFGQCIDCASGTF 120  
QY 121 SGHEGCKPWTDCQFGFLVFPGNKTHNAVCPGSPAPPLGWLTVVLLAACAACVLL 180  
DB 121 SGHEGCKPWTDCQFGFLVFPGNKTHNAVCPGSPAPPLGWLTVVLLAACAACVLL 180  
QY 181 TSAQLGLHIWQL-----RKTQLLLEVPSTEDARSCOFFPEERGERSAEKGRLGLDW 233  
DB 181 TSAQLGLHIWQLRSCQWMPRETQLLLEVPSTEDARSCOFFPEERGERSAEKGRLGLDW 240  
QY 234 V 234  
DB 241 V 241

RESULT 2  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-852-9196  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

Query Match 97.6%; Score 1308; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 9.3e-112;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 MGAFAALCGLALLCALSIGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFAALCGLALLCALSIGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGQVQSGKFSFGQCIDCASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGQVQSGKFSFGQCIDCASGTFSGGHEG 120  
QY 127 HCKPWTDCQFGFLVFPGNKTHNAVCPGSPAPPLGWLTVVLLAACAACVLLLTSAQLG 186  
DB 121 HCKPWTDCQFGFLVFPGNKTHNAVCPGSPAPPLGWLTVVLLAACAACVLLLTSAQLG 180  
QY 187 LHIWOLRKTQLLLEVPSTEDARSCOFFPEERGERSAEKGRLGLDW 234  
DB 181 LHIWOLRKTQLLLEVPSTEDARSCOFFPEERGERSAEKGRLGLDW 228

RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 81.6%; Score 1093; DB 3; Length 311;



PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX other T cell disorders  
 PS Disclosure; Pages 61-62; 71pp; English.  
 XX  
 CC This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 228 AA;

Query Match 100.0%; Score 246; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. NO. 2.5e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPPGKNTKTHNAVCV 41  
 Db 108 dcasgtfsggheghckpwtcdctgfgfltvpgnkthnavcv 148

RESULT 2  
 AA195879  
 ID AAY95879 standard; Protein; 234 AA.  
 XX  
 AC AAY95879;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-like protein TR11.  
 XX  
 KW TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Signal\_peptide  
 FT Protein 26..234  
 FT /label= Mature\_protein  
 FT Domain 26..162  
 FT /label= Extracellular\_domain  
 FT Domain 163..179  
 FT /label= Transmembrane\_domain  
 FT Domain 180..234  
 FT /label= Intracellular\_domain  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 72..81  
 FT /note= "conserved domain CD-II"  
 FT Domain 84..93  
 FT /note= "conserved domain CD-III"  
 FT Domain 107..113  
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 FT Domain 128..134  
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 FT Domain 176..186  
 FT /note= "conserved domain CD-VII"  
 FT Domain 204..209  
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Domain 224..233  
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 FT Region 27..36  
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 FT Region 43..51  
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 /note= "epitope-bearing region"  
 FT Region 222..230  
 /note= "epitope-bearing region"  
 FT  
 XX WO200050459-A1.  
 PN 31-AUG-2000.  
 XX  
 PD 23-FEB-2000; 2000WO-US04572.  
 XX  
 PF 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, NI J;  
 XX  
 PI WPI; 2000-572072/53.  
 DR N-PSDB; AAA50304.  
 XX  
 PT Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis  
 PT  
 XX Claim 14(c); Fig 1A-B; 278pp; English.  
 PS  
 XX The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11, a novel 25 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
 CC TR11 activated NF-kappaB through a TRAF2-mediated mechanism.  
 CC Expression is activation-inducible. The TR11 ligand is constitutively  
 CC expressed in an endothelial cell line. This suggests that TR11 and  
 CC its ligand may be involved in activated T-cell trafficking.  
 CC The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
 CC (see AAA50304-06) and highly conserved encoded proteins (see  
 CC AAY95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency,  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:24 ; Search time 126.12 Seconds  
(without alignments)  
19.708 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_114\_154

Perfect score: 246

Sequence: 1 DCASGTGSGHGCKPWT.....TQFGFLTVFPGKTHNAVCV 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
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12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
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20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	246	100.0	228	19 AAW37840	Truncated human 31
2	246	100.0	234	21 AAY95879	Human tumour necro
3	246	100.0	234	21 AAY52158	Tumour necrosis fa
4	246	100.0	235	21 AAY44825	Human molecule ass
5	246	100.0	240	21 AAY95881	Human tumour necro
6	246	100.0	240	21 AAY52160	TR11SV2 amino acid
7	246	100.0	241	19 AAW37839	Amino acid sequenc
8	246	100.0	241	20 AAY08605	Human TNF receptor
9	246	100.0	241	20 AAB27651	Human protein PRO3
10	246	100.0	241	21 AAB33431	Human PRO364 prote
11	246	100.0	241	21 AAY95880	Human tumour necro

12	246	100.0	241	21 AAY95895	Human tumour necro
13	246	100.0	241	21 AAB24409	Human PRO364 prote
14	246	100.0	241	21 AAY71467	Human PRO364 prote
15	246	100.0	241	21 AAY52159	TR11SV1 amino acid
16	246	100.0	241	22 AAB20115	Human immunostimul
17	246	100.0	241	22 AAB47054	Human PRO364. Hom
18	246	100.0	241	22 AAB50910	Human PRO364 prote
19	246	100.0	241	22 AAB50982	Human PRO364 prote
20	246	100.0	241	22 AAB53090	Human angiogenesis
21	246	100.0	311	19 AAW37842	Human 312C2 protei
22	196	79.7	316	22 AAB47055	Polypeptide encode
23	196	79.7	317	20 AAY06645	PRO364-related EST
24	192	78.0	222	19 AAW49018	Mouse glucocortico
25	192	78.0	228	19 AAW49016	Mouse glucocortico
26	192	78.0	228	19 AAW37838	Amino acid sequenc
27	192	78.0	294	19 AAW49017	Mouse glucocortico
28	96	39.0	277	16 AAR74737	ACT-4 cell surface
29	96	39.0	277	16 AAR79904	ACT-4-h-1 receptor
30	96	39.0	277	22 AAB35329	Human OX40 protein
31	96	39.0	277	22 AAB50522	Human tumour necro
32	95	38.6	206	16 AAR81881	Mouse type-II memb
33	95	38.6	206	19 AAW48977	Mouse OX40 extrace
34	95	38.6	277	16 AAR76996	Deduced sequence e
35	95	38.6	438	16 AAR81882	Plasmid pDC406/OX4
36	93	37.8	219	18 AAW48976	A novel human h4-1
37	93	37.8	219	18 AAW31759	Human h4-1BBSV rec
38	93	37.8	219	20 AAW92523	Human h4-1BBSV rec
39	93	37.8	219	20 AAW92524	Human receptor ind
40	93	37.8	255	16 AAR74087	H4-1BB receptor pr
41	93	37.8	255	16 AAR70977	Human 4-1BB polype
42	93	37.8	255	18 AAW64197	Human 4-1BB recept
43	93	37.8	255	18 AAW26658	Human CD137 protei
44	93	37.8	255	20 AAY33214	Human receptor pro
45	93	37.8	255	20 AAY28688	

#### ALIGNMENTS

RESULT 1  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX  
Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
OS Homo sapiens.  
XX  
XX WO9806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
XX 14-AUG-1997; 97WO-US13931.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM, Randall TD, Zlotnik A;  
XX  
XX WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PT Isolated 312C2 T cell gene - used to develop products for treating,

FT Modified-site /note= "Potential phosphorylation site"  
 FT 48  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 62  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 82  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 205  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 223  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 140  
 FT Modified-site /note= "N-glycosylated"  
 XX  
 PN WO200005374-A2.  
 XX  
 XX 03-FEB-2000.  
 XX  
 PF 21-JUL-1999; 99WO-US16537.  
 XX  
 XX 22-JUL-1998; 98US-0093827.  
 PR  
 XX (INCY-) INCYTE PHARM INC.  
 PA  
 XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 PI  
 XX WPI; 2000-182699/16.  
 DR  
 DR N-PSDB; AA249948.  
 XX  
 XX Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 PT  
 PS Claim 1; Pages 64-65; 67pp; English.  
 XX  
 XX The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMN0706  
 CC cDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotrophic, antiinflammatory, antipsoriatic, cytostatic, antiaschmatic,  
 CC dermatologic, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 SQ Sequence 235 AA;  
  
 Query Match 100.0%; Score 246; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred No. 2.6e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTFPGNKTNAVCV 41  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 108 dcasgtfsgghegckpwtctqfgfltfpgnktnavcv 148  
  
 RESULT 5  
 AAY95881  
 ID AAY95881 standard; Protein; 240 AA.  
 XX  
 AC AAY95881;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 XX Human tumour necrosis factor receptor-like protein TR11SV2.  
 DE  
 DE TR11SV2; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;

KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /label= Signal\_peptide  
 FT 20..240  
 FT /label= Mature\_protein  
 FT 20..168  
 FT Domain  
 FT /label= Extracellular\_domain  
 FT 169..185  
 FT /label= Transmembrane\_domain  
 FT 186..240  
 FT /label= Intracellular\_domain  
 FT 152  
 FT Modified-site  
 FT /note= "N-glycosylated"  
 FT 57..68  
 FT Domain  
 FT /note= "conserved domain CD-I"  
 FT 78..87  
 FT Domain  
 FT /note= "conserved domain CD-II"  
 FT 91..100  
 FT Domain  
 FT /note= "conserved domain CD-III"  
 FT 114..121  
 FT Domain  
 FT /note= "conserved domain CD-IV"  
 FT 134..140  
 FT Domain  
 FT /note= "conserved domain CD-V"  
 FT 159..166  
 FT Domain  
 FT /note= "conserved domain CD-VI"  
 FT 182..192  
 FT Domain  
 FT /note= "conserved domain CD-VII"  
 FT 210..215  
 FT Domain  
 FT /note= "conserved domain CD-IX"  
 FT 230..239  
 FT Domain  
 FT /note= "conserved domain CD-X"  
 FT 20..28  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 24..32  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 37..45  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 48..56  
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 FT /note= "epitope-bearing region"  
 FT 67..75  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 106..114  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 130..139  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 149..157  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 162..170  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 209..217  
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 FT /note= "epitope-bearing region"  
 FT 228..236  
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 XX  
 PN WO200050459-A1.  
 XX  
 XX 31-AUG-2000.  
 PD  
 XX 23-FEB-2000; 2000WO-US04572.  
 PF  
 XX 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Ruben SM, Ni J;  
 PI  
 XX WPI; 2000-572072/53.  
 DR

CC polypeptides may also be used. Methods for screening for  
 XX agonist/antagonist compounds are also provided.

SQ Sequence 234 AA;

Query Match 100.0%; Score 246; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPPGNKTHNAVCV 41  
 |||||  
 Db 114 dcasgtsfsgghegckpwtcdctqfgfltvppgnkthnavcv 154

RESULT 3

AAAY52158  
 ID AA52158 standard; Protein; 234 AA.

XX  
 AC AA52158;

XX  
 DT 01-FEB-2000 (first entry)

XX DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.

XX KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;  
 KW G1TR; growth; differentiation; cell death; immune deficiency disorder;  
 KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
 KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW inflammatory condition.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /label= Signal\_peptide  
 FT 26..234  
 FT /label= TR11  
 FT 26..162  
 FT /note= "Extracellular domain"  
 FT 163..179  
 FT /note= "Transmembrane domain"  
 FT 180..234  
 FT /note= "Intracellular domain"

XX PN W09920758-A1.

XX PD 29-APR-1999.

XX PF 21-OCT-1998; 98WO-US22085.

XX PR 21-OCT-1997; 97US-0063212.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Ruben SM;

XX DR WPI; 2000-061922/05.

XX DR N-PSDB; AA237762.

XX PT New tumour necrosis factor receptor-like polypeptides used to, e.g.

XX PT treat Digeorge syndrome -

XX PS Claim 14; Fig 1; 167pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor  
 XX receptor-like protein (TR11 receptor). The invention relates to TR11 and  
 CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
 CC determined by sequencing cloned cDNAs AA237765-237766. The TR11 receptor  
 CC and its splice variants show homology to the murine glucocorticoid  
 CC induced tumour necrosis factor receptor family-related gene (G1TR).  
 CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation

CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpasture's syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.

XX SQ Sequence 234 AA;

Query Match 100.0%; Score 246; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPPGNKTHNAVCV 41  
 |||||  
 Db 114 dcasgtsfsgghegckpwtcdctqfgfltvppgnkthnavcv 154

RESULT 4

AAAY44825

ID AA44825 standard; Protein; 235 AA.

XX  
 AC AA44825;

XX  
 DT 18-MAY-2000 (first entry)

XX DE Human molecule associated with cell proliferation, MACP-5.

XX KW Human; molecule associated with cell proliferation; MACP-5;  
 KW Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;  
 KW anti-inflammatory; antipsoriatic; anti-HIV; antisthmatic; anaemia;  
 KW dermatological; antidiabetic; nephrotropic; antichyroid; thyromimetic;  
 KW immunosuppressive; osteopathic; antiarthritic; uropathic; antitumor;  
 KW ophthalmological; diagnosis; treatment; prevention; immune disorder;  
 KW cell proliferative disorder; actinic keratosis; arteriosclerosis;  
 KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Region 1..19  
 FT /label= Signature\_sequence  
 FT 68..96  
 FT /label= Signature\_sequence  
 FT 109..147  
 FT /label= Signature\_sequence  
 FT 122..129  
 FT /label= Signature\_sequence  
 FT 157..175  
 FT /label= Signature\_sequence  
 FT 165..186  
 FT /label= Signature\_sequence  
 FT 37  
 FT Modified-site

DT 28-JUL-1998 (first entry)  
 XX Amino acid sequence of the human 312C2 T cell protein.  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT CDS 1..726  
 FT /tag= a  
 FT /product= "human 312C2 protein"  
 XX WO9806842-A1.  
 XX 19-FEB-1998.  
 XX 14-AUG-1997; 97WO-US13931.  
 XX 07-OCT-1996; 96US-0027901.  
 XX 16-AUG-1996; 96US-0689943.  
 XX (SCHE ) SCHERING CORP.  
 XX Gorman DM, Randall TD, Zlotnik A;  
 XX WPI: 1998-159534/14.  
 XX N-PSDB; AAV19153.  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 XX e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX other T cell disorders  
 XX Claim 2; Pages 59-60; 71pp; English.  
 XX This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX Sequence 241 AA;  
 SQ  
 Query Match 100.0%; Score 246; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTHNAVCV 41  
 ||||||||||||||||||||||||||||||||||||||||||||  
 DB 114 dcasgtfsgghegchckpwtctqfgfltvfpgnkthnavcv 154  
 RESULT 8  
 ID AAY06605  
 XX AAY06605 standard; Protein; 241 AA.  
 AC AAY06605;  
 XX 26-OCT-1999 (first entry)  
 DT Human TNF receptor homologue PRO364.  
 DE Tumour necrosis factor receptor; human; apoptosis;  
 KW PRO364; tumour necrosis factor receptor; human; apoptosis;

KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT Peptide 1..25 "signal peptide"  
 FT Protein 26..241  
 FT Modified-site 146  
 FT Domain 162..180  
 FT /note= "N-glycosylated"  
 FT /note= "transmembrane domain"  
 XX WO9940196-A1.  
 XX 12-AUG-1999.  
 XX 09-FEB-1999; 99WO-US02642.  
 XX 09-FEB-1998; 98US-0024087.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 XX Pitti RM, Wood WI;  
 XX WPI: 1999-494296/41.  
 XX N-PSDB; AAX87670.  
 XX Tumour necrosis factor receptor homologue - useful for, e.g.  
 XX modulating apoptosis and NF-KB activation and proinflammatory or  
 XX autoimmune responses  
 XX Claim 17; Fig 2A; 104pp; English.  
 XX The present sequence represents human PRO364, a novel member of the  
 CC tumour necrosis factor receptor family. The sequence was deduced  
 CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
 CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or  
 CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.  
 XX Sequence 241 AA;  
 SQ  
 Query Match 100.0%; Score 246; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTHNAVCV 41  
 ||||||||||||||||||||||||||||||||||||||||||||  
 DB 114 dcasgtfsgghegchckpwtctqfgfltvfpgnkthnavcv 154  
 RESULT 9  
 ID AAB27651  
 AAB27651 standard; Protein; 241 AA.



XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI: 2000-572271/53.

DR N-PSDB; AAC58596.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of

PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

XX Claim 33; Fig 36; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can

CC be used in the treatment of immune related diseases. The human PRO

CC proteins, anti-PRO antibodies, agonists and antagonists are useful for

CC treating and diagnosing immune related disorders. The disorders are

CC selected from systemic lupus erythematosus, rheumatoid arthritis,

CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,

CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems, hepatobiliary diseases, inflammatory

CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,

CC autoimmune or immune-mediated skin diseases, allergic diseases,

CC immunological diseases of the lung, and transplantation associated

CC diseases including graft rejection and graft-versus-host-disease.

CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and

CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX Sequence 241 AA;

XX

QY 1 DCASGTFSGGHEGCKPWTCTCGFTVFPGNKTHNAVCV 41

Db 114 dcasgtfsgghegckpwtctcgftvfpgnkthnavcv 154

|||||

RESULT 11

AAAY5880

ID AAY5880 standard; Protein: 241 AA.

XX

AC AAY5880;

XX

DT 20-NOV-2000 (first entry)

XX

DE Human tumour necrosis factor receptor-like protein TR11SV1.

XX

XX TR11SV1; human; tumour necrosis factor receptor-like protein;

KW immunodeficiency; autoimmune disease; rheumatoid arthritis;

KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;

KW dermatological; antiinflammatory; therapy; diagnosis.

XX

XX Homo sapiens.

XX

PH Key Location/Qualifiers

FT Domain 1...162

FT /label= Extracellular\_domain

FT Domain 163...179

FT /label= Transmembrane\_domain

FT Domain 180...241

FT /label= Intracellular\_domain

FT Modified-site 146

FT

FT Domain

FT /note= "N-glycosylated"

FT 51...61

FT /note= "conserved domain CD-I"

FT 72...81

FT /note= "conserved domain CD-II"

FT 85...94

FT /note= "conserved domain CD-III"

FT 108...115

FT /note= "conserved domain CD-IV"

FT 128...134

FT /note= "conserved domain CD-V"

FT 153...160

FT /note= "conserved domain CD-VI"

FT 176...186

FT /note= "conserved domain CD-VII"

FT 195...201

FT /note= "conserved domain CD-VIII"

FT 211...216

FT /note= "conserved domain CD-IX"

FT 231...240

FT /note= "conserved domain CD-X"

FT 2...10

FT /note= "epitope-bearing region"

FT 11...19

FT /note= "epitope-bearing region"

FT 27...35

FT /note= "epitope-bearing region"

FT 38...46

FT /note= "epitope-bearing region"

FT 42...50

FT /note= "epitope-bearing region"

FT 31...46

FT /note= "epitope-bearing region"

FT 61...69

FT /note= "epitope-bearing region"

FT 99...107

FT /note= "epitope-bearing region"

FT 125...133

FT /note= "epitope-bearing region"

FT 143...151

FT /note= "epitope-bearing region"

FT 156...164

FT /note= "epitope-bearing region"

FT 196...204

FT /note= "epitope-bearing region"

FT 209...217

FT /note= "epitope-bearing region"

FT 229...237

FT /note= "epitope-bearing region"

XX WO200050459-A1.

XX

PN 31-AUG-2000.

XX

XX 23-FEB-2000; 2000WO-US04572.

XX

XX 24-FEB-1999; 99US-0121648.

PR 13-MAY-1999; 99US-0134172.

PR 16-JUL-1999; 99US-0144076.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

XX Ruben SM, NI J;

XX

DR WPI: 2000-572072/53.

DR N-PSDB; AAA50305.

XX

PT Human tumor necrosis factor receptor-like proteins useful for

PT diagnosis, prevention and treatment of disease states associated with

PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis -

XX Claim 14(1); Fig 2A-B; 278pp; English.

PS





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PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US211547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
PI Watanabe CK, Williams PM, Wood WI;
XX
XX WPI: 2000-412154/35.
DR N-PSDB; AAA77604.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating a cardiovascular, endothelial or
PT angiogenic disorders in mammals.
XX
XX Claim 72; Fig 44; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PRO expression such as cardiovascular, endothelial or
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 246; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.7e-24;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DCASGTFSGGHEGCKPWTDCQTQFGFLTVPGNKTHNAVCV 41
Db 114 dcasgtfsgghegckpwtcdctqfgfltvpgnkhnavcv 154
RESULT 14
AA771467
ID AA771467 standard; Protein; 241 AA.
XX
XX AA771467;
XX
XX 08-NOV-2000 (first entry)
XX
XX Human PRO364 protein.
XX
XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
KW breast; prostate; colon; lung; renal; ovarian; central nervous system;
KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
KW tumour necrosis factor receptor; GTR protein homologue.
XX
XX Homo sapiens.
XX
XX Query Match 100.0%; Score 246; DB 21; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-24;
XX Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Key Location/Qualifiers
XX Peptide 1..25
XX /label= Signal_peptide
XX Modified-site 5..11
XX /note= "N-myristoylation site"
XX Modified-site 8..14
XX /note= "N-myristoylation site"

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FT Modified-site 25..31
FT /note= "N-myristoylation site"
FT Protein 26..241
FT /label= Mature_PRO364_protein
FT Modified-site 30..36
FT /note= "N-myristoylation site"
FT Modified-site 33..39
FT /note= "N-myristoylation site"
FT Modified-site 118..124
FT /note= "N-myristoylation site"
FT Modified-site 122..128
FT /note= "N-myristoylation site"
FT Modified-site 146..150
FT /note= "Asn is N-glycosylated"
FT Modified-site 156..162
FT /note= "N-myristoylation site"
FT Domain 163..183
FT /label= Transmembrane_domain
FT Binding-site 166..177
FT /note= "Prokaryotic membrane lipoprotein lipid
FT attachment site"
FT Region 171..193
FT /note= "Leucine zipper pattern"
XX
XX WO2000032778-A2.
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US28409.
XX
XX 01-DEC-1998; 98WO-US25108.
XX 16-DEC-1998; 98US-0112850.
XX 22-DEC-1998; 98US-0113296.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
XX
XX WPI: 2000-412325/35.
XX N-PSDB; AAD01240.
XX
XX New composition useful for inhibiting neoplastic cell growth and for
XX treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
XX their antagonists.
XX
XX Claim 31; Fig 4; 108pp; English.
XX
XX The present sequence is the human PRO364 protein, encoded by the cDNA
XX clone, designated as DNA47365-1206. It is isolated from human small
XX intestine tissue cDNA library, identified using probes based on the
XX consensus sequence DNA44825, relative to the Incyte expressed sequence
XX tag (EST) 3003460. This EST has homology to tumour necrosis factor
XX receptor (TNFR) family of polypeptides. PRO364 sequence also shows
XX homology to members of the TNFR family and mouse GTR protein.
XX This clone is assigned the ATCC deposit No: 209436. PRO364 functions as
XX a neoplastic cell growth inhibitor and is used for treating tumours,
XX using an effective amount of PRO655, PRO364 and PRO344. This composition
XX is especially useful for treatment of human cancers such as breast,
XX prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 246; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.7e-24;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DCASGTFSGGHEGCKPWTDCQTQFGFLTVPGNKTHNAVCV 41
Db 114 dcasgtfsgghegckpwtcdctqfgfltvpgnkhnavcv 154

```

XX The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR1SV1, a novel 26 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC cDNA (see AA50305) discovered in a PHA-stimulated T-cell library.  
 CC The invention provides TR1L, TR1SV1 and TR1SV2 nucleic acids  
 CC (see AA50304-06) and highly conserved encoded proteins (see  
 CC AA95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. TR1L, TR1SV1 and/or TR1SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency,  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR1L, TR1SV1 and/or TR1SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 246; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVPFGNKTHNAVCV 41  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 114 dcasgtsfggheghckpwtcdctqfgfltfvpgnkthnavcv 154

RESULT 12  
 AAY95895  
 ID AAY95895 standard; Protein; 241 AA.  
 XX  
 AC AAY95895;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-like protein TR11 mutein.  
 XX  
 KW TR1L; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
 KW mutant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200050459-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 23-FEB-2000; 2000WO-US04572.  
 XX  
 PR 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, N1 J;  
 XX  
 DR WPI; 2000-572072/53.  
 XX  
 PT Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis  
 XX  
 PS Disclosure; 294-295; 278pp; English.  
 XX  
 CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR1L (see also AA95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR1L, TR1SV1 and TR1SV2 proteins (see AA95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR1L, TR1SV1 and/or TR1SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunoglobulin  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR1L, TR1SV1 and/or TR1SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 246; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGHCKPWTDCTQFGFLTVPFGNKTHNAVCV 41  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 114 dcasgtsfggheghckpwtcdctqfgfltfvpgnkthnavcv 154

RESULT 13  
 AAB24409  
 ID AAB24409 standard; Protein; 241 AA.  
 XX  
 AC AAB24409;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO364 protein sequence SEQ ID NO:117.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.

---

RESULT	15	
AAV52159		
ID	AAV52159	standard; Protein; 241 AA.
XX		
AC	AAV52159;	
XX		
DT	01-FEB-2000	(first' entry)
XX		
DE	TR11SV1	amino acid sequence.
XX		
KW	Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;	
KW	GTR; growth; differentiation; cell death; immune deficiency disorder;	
KW	Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;	
KW	Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;	
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease;	
XX	inflammatory condition.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
Domain	1..162	
FT	/note= "Extracellular domain"	
FT	163..179	
FT	/note= "Transmembrane domain"	
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FT	/note= "Intracellular domain"	
XX		
PN	WO9920758-A1.	
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PD	29-APR-1999.	
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PF	21-OCT-1998; 98WO-US22085.	
XX		
PR	21-OCT-1997; 97US-0063212.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	N1 J, Ruben SM;	
XX		
DR	WPI; 2000-061922/05.	
XX	N-PSDB; AA237763.	
XX		
PT	New tumour necrosis factor receptor-like polypeptides used to, e.g.	
PT	treat Digeorge syndrome -	
XX		
PS	Claim 14; Fig 2; 167pp; English.	

```

CC They can also be used to repair, replace, or protect tissue damaged by
CC congenital defects, trauma, age, disease, surgery, including cosmetic
CC plastic surgery, fibrosis, reperfusion injury, peripheral nerve
CC injuries, neuropathies, and central nervous system disease (e.g.
CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can
CC also be used for detection, diagnosis and prognosis.
XX
XX
SQ Sequence      241 AA;

Query Match      100.0%; Score 246; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.7e-24;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 DCASGTFSGHGHCXKPWDTCQFGELTVFPGNKTHNAVCV 41
      |||||
Db 114 dcasgtfsgghgchckpwtcdtqfglftvpgnktthnavcv 154
      |||||

```

PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX other T cell disorders  
 XX  
 XX Disclosure: Pages 61-62; 71pp; English.  
 XX  
 CC This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 228 AA;

Query Match 100.0%; Score 252; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. NO. 4e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCDEPCTTCRHHCPCPGQVQSGKFSFGQCI 40  
 |||||  
 Db 68 cvqpefhcgdpctctrhpcpgqvgvsgkfsfgfqi 107

RESULT 2  
 AAY95879  
 ID AAY95879 standard; Protein: 234 AA.  
 XX  
 AC AAY95879;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-like protein Trl1.  
 XX  
 KW Trl1; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Signal\_peptide  
 FT Protein 26..234  
 FT /label= Mature\_protein  
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 FT /label= Extracellular\_domain  
 FT Domain 163..179  
 FT /label= Transmembrane\_domain  
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 FT /note= "N-glycosylated"  
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 FT /note= "epitope-bearing region"  
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 XX  
 XX WO200050459-A1.  
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 XX 31-AUG-2000.  
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 XX 23-FEB-2000; 2000WO-US04572.  
 XX  
 XX 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, NI J;  
 XX  
 XX WPI: 2000-572072/53.  
 XX N-PSDB; AAA50304.  
 XX  
 XX Human tumor necrosis factor receptor-like proteins useful for  
 XX diagnosis, prevention and treatment of disease states associated with  
 XX aberrant cell survival such as autoimmune disease and rheumatoid  
 XX arthritis  
 XX  
 XX Claim 14(c); Fig 1A-B; 278pp; English.  
 PS  
 XX  
 CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein Trl1, a novel 25 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
 CC Trl1 activated NF-kappaB through a TRAF2-mediated mechanism.  
 CC Expression is activation-inducible. The Trl1 ligand is constitutively  
 CC expressed in an endothelial cell line. This suggests that Trl1 and  
 CC its ligand may be involved in activated T-cell trafficking.  
 CC The invention provides Trl1, Trl1SV1 and Trl1SV2 nucleic acids  
 CC (see AAA50304-06) and highly conserved encoded proteins (see  
 CC AAY95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. Trl1, Trl1SV1 and/or Trl1SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency,  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. Trl1, Trl1SV1 and/or Trl1SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: - September 4, 2001, 15:56:24 ; Search time 126.12 Seconds  
(without alignments)  
19.227 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_74\_113

Perfect score: 252

Sequence: 1 CVQPEFHGDPCTTCHHPGPGQGVQSGKFSFGQCI 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	252	100.0	228	19 AAW37840	Truncated human 31
2	252	100.0	234	21 AAY95879	Human tumour necro
3	252	100.0	234	21 AAY52158	Tumour necrosis fa
4	252	100.0	235	21 AAY44825	Human molecule ass
5	252	100.0	240	21 AAY95881	Human tumour necro
6	252	100.0	240	21 AAY52160	TRILSV2 amino acid
7	252	100.0	241	19 AAW37839	Amino acid sequenc
8	252	100.0	241	20 AAY06605	Human TNF receptor
9	252	100.0	241	21 AAB27651	Human protein PRO3
10	252	100.0	241	21 AAB32431	Human PRO364 prote
11	252	100.0	241	21 AAY95880	Human tumour necro

12	252	100.0	241	21 AAY95895	Human tumour necro
13	252	100.0	241	21 AAB24409	Human PRO364 prote
14	252	100.0	241	21 AAY71467	Human PRO364 prote
15	252	100.0	241	21 AAY52159	TRILSV1 amino acid
16	252	100.0	241	22 AAB20115	Human immunostimul
17	252	100.0	241	22 AAB47054	Human PRO364. Hom
18	252	100.0	241	22 AAB50910	Human PRO364 prote
19	252	100.0	241	22 AAB50982	Human PRO364 prote
20	252	100.0	241	22 AAB53090	Human angiogenesis
21	252	100.0	311	19 AAW37842	Human 312C2 protei
22	252	100.0	316	22 AAB47055	Polyptide encode
23	252	100.0	317	20 AAY06645	PRO364-related EST
24	207.5	82.3	232	19 AAW37841	Human 312C2 protei
25	168	66.7	222	19 AAW49018	Mouse glucocortico
26	168	66.7	228	19 AAW49016	Mouse glucocortico
27	168	66.7	228	19 AAW37838	Amino acid sequenc
28	168	66.7	224	19 AAW49017	Mouse glucocortico
29	125	49.6	89	21 AAY76013	Murine TNF-alpha f
30	125	49.6	89	22 AAB55952	Skin cell protein, 41bb
31	67	26.6	191	22 AAB66986	41bb protein. Uni
32	67	26.6	256	16 AAR70978	4-1BB receptor pro
33	67	26.6	256	16 AAR64199	Murine 4-1BB polyp
34	67	26.6	256	17 AAW04173	Mouse receptor 4-1
35	67	26.6	256	18 AAW26659	Mouse 4-1BB recept
36	67	26.6	256	20 AAY33215	Murine CD137 prote
37	67	26.6	256	20 AAY28687	Mouse Receptor 4-1
38	64.5	25.6	255	21 AAY58213	Canine mature CD40
39	64.5	25.6	274	21 AAY58212	Canine CD40. Cani
40	64	25.4	478	22 AAB48033	EGF receptor relat
41	63	25.0	185	19 AAW60046	Human TNF receptor
42	63	25.0	185	21 AAY94716	Human TR2-receptor
43	63	25.0	186	21 AAY79206	Soluble herpesviru
44	63	25.0	193	21 AAY79204	Soluble herpesviru
45	63	25.0	197	21 AAY79205	Soluble herpesviru

#### ALIGNMENTS

RESULT 1  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX  
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX  
OS Homo sapiens.  
XX  
PN WO9806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 14-AUG-1997; 97WO-US13931.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM, Randall TD, Zlotnik A;  
XX WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PT Isolated 312C2 T cell gene - used to develop products for treating,

FT Modified-site /note= "Potential phosphorylation site"  
 FT 48  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 62  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 82  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 205  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 223  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 140  
 FT Modified-site /note= "N-glycosylated"  
 FT  
 PN W0200005374-A2.  
 XX  
 XX 03-FEB-2000.  
 PD  
 XX  
 XX 21-JUL-1999; 99WO-US16637.  
 PF  
 XX 22-JUL-1998; 98US-0093827.  
 PR  
 XX (INCY-) INCYTE PHARM INC.  
 PA  
 XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 PI  
 XX WPI; 2000-182699/16.  
 XX N-PSDB; AA249948.  
 DR  
 XX Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 PT  
 XX Claim 1; Pages 64-65; 67pp; English.  
 PS  
 XX The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from incyte clone 2809903 isolated from TLYMN0706  
 CC cDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotrophic, antiinflammatory, antipsoriatic, cytostatic, antilashmatic,  
 CC dermatologic, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 SQ Sequence 235 AA;  
 Query Match 100.0%; Score 252; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CVQPEHCGDPCCCTCRHHPGPGQVGSQGFQFCI 40  
 Db 68 cvqpehcgdpccctcrhbpqpgvgqgkfsfgfqi 107  
 RESULT 5  
 ID AAY95881  
 XX AAY95881 standard; Protein; 240 AA.  
 AC  
 XX AAY95881;  
 XX  
 XX 20-NOV-2000 (first entry)  
 DT  
 XX Human tumour necrosis factor receptor-like protein TR11SV2.  
 DE  
 XX TR11SV2; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; anti-rheumatic; antiarthritic; haemostatic;  
 DR

KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /label= Signal\_peptide  
 FT 20..240  
 FT /label= Mature\_protein  
 FT 20..168  
 FT Domain  
 FT /label= Extracellular\_domain  
 FT 169..185  
 FT /label= Transmembrane\_domain  
 FT 186..240  
 FT /label= Intracellular\_domain  
 FT 152  
 FT /note= "N-glycosylated"  
 FT 57..68  
 FT /note= "conserved domain CD-I"  
 FT 78..87  
 FT /note= "conserved domain CD-II"  
 FT 91..100  
 FT /note= "conserved domain CD-III"  
 FT 114..121  
 FT /note= "conserved domain CD-IV"  
 FT 134..140  
 FT /note= "conserved domain CD-V"  
 FT 159..166  
 FT /note= "conserved domain CD-VI"  
 FT 182..192  
 FT /note= "conserved domain CD-VII"  
 FT 210..215  
 FT /note= "conserved domain CD-IX"  
 FT 230..239  
 FT /note= "conserved domain CD-X"  
 FT 20..28  
 FT /note= "epitope-bearing region"  
 FT 24..32  
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 FT 37..45  
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 FT 48..56  
 FT /note= "epitope-bearing region"  
 FT 67..75  
 FT /note= "epitope-bearing region"  
 FT 106..114  
 FT /note= "epitope-bearing region"  
 FT 130..139  
 FT /note= "epitope-bearing region"  
 FT 149..157  
 FT /note= "epitope-bearing region"  
 FT 162..170  
 FT /note= "epitope-bearing region"  
 FT 209..217  
 FT /note= "epitope-bearing region"  
 FT 228..236  
 FT /note= "epitope-bearing region"  
 XX W02000050459-AL.  
 PN  
 XX 31-AUG-2000.  
 PD  
 XX 23-FEB-2000; 2000WO-US04572.  
 PF  
 XX 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Ruben SM, Ni J;  
 PI  
 XX WPI; 2000-572072/53.  
 DR

CC polypeptides may also be used. Methods for screening for  
 XX agonist/antagonist compounds are also provided.

SQ Sequence 234 AA;

Query Match 100.0%; Score 252; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 4.1e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRHHPGCGVQSGKFSFGFCI 40

Db 74 cvqpefhcgdpctctcrhhpcppgvgqgkfsfgfc1 113

RESULT 3

AAV52158

ID AAV52158 standard; Protein; 234 AA.

XX AC AAV52158;

XX DT 01-FEB-2000 (first entry)

XX DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.

XX KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;

XX KW G1TR; growth; differentiation; cell death; immune deficiency disorder;

XX KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;

XX KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;

XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease;

XX KW inflammatory condition.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..25

XX FT Protein /label= Signal\_peptide

XX FT FT 26..234

XX FT FT /label= TR11

XX FT Domain 26..162

XX FT /note= "Extracellular domain"

XX FT Domain 163..179

XX FT /note= "Transmembrane domain"

XX FT Domain 180..234

XX FT /note= "Intracellular domain"

XX PN W09920758-A1.

XX PD 29-APR-1999.

XX PF 21-OCT-1998; 98WO-US22085.

XX PR 21-OCT-1997; 97US-0063212.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Ruben SM;

XX XX WPI; 2000-061922/05.

XX DR N-PSDB; AAZ37762.

XX XX New tumour necrosis factor receptor-like polypeptides used to, e.g.

XX FT treat Digeorge syndrome -

XX PS Claim 14; Fig 1; 167pp; English.

XX CC This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor-like protein (TR11 receptor). The invention relates to TR11 and  
 CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
 CC determined by sequencing cloned cDNAs AAZ37765-z37766. The TR11 receptor  
 CC and its splice variants show homology to the murine glucocorticoid  
 CC induced tumour necrosis factor receptor family-related gene (G1TR).  
 CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation

CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.

XX SQ Sequence 234 AA;

Query Match 100.0%; Score 252; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 4.1e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRHHPGCGVQSGKFSFGFCI 40

Db 74 cvqpefhcgdpctctcrhhpcppgvgqgkfsfgfc1 113

RESULT 4

AAV44825

ID AAV44825 standard; Protein; 235 AA.

XX AC AAV44825;

XX DT 18-MAY-2000 (first entry)

XX DE Human molecule associated with cell proliferation, MACP-5.

XX KW Human; molecule associated with cell proliferation; MACP-5;

XX KW Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;

XX KW anti-inflammatory; antipapillary; anti-HIV; antithymic; anaemia;

XX KW dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic;

XX KW immunosuppressive; osteopathic; antiarthritic; urapathic; antitumor;

XX KW ophthalmological; diagnosis; treatment; prevention; immune disorder;

XX KW cell proliferative disorder; actinic keratosis; arteriosclerosis;

XX KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 1..19

XX FT /label= Signature\_sequence

XX FT Region 68..96

XX FT /label= Signature\_sequence

XX FT Region 109..147

XX FT /label= Signature\_sequence

XX FT Region 122..129

XX FT /label= Signature\_sequence

XX FT Region 157..175

XX FT /label= Signature\_sequence

XX FT Region 165..186

XX FT /label= Signature\_sequence

XX FT Modified-site 37



DT	28-JUL-1998	(first entry)
XX		
XX		Amino acid sequence of the human 312C2 T cell protein.
XX		
KW	Human 312C2 T cell protein;	thymus cell; spleen cell; T cell;
KW	antigen-specific T cell proliferation;	cytokine production by T-cell;
KW	apoptosis; cancer;	haematopoietic cells; lymphoid cell;
KW	autoimmune disorders.	
XX		
XX	Homo sapiens.	
OS		
XX		
XX		
Key	Location/Qualifiers	
CDS	1..726	
FT	/*tag= a	
FT	/product= "human 312C2 protein"	
XX		
XX	W09806842-A1.	
PN		
XX		
PD	19-FEB-1998.	
XX		
XX	14-AUG-1997;	97WO-US13931.
XX		
XX		
PR	07-OCT-1996;	96US-0027901.
PR	16-AUG-1996;	96US-0689943.
XX		
XX	(SCHE ) SCHERING CORP.	
XX		
XX	Gorman DM, Randall TD, Zlotnik A;	
PI		
XX		
XX	WPI; 1998-159534/14.	
DR	N-PSDB; AAV19153.	
XX		
XX		
PT	Isolated 312C2 T cell gene -	used to develop products for treating,
PT	e.g. cancers, auto-immune disorders,	transplantation rejection and
PT	other T cell disorders	
XX		
XX	Claim 2; Pages 59-60; 71pp; English.	
XX		
XX	This is the amino acid sequence encoding the human 312C2 T cell	
CC	protein. The 312C2 proteins are expressed in thymus cells and are	
CC	induced on T cells and spleen cells following activation. Engagement	
CC	of 312C2 stimulates proliferation of T cell clones, antigen-specific	
CC	proliferation and cytokine production by T-cells, and potentiates T	
CC	cell expansion or apoptosis. The products can be used in the	
CC	treatment of conditions associated with abnormal physiology or	
CC	development, including abnormal proliferation, e.g. cancerous	
CC	conditions or degenerative conditions. They can be used in the	
CC	regulation or development of haematopoietic cells; e.g. lymphoid cells	
CC	which affect immunological responses, e.g. autoimmune disorders.	
XX		
SQ	Sequence	241 AA;
	Query Match	100.0%; Score 252; DB 19; Length 241;
	Best Local Similarity	100.0%; Pred. No. 4.2e-20;
	Matches	40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CVQPEFHCGDPCCCTCRHHPCPGGQVQSQKFSGFOCI 40
Db	74	cvqpefhcgdpccctcrhhpcpggqvggkfstgfqci 113
RESULT	8	
AAV06605		
ID	AAV06605 standard; Protein;	241 AA.
XX		
XX	AAV06605;	
AC		
XX		
DT	26-OCT-1999	(first entry)
XX		
DE	Human TNF receptor homologue	PRO364.
XX		
XX	PRO364; tumour necrosis factor receptor; human; apoptosis;	

KW	Inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy.
KX	Homo sapiens.
OS	
XX	Key Location/Qualifiers
FH	Peptide 1..25
FT	/note= "signal peptide"
FT	Protein 26..241
FT	/note= "mature protein"
FT	Modified-site 146
FT	/note= "N-glycosylated"
FT	Domain 162...180
FT	/note= "transmembrane domain"
XX	
WN	WO9940196-A1.
XX	
PD	12-AUG-1999.
XX	
PF	09-FEB-1999; 99WO-US02642.
XX	
PR	09-FEB-1998; 98US-0024087.
XX	
PA	(GETH ) GENENTECH INC.
XX	
PI	Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;
PI	Pitti RM, Wood WT;
XX	
DR	NPI; 1999-494296/41.
DR	NP-PSDB; AAX87670.
PT	Tumour necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune responses
XX	
PS	Claim 17; Fig 2A; 104pp; English.
CC	The present sequence represents human PRO364, a novel member of the tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the recombinant production of PRO364 polypeptides, e.g. in CHO, Escherichia coli or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present sequence, where X is any one of amino acid residues 157-167 of PRO364. PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammalian cells (claimed). Chimeric molecules comprising a PRO364 polypeptide fused to a heterologous sequence such as epitope tag or immunoglobulin Fc region are also claimed. PRO364 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PRO364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as inhibitors.
XX	
SQ	Sequence 241 AA:
	Query Match 100.0%; Score 252; DB 20; Length 241;
	Best Local Similarity 100.0%; Pred.No. 4.2e-20;
	Matches 40; Conservative 0; Mismatches 0; Indels 0; Gap
QY	1 CVQPEFHCGBPCTTCRRHPGPGGVQSQRKSFSGFCI 40
Db	74 cvqpefhcgpccttcrhhpcppggvqsqrkfsfgfci 113
RESULT	9
AAB27651	
ID	AAB27651 standard; Protein: 241 AA.

DR N-PSDB; AAA50306.

XX Human tumor necrosis factor receptor-like proteins useful for

PT diagnosis, prevention and treatment of disease states associated with

PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis

XX

PS Claim 14(n); Fig 3A-B; 278pp; English.

XX

CC The present sequence is that of human tumour necrosis factor

CC receptor-like protein TR11SV2, a novel 26 kDa protein which shows

CC 58.6% identity to murine glucocorticoid induced tumour necrosis

CC factor receptor family-related gene. The sequence was deduced from

CC a cDNA clone (see AAA50306) discovered in an activated T-cell library.

CC The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids

CC (see AAA50304-06) and highly conserved encoded proteins (see

CC AA95879-81), as well as vectors, host cells and recombinant methods for

CC their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful

CC for treating, preventing, prognosis and/or diagnosis of an

CC immunodeficiency, especially common variable immunodeficiency,

CC X-linked agammaglobulinemia, severe combined immunodeficiency

CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin

CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2

CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis

CC and/or diagnose an autoimmune disease, especially rheumatoid

CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura

CC or IgA nephropathy. The polypeptides, polynucleotides and/or

CC antibodies can be administered to cells in vitro, ex vivo or in

CC vivo or to a multicellular organism. Soluble forms of the

CC polypeptides may also be used. Methods for screening for the

CC agonist/antagonist compounds are also provided.

XX

SQ Sequence 240 AA;

Query Match 100.0%; Score 252; DB 21; Length 240;

Best Local Similarity 100.0%; Pred. No. 4.2e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTCRHHPCPPGQGVQSGKFSFGFCI 40

DB 80 CVQPEFHCGDPCCTCRHHPCPPGQGVQSGKFSFGFCI 119

RESULT 6

AAV52160

ID AAV52160 standard; Protein; 240 AA.

XX

AC AAV52160;

XX

DT 01-FEB-2000 (first entry)

XX

DE TR11SV2 amino acid sequence.

XX

KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;

KW G1R; growth; differentiation; cell death; immune deficiency disorder;

KW Digorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;

KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease;

KW inflammatory condition.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Signal\_peptide

FT Protein 20..240

FT /label= TR11SV2

FT Domain 20..168

FT /note= "Extracellular domain"

FT Domain 169..185

FT /note= "Transmembrane domain"

FT Domain 186..240

FT

XX

PN WO9920758-A1.

XX

PD 29-APR-1999.

XX

PF 21-OCT-1998; 98WO-US22085.

XX

PR 21-OCT-1997; 97US-0063212.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ni J, Ruben SM;

XX

WPI; 2000-061922/05.

XX

N-PSDB; AA237764.

DR

DR New tumour necrosis factor receptor-like polypeptides used to, e.g.

PT treat Digorge syndrome

PT

PS Claim 14; Fig 3; 167pp; English.

XX

CC This is the amino acid sequence of the human tumour necrosis factor

CC receptor-like protein splice variant 2 (TR11SV2 receptor). The invention

CC relates to TR11 and two splice variants TR11SV1 and TR11SV2. The

CC nucleotide sequences were determined by sequencing cloned cDNAs

CC AA237765-237766. The TR11 receptor and its splice variants show homology

CC to the murine glucocorticoid induced tumour necrosis factor receptor

CC family related gene (G1TR). TR11, TR11SV1 and TR11SV2 polypeptides may

CC be involved in the regulation of cell-type specific receptor-mediated

CC cell growth, differentiation, and ultimately, cell death. They can be

CC used for screening for agonists/antagonists. The polypeptides, agonists

CC or antagonists can be used for treating a disease state associated with

CC aberrant cell survival. They can be used for treating immune deficiency

CC disorders, Digorge syndrome, HIV infection, severe combined

CC immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation

CC disorders, blood platelet disorders or wounds resulting from trauma or

CC surgery. They can also be used to treat heart attacks, strokes,

CC Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures

CC syndrome, Grave's disease, multiple sclerosis, myasthenia gravis,

CC Stiff-Man syndrome, systemic lupus erythematosus, Gullain-Barre

CC syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory

CC eye disease, anaphylaxis, hypersensitivity to an antigenic molecule,

CC organ rejection or graft versus host disease, inflammatory conditions,

CC ischaemia-reperfusion injury, complement-mediated hyperacute rejection,

CC nephritis, cytokine or chemokine induced lung injury, inflammatory bowel

CC disease, Crohn's disease, hyperproliferative disorders, or infections.

CC They can also be used to repair, replace, or protect tissue damaged by

CC congenital defects, trauma, age, disease, surgery, including cosmetic

CC plastic surgery, fibrosis, reperfusion injury, peripheral nerve

CC injuries, neuropathies, and central nervous system disease (e.g.

CC Alzheimer's disease, Parkinson's disease, Huntington's disease,

CC anyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can

CC also be used for detection, diagnosis and prognosis.

XX

SQ Sequence 240 AA;

Query Match 100.0%; Score 252; DB 21; Length 240;

Best Local Similarity 100.0%; Pred. No. 4.2e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTCRHHPCPPGQGVQSGKFSFGFCI 40

DB 80 CVQPEFHCGDPCCTCRHHPCPPGQGVQSGKFSFGFCI 119

RESULT 7

AAW37839

ID AAW37839 standard; Protein; 241 AA.

XX

AC AAW37839;

XX

```

XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
XX PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
XX PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX DR WPI: 2000-572271/53.
XX DR N-PSDB; AAC58536.
XX
XX PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX PS Claim 33; Fig 36; 309pp; English.
XX
XX CC The present invention describes sixty four human PRO proteins which can
XX CC be used in the treatment of immune related diseases. The human PRO
XX CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
XX CC treating and diagnosing immune related disorders. The disorders are
XX CC selected from systemic lupus erythematosus, rheumatoid arthritis,
XX CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
XX CC immune-mediated renal disease, demyelinating diseases of the central
XX CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
XX CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
XX CC autoimmune or immune-mediated skin diseases, allergic diseases,
XX CC immunological diseases of the lung, and transplantation associated
XX CC diseases including graft rejection and graft-versus-host-disease.
XX CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
XX CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
XX CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
XX CC sequences given in the exemplification of the present invention.
XX SQ Sequence 241 AA;

Query Match 100.0%; Score 252; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTCRHHPCPGQGVOSQCKFSGFQCI 40
Db |||||
74 cvqpefhcgdpccctcrhhpcpgpgvgqgkfsfgfqi 113

RESULT 11
ID AAY95880
XX AC AAY95880 standard; Protein; 241 AA.
XX AC AAY95880;
XX
XX DT 20-NOV-2000 (first entry)
XX
XX DE Human tumour necrosis factor receptor-like protein TR11SV1.
XX
XX KW TR11SV1; human; tumour necrosis factor receptor-like protein;
XX KW immunodeficiency; autoimmune disease; rheumatoid arthritis;
XX KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;
XX KW dermatological; antiinflammatory; therapy; diagnosis.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Domain 1...162
XX FT /label= Extracellular_domain
XX FT Domain 163...179
XX FT /label= Transmembrane_domain
XX FT Domain 180...241
XX FT /label= Intracellular_domain
XX FT Modified-site 146

```

```

FT Domain
FT /note= "N-glycosylated"
FT 51..61
FT /note= "conserved domain CD-I"
FT 72..81
FT /note= "conserved domain CD-II"
FT 85..94
FT /note= "conserved domain CD-III"
FT 108..115
FT /note= "conserved domain CD-IV"
FT 128..134
FT /note= "conserved domain CD-V"
FT 153..160
FT /note= "conserved domain CD-VI"
FT 176..186
FT /note= "conserved domain CD-VII"
FT 195..201
FT /note= "conserved domain CD-VIII"
FT 211..216
FT /note= "conserved domain CD-IX"
FT 231..240
FT /note= "conserved domain CD-X"
FT 2..10
FT /note= "epitope-bearing region"
FT 11..19
FT /note= "epitope-bearing region"
FT 27..35
FT /note= "epitope-bearing region"
FT 38..46
FT /note= "epitope-bearing region"
FT 42..50
FT /note= "epitope-bearing region"
FT 31..46
FT /note= "epitope-bearing region"
FT 61..69
FT /note= "epitope-bearing region"
FT 99..107
FT /note= "epitope-bearing region"
FT 125..133
FT /note= "epitope-bearing region"
FT 143..151
FT /note= "epitope-bearing region"
FT 156..164
FT /note= "epitope-bearing region"
FT 196..204
FT /note= "epitope-bearing region"
FT 209..217
FT /note= "epitope-bearing region"
FT 229..237
FT /note= "epitope-bearing region"
XX WO200050459-A1.
XX
XX PD 31-AUG-2000.
XX
XX PF 23-FEB-2000; 2000WO-US04572.
XX
XX PR 24-FEB-1999; 99US-0121648.
XX PR 13-MAY-1999; 99US-0134172.
XX PR 16-JUL-1999; 99US-0144076.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ruben SM, NI J;
XX
XX DR WPI; 2000-572072/53.
XX DR N-PSDB; AAA50305.
XX
XX PT Human tumor necrosis factor receptor-like proteins useful for
XX PT diagnosis, prevention and treatment of disease states associated with
XX PT aberrant cell survival such as autoimmune disease and rheumatoid
XX PT arthritis -
XX PS Claim 14(1); Fig 2A-B; 278pp; English.

```

```

XX AAB27651;
AC 26-JAN-2001 (first entry)
DT Human protein PRO364.
DE
XX
XX Cardiovascular; endothelial; angiogenic disorder; PRO179;
KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;
KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= "Signal peptide"
XX
PN WO200053757-A2.
XX
XX 14-SEP-2000.
XX
XX 24-FEB-2000; 2000WO-US05004.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 02-JUN-1999; 99WO-US12252.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 02-DEC-1999; 99WO-US28565.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME,
PI Goddard A, Gurney AL, Hillian KJ, Marsters SA, Paoni NF, Pitti RM;
PI Watanabe CK, Williams PM, Wood WI;
XX
XX WPI: 2000-611444/58.
XX N-PSDB; AAA99903.
XX
XX Novel PRO polypeptides and agonists and antagonists of them, used to
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders
PT
XX
XX Claim 71; Fig 6; 181pp; English.
XX
XX The present invention relates to methods for stimulating or inhibiting
CC angiogenesis and cardiovascularization. The methods involve the use of
CC pharmaceutical compositions based on the following proteins, PRO179,
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,
CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These
CC proteins were identified by isolating cDNA clones encoding secreted
CC proteins. The proteins of the invention may be used to diagnose and
CC treat cardiovascular, endothelial or angiogenic disorders. The present
CC sequence is one of the proteins of the invention.
XX
XX Sequence 241 AA;

```

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Query Match 100.0%; Score 252; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 4, 2e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVQPEFHCGDPCCTTCRRHPCPPGGVQSGKFSFGQCI 40
Db 74 cvqpefhcgdpctcttrhrhpcppggvqsgkfsfgfqi 113

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```

RESULT 10
AAB33431
ID AAB33431 standard; Protein: 241 AA.
XX
XX AC AAB33431;
XX
XX 29-JAN-2001 (first entry)
XX
XX DE Human PRO364 protein UNQ319 SEQ ID NO:92.
XX
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
XX Homo sapiens.
XX
XX WO200053758-A2.
XX
XX 14-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05841.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 10-MAR-1999; 99US-0123618.
XX 12-MAR-1999; 99US-0123957.
XX 23-MAR-1999; 99US-0125775.
XX 12-APR-1999; 99US-0128849.
XX 20-APR-1999; 99WO-US08615.
XX 28-APR-1999; 99US-0131445.
XX 04-MAY-1999; 99US-0132371.
XX 14-MAY-1999; 99US-0134287.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 20-JUL-1999; 99US-0144758.
XX 28-JUL-1999; 99US-0145698.
XX 28-JUL-1999; 99US-0146222.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 29-OCT-1999; 99US-0162506.
XX 29-NOV-1999; 99WO-US28214.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30999.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.

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PR 13-SEP-1999; 99WO-US20944.
PR 13-SEP-1999; 99WO-US21090.
PR 13-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
PI Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2000-412154/35.
DR N-PSDB; AAA77604.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating cardiovascular, endothelial or
PT angiogenic disorders in mammals
XX
XX Claim 72; Fig 44; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
XX useful for preventing, diagnosing and treating a disorder in mammals by
XX cardiovascular, endothelial or angiogenic disorder in mammals by
XX modulating cell proliferation and angiogenesis and cardiovascularisation,
XX and for identifying agonists and antagonists of these processes. The
XX nucleic acids and the proteins they encode may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate PRO expression such as cardiovascular, endothelial or
XX angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
XX cardiac hypertrophy). For example, the nucleic acids (Ncs) and vectors
XX containing them and the PRO polypeptide may be used to treat disorders
XX associated with decreased PRO expression. AAA77510 to AAA77721 and
XX AAB24388 to AAB24435 represent nucleotide and protein sequences used in
XX the exemplification of the present invention.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 252; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVQPEFHCGDPCCTTCRHHPCPPGQVSGQKFSFGFCI 40
Db 74 cvqpefhcgdpcccttrhhpcppggvgsgqkfsfgfc 113

RESULT 14
AA71467
ID AA71467 standard; Protein: 241 AA.
XX
XX AA71467;
XX
XX 08-NOV-2000 (first entry)
XX
XX Human PRO364 protein.
DE
XX
XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
KW breast; prostate; colon; lung; renal; ovarian; central nervous system;
KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
KW tumour necrosis factor receptor; GTR protein homologue.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= Signal_peptide
FT Modified-site 5..11
FT /note= "N-myristoylation site"
FT Modified-site 8..14
FT /note= "N-myristoylation site"

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FT Modified-site 25..31
FT /note= "N-myristoylation site"
FT Protein 26..241
FT /label= Mature_PRO364_protein
FT Modified-site 30..36
FT /note= "N-myristoylation site"
FT Modified-site 33..39
FT /note= "N-myristoylation site"
FT Modified-site 118..124
FT /note= "N-myristoylation site"
FT Modified-site 122..128
FT /note= "N-myristoylation site"
FT Modified-site 146..150
FT /note= "Asn is N-glycosylated"
FT Modified-site 156..162
FT /note= "N-myristoylation site"
FT Domain 163..183
FT /label= Transmembrane_domain
FT Binding-site 166..177
FT /note= "Prokaryotic membrane lipoprotein lipid
FT attachment site"
FT Region 171..193
FT /note= "Leucine zipper pattern"
XX
XX WO200032778-A2.
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US28409.
XX
XX 01-DEC-1998; 98WO-US25108.
XX 16-DEC-1998; 98US-0112850.
XX 22-DEC-1998; 98US-0113296.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
XX
XX WPI; 2000-412325/35.
XX N-PSDB; AAD01240.
XX
XX New composition useful for inhibiting neoplastic cell growth and for
XX treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
XX their antagonists
XX
XX Claim 31; Fig 4; 108pp; English.
XX
XX The present sequence is the human PRO364 protein, encoded by the cDNA
XX clone, designated as DNA47365-1206. It is isolated from human small
XX intestine tissue cDNA library, identified using probes based on the
XX consensus sequence DNA44825, relative to the Incyte expressed sequence
XX tag (EST) 3003460. This EST has homology to tumour necrosis factor
XX receptor (TNFR) family of polypeptides. PRO364 sequence also shows
XX homology to members of the TNFR family, and mouse GTR protein.
XX This clone is assigned the ATCC deposit No: 209436. PRO364 functions as
XX a neoplastic cell growth inhibitor and is used for treating tumours
XX using an effective amount of PRO655, PRO364 and PRO344. This composition
XX is especially useful for treatment of human cancers such as breast,
XX prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 252; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVQPEFHCGDPCCTTCRHHPCPPGQVSGQKFSFGFCI 40
Db 74 cvqpefhcgdpcccttrhhpcppggvgsgqkfsfgfc 113

```

XX The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR1SV1, a novel 26 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC cDNA (see AAAS0305) discovered in a PHA-stimulated T-cell library.  
 CC The invention provides TR11, TR1SV1 and TR1SV2 nucleic acids  
 CC (see AAAS0304-06) and highly conserved encoded proteins (see  
 CC AAY95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. TR11, TR1SV1 and/or TR1SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR1SV1 and/or TR1SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX Sequence 241 AA;

Query Match 100.0%; Score 252; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTCRHHPCPPGQVSGQKFSFGFCI 40  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 74 cvqpefhcgdpctcttrhhpcppgqvgqskfsfgfqi 113

## RESULT 12

AAY95895  
 ID AAY95895 standard; Protein; 241 AA.  
 XX  
 AC AAY95895;  
 XX  
 DT 20-NOV-2000 (first entry).  
 XX  
 DE Human tumour necrosis factor receptor-like protein TR11 mutein.  
 XX  
 KW TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
 KW mutant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200050459-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 23-FEB-2000; 2000WO-US04572.  
 XX  
 PR 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Ni J;  
 XX  
 DR WPI; 2000-572072/53.  
 XX  
 PT Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis  
 XX  
 PS Disclosure; 294-295; 278pp; English.  
 XX  
 CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR11, TR1SV1 and TR1SV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR11, TR1SV1 and/or TR1SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR1SV1 and/or TR1SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX Sequence 241 AA;

Query Match 100.0%; Score 252; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTCRHHPCPPGQVSGQKFSFGFCI 40  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 74 cvqpefhcgdpctcttrhhpcppgqvgqskfsfgfqi 113

## RESULT 13

AAB24409  
 ID AAB24409 standard; Protein; 241 AA.  
 XX  
 AC AAB24409;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO364 protein sequence SEQ ID NO:117.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.

---

## RESULT 15

AAV52159  
ID AAV52159 standard; Protein; 241 AA.XX AC AAV52159;  
XX DT 01-FEB-2000 (first entry)XX DE TR1LSV1 amino acid sequence.  
XX KW Tumour necrosis factor receptor-like protein; TR1L; TR1LSV1; TR1LSV2;  
KW G1TR; growth; differentiation; cell death; immune deficiency disorder;  
KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
KW inflammatory condition.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT Domain 1..162  
FT /note= "Extracellular domain"  
FT Domain 163..179  
FT /note= "Transmembrane domain"  
FT Domain 180..241  
FT /note= "Intracellular domain"

XX PN W09920758-A1.

XX PD 29-APR-1999.

XX PF 21-OCT-1998; 98WO-US22085.

XX PR 21-OCT-1997; 97US-0063212.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Ruben SM;

XX DR WPI; 2000-061922/05.  
XX DR N-PSDB; AAZ37763.XX PT New tumour necrosis factor receptor-like polypeptides used to, e.g.  
XX PT treat Digeorge syndrome -

XX PS Claim 14; Fig 2; 167pp; English.

This is the amino acid sequence of the human tumour necrosis factor receptor-like protein splice variant 1 (TR1LSV1 receptor). The invention relates to TR1L and two splice variants TR1LSV1 and TR1LSV2. The nucleotide sequences were determined by sequencing cloned cDNAs AAZ37765-37766. The TR1L receptor and its splice variants show homology to the murine glucocorticoid-induced tumour necrosis factor receptor family related gene (G1TR). TR1L, TR1LSV1 and TR1LSV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, Digeorge syndrome, HIV infection, severe combined immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections.

CC They can also be used to repair, replace, or protect tissue damaged by  
CC congenital defects, trauma, age, disease, surgery, including cosmetic  
CC plastic surgery, fibrosis, reperfusion injury, peripheral nerve  
CC injuries, neuropathies, and central nervous system disease (e.g.  
CC Alzheimer's disease, Parkinson's disease, Huntington's disease,  
CC anyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can  
CC also be used for detection, diagnosis and prognosis.

XX SQ Sequence 241 AA;

Query Match 100.0%; Score 252; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 CVQPEFHGCDPCCTCRHHPCPPGGVQSGKFSFGFCI 40  
|||||  
Db 74 cvqpefhcgdpccctcrhhpcppggvgsgkfsfgfc 113Search completed: September 4, 2001, 15:56:24  
Job time: 341 sec



PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX other T cell disorders  
 PS Disclosure; Pages 61-62; 71pp; English.  
 CC This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone\_A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX SQ Sequence 228 AA;

Query Match 100.0%; Score 255; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGECCEWDCM 41  
 |||||  
 Db 27 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGECCEWDCM 67

RESULT 2  
 AAW37841  
 ID AAW37841 standard; Protein; 232 AA.  
 AC AAW37841;  
 DT 28-JUL-1998 (first entry)  
 XX Human 312C2 protein from clone\_A5 amino acid sequence.  
 DE Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 XX antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX Homo sapiens.  
 OS WO9806842-A1.  
 PN 19-FEB-1998.  
 PD 14-AUG-1997; 97WO-US13931.  
 PF 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX (SCHE ) SCHERING CORP.  
 PA Gorman DM, Randall TD, Zlotnik A;  
 PI WPI; 1998-159534/14.  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 PS Disclosure; Pages 62-63; 71pp; English.  
 CC This is the amino acid sequence of the human 312C2 T cell protein from  
 CC clone\_A5, which is identical to sequence AAW37838 for the first 105  
 CC amino acid residues. It is thought that divergence may be due to  
 CC an unspliced intron. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,

CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX SQ Sequence 232 AA;

Query Match 100.0%; Score 255; DB 19; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGECCEWDCM 41  
 |||||  
 Db 27 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGECCEWDCM 67

RESULT 3  
 AAY95879  
 ID AAY95879 standard; Protein; 234 AA.  
 XX AC AAY95879;  
 XX 20-NOV-2000 (first entry)  
 DT Human tumour necrosis factor receptor-like protein TR11.  
 DE TR11; human; tumour necrosis factor receptor-like protein;  
 XX immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX Homo sapiens.  
 OS

Key	Location/Qualifiers
FT Peptide	1..25
FT Protein	/label= Signal_peptide
FT Protein	26..234
FT Domain	/label= Mature_protein
FT Domain	26..162
FT Domain	/label= Extracellular_domain
FT Domain	163..179
FT Domain	/label= Transmembrane_domain
FT Domain	180..234
FT Modified-site	/label= Intracellular_domain
FT Domain	146
FT Domain	/note= "N-glycosylated"
FT Domain	72..81
FT Domain	/note= "conserved domain CD-II"
FT Domain	84..93
FT Domain	/note= "conserved domain CD-III"
FT Domain	107..113
FT Domain	/note= "conserved domain CD-IV"
FT Domain	128..134
FT Domain	/note= "conserved domain CD-V"
FT Domain	153..160
FT Domain	/note= "conserved domain CD-VI"
FT Domain	176..186
FT Domain	/note= "conserved domain CD-VII"
FT Domain	204..209
FT Domain	/note= "conserved domain CD-IX"
FT Domain	224..233
FT Region	/note= "conserved domain CD-X"
FT Region	27..36
FT Region	/note= "epitope-bearing region"
FT Region	43..51
FT Region	/note= "epitope-bearing region"
FT Region	59..67
FT Region	/note= "epitope-bearing region"
FT Region	56..64

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:23 ; Search time 126.12 Seconds  
(without alignments)  
19.708 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_73

Perfect score: 255

Sequence: 1 GCGPGKLLGTGTARCCRV.....TTRCCRDYPGECCSEWDCM 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*

1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT.\*  
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT.\*  
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5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT.\*  
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11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT.\*  
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT.\*  
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14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT.\*  
15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT.\*  
16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT.\*  
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT.\*  
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT.\*  
19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	255	100.0	228	AAW37840	Truncated human 31
2	255	100.0	232	AAW37841	Human 312C2 protei
3	255	100.0	234	AAAY95879	Human tumour necro
4	255	100.0	234	AAAY52158	Tumour necrosis fa
5	255	100.0	235	AAAY44825	Human molecule ass
6	255	100.0	241	AAW37839	Amino acid sequenc
7	255	100.0	241	AAAY06605	Human TNF receptor
8	255	100.0	241	AAAB27651	Human protein PRO3
9	255	100.0	241	AAAB33431	Human PRO364 prote
10	255	100.0	241	AAAY95895	Human tumour necro
11	255	100.0	241	AAAB24409	Human PRO364 prote

12	255	100.0	241	21	AAV71467	Human PRO364 prote
13	255	100.0	241	22	AAAB20115	Human immunostimul
14	255	100.0	241	22	AAAB47054	Human PRO364. Hom
15	255	100.0	241	22	AAAB50910	Human PRO364 prote
16	255	100.0	241	22	AAAB50982	Human PRO364 prote
17	255	100.0	241	22	AAAB53090	Human angiogenesis
18	255	100.0	311	19	AAW37842	Human 312C2 protei
19	255	100.0	316	22	AAAB47055	Polypeptide encode
20	255	100.0	317	20	AAAY06645	PRO364-related EST
21	239	93.7	240	21	AAAY95881	Human tumour necro
22	239	93.7	240	21	AAAY52160	TR11SV2 amino acid
23	87.5	34.3	89	21	AAV76013	Murine TNF-alpha f
24	87.5	34.3	89	22	AAAB55952	Skin cell protein,
25	87.5	34.3	222	19	AAW49018	Mouse glucocortic
26	87.5	34.3	228	19	AAW49016	Mouse glucocortic
27	87.5	34.3	228	19	AAW37838	Amino acid sequenc
28	87.5	34.3	294	19	AAW49017	Mouse glucocortic
29	81.5	32.0	241	21	AAAY95880	Human tumour necro
30	81.5	32.0	241	21	AAAY52159	TR11SV1 amino acid
31	65.5	25.7	150	20	AAW98148	TRAIN-R short, sol
32	65.5	25.7	328	20	AAW06400	Human NTR-5 recept
33	65.5	25.7	417	19	AAW70386	Amino acid sequenc
34	65.5	25.7	417	20	AAW98146	Human TRAIN-R. Ho
35	65.5	25.7	417	21	AAAB33474	Human PRO4333 prot
36	65.5	25.7	423	19	AAW70387	Amino acid sequenc
37	65.5	25.7	423	20	AAW85724	Novel protein (Clo
38	65.5	25.7	423	20	AAW93581	Human hAPO4-alpha
39	65.5	25.7	423	21	AAAB23547	Human Troy protein
40	64	25.1	109	17	AAW84086	T-lymphocyte stimu
41	64	25.1	443	18	AAW27441	Oil seed rape cyst
42	62	24.3	127	21	AAAB51446	Human secreted pro
43	62	24.3	127	21	AAAB51450	Human secreted pro
44	61.5	24.1	150	20	AAW06523	Mouse STRIPE2 (Tan
45	61.5	24.1	150	20	AAV22224	Mouse TNFR superfa

#### ALIGNMENTS

RESULT 1  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
XX Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
DE  
DE Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX Homo sapiens.  
XX  
XX WO9806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
XX 14-AUG-1997; 97WO-US13931.  
XX  
XX 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
XX Gorman DM, Randall TD, Zlotnik A;  
XX WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PT Isolated 312C2 T cell gene - used to develop products for treating,

CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.  
 XX  
 XX  
 SQ Sequence 234 AA;

Query Match 100.0%; Score 255; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41  
 Db 33 gcgpgrrlllgtgdarcrcrvhttrccrdypgeccsewdcm 73  
 |||||

RESULT 5  
 AAY44825  
 ID AAY44825 standard; Protein: 235 AA.  
 AC AAY44825;  
 XX  
 XX 18-MAY-2000 (first entry)  
 XX Human molecule associated with cell proliferation, MACP-5.  
 DE Human; molecule associated with cell proliferation, MACP-5;  
 KW Inocyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;  
 KW anti-inflammatory; antiproliferative; anti-HIV; antiasthmatic; anaemia;  
 KW dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic;  
 KW immunosuppressive; osteopathic; antiarthritic; uropathic; antitumor;  
 KW ophthalmological; diagnosis; treatment; prevention; immune disorder;  
 KW cell proliferative disorder; actinic keratosis; arteriosclerosis;  
 KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..19 /label= Signature\_sequence  
 FT Region 68..96 /label= Signature\_sequence  
 FT Region 109..147 /label= Signature\_sequence  
 FT Region 122..129 /label= Signature\_sequence  
 FT Region 157..175 /label= Signature\_sequence  
 FT Region 165..186 /label= Signature\_sequence  
 FT Region 37 /label= Signature\_sequence  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT Modified-site 48 /note= "Potential phosphorylation site"  
 FT Modified-site 62 /note= "Potential phosphorylation site"  
 FT Modified-site 82 /note= "Potential phosphorylation site"  
 FT Modified-site 205 /note= "Potential phosphorylation site"  
 FT Modified-site /note= "Potential phosphorylation site"

FT Modified-site 223 /note= "Potential phosphorylation site"  
 FT Modified-site 140 /note= "N-glycosylated"  
 XX  
 PN WO200005374-A2.  
 PD 03-FEB-2000.  
 XX  
 XX 21-JUL-1999; 99WO-US16637.  
 PR 22-JUL-1998; 98US-0093827.  
 XX (INCY-) INCYTE PHARM INC.  
 PA  
 XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 PI WPI: 2000-182699/16.  
 DR N-PSDB: AAZ49948.  
 XX  
 XX Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 XX  
 PS Claim 1; Pages 64-65; 67pp; English.  
 XX  
 CC The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from Inocyte clone 2809903 isolated from TLYMN0T06  
 CC CDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotropic, antiinflammatory, antiproliferative, cytostatic, antiasthmatic,  
 CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antitumor,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 SQ Sequence 235 AA;

Query Match 100.0%; Score 255; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41  
 Db 27 gcgpgrrlllgtgdarcrcrvhttrccrdypgeccsewdcm 67  
 |||||

RESULT 6  
 AAW37839  
 ID AAW37839 standard; Protein: 241 AA.  
 XX  
 AC AAW37839;  
 XX  
 XX 28-JUL-1998 (first entry)  
 XX  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 XX Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..726 /tag= a  
 FT /product= "human 312C2 protein"  
 XX

FT	Region	/note= "epitope-bearing region"
FT		66..71
FT	Region	/note= "epitope-bearing region"
FT		99..107
FT	Region	/note= "epitope-bearing region"
FT		125..133
FT	Region	/note= "epitope-bearing region"
FT		143..151
FT	Region	/note= "epitope-bearing region"
FT		156..164
FT	Region	/note= "epitope-bearing region"
FT		203..211
FT	Region	/note= "epitope-bearing region"
FT		222..230
FT	Region	/note= "epitope-bearing region"
XX		
XX	WO200050459-A1.	
XX	31-AUG-2000.	
XX		
XX	23-FEB-2000; 2000WO-US04572.	
PR	24-FEB-1999; 99US-0121648.	
PR	13-MAY-1999; 99US-0134172.	
PR	16-JUL-1999; 99US-0144076.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
XX	Ruben SM, N1 J;	
PI		
XX		
DR	WPI; 2000-572072/53.	
DR	N-PSDB; AAA50304.	
XX		
PT	Human tumor necrosis factor receptor-like proteins useful for	
PT	diagnosis, prevention and treatment of disease states associated with	
PT	aberrant cell survival such as autoimmune disease and rheumatoid	
PT	arthritis	
XX		
XX	Claim 14(c); Fig 1A-B; 278pp; English.	
PS		
XX		
CC	The present sequence is that of human tumour necrosis factor	
CC	receptor-like protein Trll, a novel 25 kDa protein which shows	
CC	58.6% identity to murine glucocorticoid induced tumour necrosis	
CC	factor receptor family-related gene. The sequence was deduced from	
CC	a cDNA clone (see AAA50304) discovered in a T-helper cell library.	
CC	Trll activated NF-kappaB through a TRAF2-mediated mechanism.	
CC	Expression is activation-inducible. The Trll ligand is constitutively	
CC	expressed in an endothelial cell line. This suggests that Trll and	
CC	its ligand may be involved in activated T-cell trafficking.	
CC	The invention provides Trll, TrllSV1 and TrllSV2 nucleic acids	
CC	(see AAA50304-06) and highly conserved encoded proteins (see	
CC	AA95879-81), as well as vectors, host cells and recombinant methods for	
CC	their production. Trll, TrllSV1 and/or TrllSV2 polypeptides are useful	
CC	for treating, preventing, prognosis and/or diagnosis of an	
CC	immunodeficiency, especially common variable immunodeficiency,	
CC	X-linked agammaglobulinemia, severe combined immunodeficiency,	
CC	(SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin	
CC	deficiency with hyper IgM. Trll, TrllSV1 and/or TrllSV2	
CC	antagonists (e.g. antibodies) are used to treat, prevent, prognosis	
CC	and/or diagnose an autoimmune disease, especially rheumatoid	
CC	arthritis, systemic lupus erythematosus, thrombocytopenia purpura	
CC	or IgA nephropathy. The polypeptides, polynucleotides and/or	
CC	antibodies can be administered to cells in vitro, ex vivo or in	
CC	vivo or to a multicellular organism. Soluble forms of the	
CC	polypeptides may also be used. Methods for screening for	
CC	agonist/antagonist compounds are also provided.	
XX		
SQ	Sequence 234 AA;	
	Query Match 100.0%; Score 255; DB 21; Length 234;	
	Best Local Similarity 100.0%; Pred. No. 6.3e-20;	
	Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Qy 1 GCGPGRLLLTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41  
 |||||  
 Db 33 gcgpgrllltgtgdarcrcrvhttrccrdypgeccsewdcm 73

## RESULT 4

AA52158  
 ID AAY52158 standard; Protein; 234 AA.

XX AC AAY52158;

XX DT 01-FEB-2000 (first entry)

XX DE Tumour necrosis factor receptor-like protein (Trll) amino acid sequence.

XX KW Tumour necrosis factor receptor-like protein; Trll; TrllSV1; TrllSV2;  
 KW GTR; growth; differentiation; cell death; immune deficiency disorder;  
 KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anemia;  
 KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW inflammatory condition.

XX OS Homo sapiens.

Key	Location/Qualifiers
FT Peptide	1..25
FT Protein	/label= Signal_peptide
FT Domain	26..234
FT Domain	/label= Trll
FT Domain	26..162
FT Domain	/note= "Extracellular domain"
FT Domain	163..179
FT Domain	/note= "Transmembrane domain"
FT Domain	180..234
FT Domain	/note= "Intracellular domain"

XX PN WO9920758-A1.

XX PD 29-APR-1999.

XX PF 21-OCT-1998; 98WO-US22085.

XX PR 21-OCT-1997; 97US-0063212.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI N1 J, Ruben SM;

XX DR WPI; 2000-061922/05.

XX DR N-PSDB; AA237762.

XX PT New tumour necrosis factor receptor-like polypeptides used to, e.g.

XX PS Claim 14; Fig 1; 167pp; English.

XX CC This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor-like protein (Trll receptor). The invention relates to Trll and  
 CC two splice variants TrllSV1 and TrllSV2. The nucleotide sequences were  
 CC determined by sequencing cloned cDNAs AA237765-237766. The Trll receptor  
 CC and its splice variants show homology to the murine glucocorticoid  
 CC induced tumour necrosis factor receptor family-related gene (GTR).  
 CC Trll, TrllSV1 and TrllSV2 polypeptides may be involved in the regulation  
 CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,

FT XX /label= "Signal peptide"  
 PN KW2000053757-A2.  
 XX 14-SEP-2000.  
 XX 24-FEB-2000; 2000WO-US05004.  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX WPI: 2000-611444/58.  
 DR N-PSDB; AAA99903.  
 XX Novel PRO polypeptides and agonists and antagonists of them, used to  
 PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
 PT -  
 XX Claim 71; Fig 6; 181pp; English.  
 XX The present invention relates to methods for stimulating or inhibiting  
 CC angiogenesis and cardiovascularization. The methods involve the use of  
 CC pharmaceutical compositions based on the following proteins, PRO179,  
 CC PRO238, PRO364, PRO844, PRO876, PRO1760, PRO205, PRO321, PRO333,  
 CC PRO840, PRO877, PRO878, PRO882, PRO885 or PRO887. These  
 CC proteins were identified by isolating cDNA clones encoding secreted  
 CC proteins. The proteins of the invention may be used to diagnose and  
 CC treat cardiovascular, endothelial or angiogenic disorders. The present  
 CC sequence is one of the proteins of the invention.  
 XX Sequence 241 AA;  
 SQ  
 Query Match 100.0%; Score 255; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. NO. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPGRLLLTGTDARCRVHTTRCCRDYFGCECCSEWDCM 41  
 |||||  
 DB 33 gcgpgrrlllgtgdarcrcrvhttrccrdyfgceccsewdcm 73  
 RESULT 9  
 AAB33431  
 ID AAB33431 standard; Protein; 241 AA.  
 XX AC  
 AC AAB33431;  
 XX DT  
 DT 29-JAN-2001 (first entry)  
 XX DE  
 DE Human PRO364 protein UNQ319 SEQ ID NO:92.  
 XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW  
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.  
 XX Homo sapiens.  
 OS  
 XX WO200053758-A2.  
 PN 14-SEP-2000.  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99US-0146222.  
 PR 08-SEP-1999; 99WO-US20111.  
 PR 13-SEP-1999; 99WO-US20594.  
 PR 15-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX WPI: 2000-572271/53.  
 DR N-PSDB; AAC58596.  
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX Claim 33; Fig 36; 309pp; English.  
 PS  
 XX

PN W09806842-A1.  
 XX PD 19-FEB-1998.  
 XX PF 14-AUG-1997; 97WO-US13931.  
 XX PR 07-OCT-1996; 96US-0027901.  
 XX PR 16-AUG-1996; 96US-0689943.  
 XX PA (SCHE ) SCHERING CORP.  
 XX PI Gorman DM, Randall TD, Zlotnik A;  
 XX PI WPI; 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 XX PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX PS Claim 2; Pages 59-60; 71pp; English.  
 XX CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX SQ Sequence 241 AA;  
 Query Match 100.0%; Score 255; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGECCECCSEWDCM 41  
 Db 33 gcgpgrrlllgtgdarccrvhttrccrdypgeccsewdcn 73  
 RESULT 7  
 ID AAY06605  
 AC AAY06605 standard; Protein; 241 AA.  
 XX AC AAY06605;  
 XX DT 26-OCT-1999 (first entry)  
 XX DE Human TNF receptor homologue PRO364.  
 XX KW PRO364; tumour necrosis factor receptor; human; apoptosis;  
 KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /note= "signal peptide"  
 FT Modified-site 146 /note= "mature protein"  
 FT Domain /note= "N-glycosylated"  
 FT /note= "transmembrane domain"  
 XX W09940196-A1.

XX PD 12-AUG-1999.  
 XX PF 09-FEB-1999; 99WO-US02642.  
 XX PR 09-FEB-1998; 98US-0024087.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 XX PI Pitti RM, Wood WI;  
 DR WPI; 1999-494296/41.  
 DR N-PSDB; AAX87670.  
 XX PT Tumour necrosis factor receptor homologue - useful for, e.g.  
 PT modulating apoptosis and NF-KB activation and proinflammatory or  
 PT autoimmune responses  
 XX PS Claim 17; Fig 2A; 104pp; English.  
 XX CC The present sequence represents human PRO364, a novel member of the  
 CC tumour necrosis factor receptor family. The sequence was deduced  
 CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
 CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or  
 CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.  
 XX SQ Sequence 241 AA;  
 Query Match 100.0%; Score 255; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGECCECCSEWDCM 41  
 Db 33 gcgpgrrlllgtgdarccrvhttrccrdypgeccsewdcn 73  
 RESULT 8  
 AAB27651  
 ID AAB27651 standard; Protein; 241 AA.  
 XX AC AAB27651;  
 XX DT 26-JAN-2001 (first entry)  
 XX DE Human protein PRO364.  
 XX KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
 KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
 KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
 KW gene therapy.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..25

PR 29-OCT-1999; 99US-0162506.  
 PA (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX WPI; 2000-412154/35.  
 DR N-PSDB; AAA77604.  
 XX Nucleic acids encoding PRO polypeptides useful for preventing,  
 PT diagnosing and treating a cardiovascular, endothelial or  
 PT angiogenic disorders in mammals -  
 XX  
 PS Claim 72; Fig 44; 315pp; English.  
 XX The present invention describes nucleic acids encoding PRO polypeptides  
 CC useful for preventing, diagnosing and treating a disorder in mammals by  
 CC cardiovascular, endothelial or angiogenic disorder in mammals by  
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
 CC and for identifying agonists and antagonists of these processes. The  
 CC nucleic acids and the proteins they encode may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PRO expression such as cardiovascular, endothelial or  
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and  
 CC cardiac hypertrophy). For example, the nucleic acids (NGs) and vectors  
 CC containing them and the PRO polypeptide may be used to treat disorders  
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
 CC the exemplification of the present invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 255; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41  
 |||||  
 DB 33 gcgpglllgtgdarcrcrvhttrccrdypgeccsewdcm 73

RESULT 12  
 AAY71467  
 ID AAY71467 standard; Protein; 241 AA.  
 XX  
 AC AAY71467;  
 XX  
 DT 08-NOV-2000 (first entry)  
 XX Human PRO364 protein.  
 DE  
 XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;  
 KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
 KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
 KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;  
 KW tumour necrosis factor receptor; GTR protein homologue.  
 XX  
 OS Homo sapiens.

Key Location/Qualifiers  
 FH Key 1..25  
 FT Peptide /label= Signal\_peptide  
 FT Modified-site 5..11 /note= "N-myristoylation site"  
 FT Modified-site 8..14 /note= "N-myristoylation site"  
 FT Modified-site 25..31 /note= "N-myristoylation site"  
 FT Protein 26..241 /label= Mature\_PRO364\_protein

FT Modified-site 30..36 /note= "N-myristoylation site"  
 FT Modified-site 33..39 /note= "N-myristoylation site"  
 FT Modified-site 118..124 /note= "N-myristoylation site"  
 FT Modified-site 122..128 /note= "N-myristoylation site"  
 FT Modified-site 146..150 /note= "N-myristoylation site"  
 FT Modified-site 156..162 /note= "N-myristoylation site"  
 FT Domain 163..183 /label= Transmembrane\_domain  
 FT Binding-site 166..177 /note= "Prokaryotic membrane lipoprotein lipid attachment site"  
 FT Region 171..193 /note= "Leucine zipper pattern"  
 XX WO200032778-A2.  
 XX 08-JUN-2000.  
 PF 30-NOV-1999; 99WO-US28409.  
 XX 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 22-DEC-1998; 98US-0113296.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
 XX WPI; 2000-412325/35.  
 DR N-PSDB; AAD01240.  
 XX  
 PT New composition useful for inhibiting neoplastic cell growth and for  
 PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
 PT their antagonists -  
 XX  
 PS Claim 31; Fig 4; 108pp; English.  
 XX  
 CC The present sequence is the human PRO364 protein, encoded by the cDNA  
 CC clone, designated as DNA47365-1206. It is isolated from human small  
 CC intestine tissue cDNA library, identified using probes based on the  
 CC consensus sequence DNA44825, relative to the Incyte expressed sequence  
 CC tag (EST) 3003460. This EST has homology to tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows  
 CC homology to members of the TNFR family and mouse GTR protein.  
 CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as  
 CC a neoplastic cell growth inhibitor and is used for treating tumours,  
 CC using an effective amount of PRO655, PRO364 and PRO344. This composition  
 CC is especially useful for treatment of human cancers such as breast,  
 CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 255; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41  
 |||||  
 DB 33 gcgpglllgtgdarcrcrvhttrccrdypgeccsewdcm 73

RESULT 13  
 AAB20115  
 ID AAB20115 standard; Protein; 241 AA.

CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 255; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGECCECCSEWDCM 41  
 |||||  
 Db 33 gcgpgrrllgtgdarcrcrvhttrccrdypgeccsewdcm 73

RESULT 10

AAY95895  
 ID AAY95895 standard; Protein; 241 AA.

XX  
 AC AAY95895;

XX 20-NOV-2000 (first entry)

XX Human tumour necrosis factor receptor-like protein TR11 mutein.

XX TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutin;  
 KW mutant.

XX Homo sapiens.

XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, NI J;

XX WPI; 2000-572072/53.

XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis

XX Disclosure; 294-295; 278pp; English.

CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.

XX Sequence 241 AA;

Query Match 100.0%; Score 255; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGECCECCSEWDCM 41  
 |||||  
 Db 33 gcgpgrrllgtgdarcrcrvhttrccrdypgeccsewdcm 73

RESULT 11

AAB24409

ID AAB24409 standard; Protein; 241 AA.

XX  
 AC AAB24409;

XX 07-NOV-2000 (first entry)

XX Human PRO364 protein sequence SEQ ID NO:117.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1998; 98WO-US25108.

XX 16-DEC-1998; 98US-0112850.

XX 12-JAN-1999; 99US-0115554.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 02-JUN-1999; 99WO-US12252.

XX 20-JUL-1999; 99US-014758.

XX 26-JUL-1999; 99US-0145698.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.





XX AAB201115;  
 AC 30-APR-2001 (first entry)  
 DT Human immunostimulant PRO364.  
 DE  
 XX PRO364; UNQ319; human; immune disease; autoimmune disease;  
 KW antirheumatic; antiarthritic; antiinflammatory; antianemic;  
 KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
 KW hepatotropic; virucide; dermatological; antipsoriatic;  
 KW antiasthmatic; antiallergic; immunostimulant.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /label= Signal\_peptide  
 FT 26..241  
 FT Domain /label= Mature\_protein  
 FT 163..183  
 FT Modified-site /note= "transmembrane domain"  
 FT 5..11  
 FT Modified-site /note= "N-myristoylation site"  
 FT 8..14  
 FT Modified-site /note= "N-myristoylation site"  
 FT 25..31  
 FT Modified-site /note= "N-myristoylation site"  
 FT 30..36  
 FT Modified-site /note= "N-myristoylation site"  
 FT 33..39  
 FT Modified-site /note= "N-myristoylation site"  
 FT 118..124  
 FT Modified-site /note= "N-myristoylation site"  
 FT 122..128  
 FT Modified-site /note= "N-myristoylation site"  
 FT 156..162  
 FT Modified-site /note= "N-myristoylation site"  
 FT 146..150  
 FT Modified-site /note= "Asn is N-glycosylated"  
 FT 166..177  
 FT Peptide /note= "prokaryotic membrane lipoprotein lipid  
 FT attachment site"  
 FT 171..193  
 FT Peptide /note= "leucine zipper pattern"  
 FT  
 XX WO200105972-A1.  
 XX  
 XX 25-JAN-2001.  
 XX  
 XX 15-MAR-2000; 2000WO-US06884.  
 XX  
 XX 20-JUL-1999; 99US-0144758.  
 XX  
 XX (GEPH) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX WPI; 2001-103149/11.  
 DR N-PSDB; AAF30057.  
 XX  
 XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes -  
 XX  
 XX Claim 20; Fig 16; 127pp; English.  
 PS  
 XX The present sequence is that of novel human immunomodulator PRO364  
 CC (UNQ319), as deduced from cDNA (see AAF30057) isolated from a  
 CC small intestine library. PRO364 (26 kDa, pI 6.34) shows sequence  
 CC homology to mouse G1TR protein and may be its human counterpart.

CC The invention provides polynucleotides (see AAF30050-62) encoding  
 CC novel human PRO proteins (see AAB20108-20) including PRO364.  
 CC Claimed compositions comprising these proteins or their agonists  
 CC are useful for increasing infiltration of inflammatory cells into  
 CC a tissue of a mammal, stimulating or enhancing an immune  
 CC response, or increasing the proliferation of T-lymphocytes in a  
 CC mammal in response to an antigen. Claimed compositions comprising  
 CC a PRO polypeptide or its antagonist have the opposite effect. A  
 CC claimed method for treating an immune related disorder, such as a T  
 CC cell disorder, involves administering a PRO polypeptide, an agonist  
 CC antibody or an antagonist antibody. The disorder is selected from  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated  
 CC renal disease, demyelinated diseases (such as multiple sclerosis),  
 CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
 CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
 CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
 CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
 CC (such as bullous skin disease, erythema multiforme and psoriasis),  
 CC allergic diseases (such as asthma, allergic rhinitis, atopic  
 CC dermatitis, food hypersensitivity and urticaria), immunologic  
 CC diseases of the lung and transplantation associated diseases (such  
 CC as graft rejection and graft-versus-host disease) (all claimed).  
 CC Claimed methods of diagnosing these disorders comprise detecting  
 CC the level of expression of the PRO gene. Also claimed are a method  
 CC of identifying a compound capable of inhibiting the expression or  
 CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
 CC and a method of stimulating the proliferation of T lymphocytes  
 CC using PRO364.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 255; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGRLLLGCTDARCCRVHTTRCCRDYPGEECCSEWDCM 41  
 Db 33 gcgpglllgtgtdarccrvhttrccrdypgeccsewdcm 73

RESULT 14  
 AAB47054  
 ID AAB47054 standard; Protein; 241 AA.

XX AAB47054;

DT 08-MAY-2001 (first entry)

XX Human PRO364.

PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
 KW hG1TR; ligand; hG1TRL; PRO175; tumour necrosis factor receptor; TNFR;  
 KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
 KW myocardial infarction; PGF\_2alpha; trauma; cancer; angiogenesis;  
 KW age-related macular degeneration; antibody; periodontal disease;  
 KW vascular-related drug targeting; atherosclerosis; hypertension;  
 KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
 KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
 KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..26  
 FT Modified-site /note= "Potential signal peptide"  
 FT 146  
 FT Domain /note= "N-glycosylated"  
 FT 162..180

CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases

Query Match	100.0%	Score 255:	DB 22;	Length 241;
Best Local Similarity	100.0%	Pred. No.	6.4e-20;	
Matches 41;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CGCGRLLLTGTGTARCCRVHTTCRRDYPGEECCSEWDCM	41	
Db	33	gcgpgrrlllgtgtarccrvhttcrrdypgеессewdcм	73	

Search completed: September 4, 2001, 15:56:24  
Job time: 341 sec

CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognose  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 SQ Sequence 234 AA;

Query Match 100.0%; Score 753; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPFHCGDPCCTTCRHH 60  
 |||||  
 DB 33 GCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPFHCGDPCCTTCRHH 92  
 |||||

QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTNAV 120  
 |||||  
 DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTNAV 152  
 |||||

QY 121 CV 122  
 ||  
 DB 153 CV 154

RESULT 3  
 AAY52158  
 ID AAY52158 standard; Protein; 234 AA.  
 XX  
 AC AAY52158;  
 DT  
 XX 01-FEB-2000 (first entry)  
 XX Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.  
 XX  
 KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;  
 KW GTR; growth; differentiation; cell death; immune deficiency disorder;  
 KW George syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
 KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; Huntingdon's disease;  
 KW inflammatory condition.  
 XX  
 OS Homo sapiens.

Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Signal\_peptide  
 FT Protein 26..234  
 FT /label= TR11  
 FT Domain 26..162  
 FT /note= "Extracellular domain"  
 FT Domain 163..179  
 FT /note= "Transmembrane domain"  
 FT Domain 180..234  
 FT /note= "Intracellular domain"

XX WO9920758-A1.  
 XX  
 XX 29-APR-1999.  
 XX  
 XX 21-OCT-1998; 98WO-US22085.  
 XX  
 XX 21-OCT-1997; 97US-0063212.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX N1 J, Ruben SM;

XX WPI; 2000-061922/05.  
 DR N-PSDB; AA237762.  
 XX  
 PT New tumour necrosis factor receptor-like polypeptides used to, e.g.  
 PT treat Digeorge syndrome -  
 XX  
 PS Claim 14; Fig 1; 167pp; English.  
 XX  
 CC This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor-like protein (TR11 receptor). The invention relates to TR11 and  
 CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
 CC determined by sequencing cloned cDNAs AA237765-237766. The TR11 receptor  
 CC and its splice variants show homology to the murine glucocorticoid  
 CC induced tumour necrosis factor receptor family-related gene (GTR).  
 CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation  
 CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.  
 XX  
 SQ Sequence 234 AA;

Query Match 100.0%; Score 753; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPFHCGDPCCTTCRHH 60  
 |||||  
 DB 33 GCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPFHCGDPCCTTCRHH 92  
 |||||

QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTNAV 120  
 |||||  
 DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTNAV 152  
 |||||

QY 121 CV 122  
 ||  
 DB 153 CV 154

RESULT 4  
 AAY44825  
 ID AAY44825 standard; Protein; 235 AA.  
 XX  
 AC AAY44825;  
 XX  
 DT 18-MAY-2000 (first entry)  
 XX Human molecule associated with cell proliferation, MACP-5.  
 XX  
 XX Human; molecule associated with cell proliferation; MACP-5;

KW Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;  
 KW anti-inflammatory; antiproliferative; anti-HIV; antitumorigenic; anaemia;  
 KW dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic;  
 KW immunosuppressive; osteopathic; antiarthritic; uropathic; antitumor;  
 KW ophthalmological; diagnosis; treatment; prevention; immune disorder;  
 KW cell proliferative disorder; actinic keratosis; arteriosclerosis;  
 KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..19  
 FT /label= Signature\_sequence  
 FT 68..96  
 FT /label= Signature\_sequence  
 FT 109..147  
 FT /label= Signature\_sequence  
 FT 122..129  
 FT /label= Signature\_sequence  
 FT 137..175  
 FT /label= Signature\_sequence  
 FT 165..186  
 FT /label= Signature\_sequence  
 FT 37  
 FT /note= "Potential phosphorylation site"  
 FT 48  
 FT /note= "Potential phosphorylation site"  
 FT 62  
 FT /note= "Potential phosphorylation site"  
 FT 82  
 FT /note= "Potential phosphorylation site"  
 FT 205  
 FT /note= "Potential phosphorylation site"  
 FT 223  
 FT /note= "Potential phosphorylation site"  
 FT 140  
 FT /note= "N-glycosylated"  
 FT  
 XX WO200005374-A2.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 21-JUL-1999; 99WO-US16637.  
 XX  
 PR 22-JUL-1998; 98US-0093827.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 XX WPI; 2000-182699/16.  
 DR N-PSDB; AA249948.  
 XX  
 PT Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 XX  
 PS Claim 1; Pages 64-65; 67pp; English.  
 XX  
 CC The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from incyte clone 2809903 isolated from TLYMN0706  
 CC CDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotropic, antiinflammatory, antiproliferative, cytostatic, antitumorigenic,  
 CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antitumor,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 SQ Sequence 235 AA;

Query Match 100.0%; Score 753; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCGPRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60  
 Db 27 GCGPRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 86  
 Qy 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTHNAV 120  
 Db 87 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTHNAV 146  
 Qy 121 CV 122  
 Db 147 cv 148  
 RESULT 5  
 AAW37839  
 ID AAW37839 standard; Protein; 241 AA.  
 XX  
 AC AAW37839;  
 XX  
 DT 28-JUL-1998 (first entry)  
 XX  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /\*tag= a  
 FT /product= "human 312C2 protein"  
 XX  
 PN WO9806842-A1.  
 XX  
 PD 19-FEB-1998.  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 XX  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Gorman DM, Randall TD, Zlotnik A;  
 XX WPI; 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 XX  
 PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:23 ; Search time 136.12 Seconds  
(without alignments)  
58.644 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_154

Perfect score: 753

Sequence: 1 GCGPGLLLGTGTARCCRV.....TQGFGLTVFGNKTHNAVCV 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT:\*

4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT:\*

5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT:\*

6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT:\*

7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT:\*

8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT:\*

9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT:\*

10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT:\*

11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT:\*

12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT:\*

13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT:\*

14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT:\*

15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT:\*

16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT:\*

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18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT:\*

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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	753	100.0	228	19 AAW37840	Truncated human 31
2	753	100.0	234	21 AAY95879	Human tumour necro
3	753	100.0	234	21 AAY52158	Tumour necrosis fa
4	753	100.0	235	21 AAY44825	Human molecule ass
5	753	100.0	241	19 AAW37839	Amino acid sequenc
6	753	100.0	241	20 AAY06605	Human TNF receptor
7	753	100.0	241	21 AAB27651	Human protein PRO3
8	753	100.0	241	21 AAB33431	Human PRO364 prote
9	753	100.0	241	21 AAY95895	Human tumour necro
10	753	100.0	241	21 AAB24409	Human PRO364 prote
11	753	100.0	241	21 AAY71467	Human PRO364 prote

12	753	100.0	241	22 AAB20115	Human immunostimul
13	753	100.0	241	22 AAB47054	Human PRO364. Hom
14	753	100.0	241	22 AAB50910	Human PRO364 prote
15	753	100.0	241	22 AAB50982	Human PRO364 prote
16	753	100.0	241	22 AAB53090	Human angiogenesis
17	753	100.0	311	19 AAW37842	Human 312C2 protel
18	737	97.9	240	21 AAY95881	Human tumour necro
19	737	97.9	240	21 AAY52160	Human tumour necro
20	703	93.4	316	22 AAB47055	TRILSV2 amino acid
21	703	93.4	317	20 AAY06645	POLYPEPTIDE ENCODE
22	579.5	77.0	241	21 AAY95880	PRO364-related EST
23	579.5	77.0	241	21 AAY52159	Human tumour necro
24	468	62.2	232	19 AAW37841	TRILSV1 amino acid
25	445.5	59.2	222	19 AAW49018	Human 312C2 protel
26	445.5	59.2	228	19 AAW49016	Mouse glucocorticoid
27	445.5	59.2	228	19 AAW37838	Mouse glucocorticoid
28	445.5	59.2	294	19 AAW49017	Amino acid sequenc
29	212.5	28.2	89	21 AAY76013	Mouse glucocorticoid
30	212.5	28.2	89	22 AAB55952	Murine TNF-alpha f
31	164	21.8	206	16 AAR81881	Skin cell protein,
32	164	21.8	206	16 AAW48977	Mouse type-II memb
33	164	21.8	438	16 AAR81882	Mouse OX40 extrace
34	164	21.8	438	19 AAW48976	Plasmid pDC406/OX4
35	154	20.5	300	21 AAB03622	OX40/Fc mutein. C
36	154	20.5	300	21 AAB03623	Monkey Fas ligand
37	152.5	20.3	255	16 AAR70977	Human Fas ligand i
38	152.5	20.3	255	16 AAR64197	H4-11B receptor pr
39	152.5	20.3	255	18 AAW26658	Human 4-11B polype
40	152.5	20.3	255	20 AAY33214	Human 4-11B recept
41	152.5	20.3	255	20 AAY28688	Human CD137 protel
42	152.5	20.3	255	22 AAB50521	Human receptor pro
43	151.5	20.1	132	21 AAY94714	Human tumour necro
44	151	20.1	300	21 AAB19710	Tumour necrosis fa
45	151	20.1	300	21 AAY96597	Human Fas ligand i
					Human FLINT. Homo

#### ALIGNMENTS

RESULT 1

AAW37840

ID AAW37840 standard; Protein; 228 AA.

AC AAW37840;

XX

XX

DT 28-JUL-1998 (first entry)

XX

XX

DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.

XX

XX

KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;

KW antigen-specific T cell proliferation; cytokine production by T-cell;

KW apoptosis; cancer; haematopoietic cells; lymphoid cell;

KW autoimmune disorders.

XX

OS Homo sapiens.

XX

XX

PN WO9806842-A1.

XX

PD 19-FEB-1998.

XX

XX

PF 14-AUG-1997; 97WO-US13931.

XX

XX

PR 07-OCT-1996; 96US-0027901.

PR 16-AUG-1996; 96US-0689943.

XX

PA (SCHE ) SCHERING CORP.

XX

XX

PI Gorman DM, Randall TD, Zlotnik A;

XX

XX

DR WPI; 1998-159534/14.

DR N-PSDB; AAV19154.

XX

XX

PT Isolated 312C2 T cell gene - used to develop products for treating,

e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders

Disclosure; Pages 61-62; 71pp; English.

This is the amino acid sequence of the truncated human 312C2 T cell protein from clone A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.

Sequence 228 AA;

Query Match 100.0%; Score 753; DB 19; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.8e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPRLLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 60  
|||  
Db 27 GCGPRLLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 86  
|||

QY 61 PCPPGQGVQSGKSFQFCIDCAGTFSGGHEGHCKPWTCTQGFGLTVPGNKTNNAV 120  
|||  
Db 87 PCPPGQGVQSGKSFQFCIDCAGTFSGGHEGHCKPWTCTQGFGLTVPGNKTNNAV 146  
|||

QY 121 CV 122  
||  
Db 147 CV 148  
||

RESULT 2  
AAAY95879  
ID RAY95879 standard; Protein; 234 AA.  
AC AAAY95879;  
XX  
XX 20-NOV-2000 (first entry)  
XX Human tumour necrosis factor receptor-like protein TR11.  
XX TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis.  
XX  
XX Homo sapiens.  
XX

Key Location/Qualifiers  
FH Peptide 1..25  
FT /label= Signal\_peptide  
FT Protein 26..234  
FT /label= Mature\_protein  
FT Domain 26..162  
FT /label= Extracellular\_domain  
FT Domain 163..179  
FT /label= Transmembrane\_domain  
FT Domain 180..234  
FT /label= Intracellular\_domain  
FT Modified-site 146  
FT /note= "N-glycosylated"  
FT Domain 72..81  
FT /note= "conserved domain CD-II"  
FT Domain 84..93  
FT /note= "conserved domain CD-III"  
FT Domain 107..113  
FT /note= "conserved domain CD-IV"  
FT

PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL; Hebert C, Hienzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK; Wood WI;  
 PI WPI; 2001-025253/03.  
 DR N-PSDB; AAC91469.  
 XX  
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -  
 XX  
 PS Claim 58; Fig 18; 218pp; English.  
 XX  
 CC The present sequence is one of thirty three novel PRO polypeptides.  
 CC The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polynuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polynuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCGPGRLLLTGTGDARCCRVHTTRCCRDYPGECCEWDCMCVQPFHCGDPCCCTCRHH 60  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 33 gcgpglllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpfhcgdpccctcrhh 92  
 Qy 61 PCPPGQGVQSQGKSFQFCIDACSTGSGHGHCCKPWTDCFTQCFLTVFPGNKTHNAV 120  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 93 pcppgqgvqsgkqsfqfqcicdca9tfgsgghgchckpwcddctqflltvfpgnkthnav 152  
 Qy 121 CV 122  
 Db ||  
 153 CV 154

RESULT 15  
 AAB50982  
 ID AAB50982 standard; Protein; 241 AA.  
 AC AAB50982;  
 XX  
 XX 21-MAR-2001 (first entry)  
 DT  
 XX Human PRO364 protein.

XX Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
 KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
 KW vulnerary; antianginal; gene therapy; cardiovascular disease;  
 KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
 KW wound healing.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200073445-A2.  
 XX  
 XX 07-DEC-2000.  
 PD  
 XX  
 XX 17-MAY-2000; 2000WO-US13705.  
 PF  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06319.  
 PR 21-MAR-2000; 2000WO-US06884.  
 PR 30-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 XX  
 (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
 PI Paonl NF, Pittl RM, Watanabe CK, Williams PM, Wood WI;  
 XX  
 WPI; 2001-025251/03.  
 DR N-PSDB; AAC90566.  
 XX  
 PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 PT disorders in a mammal -  
 XX  
 XX Claim 71; Fig 8; 182pp; English.  
 PS  
 CC The present sequence is one of seventeen novel PRO polypeptides. The PRO  
 CC nucleic acids, polypeptides, agonists and antagonists are useful for  
 CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
 CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
 CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
 CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
 CC antagonists are also used to prevent tumour angiogenesis and for treating  
 CC periodontal diseases. They are also used to stimulate wound healing and  
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder.  
 XX  
 XX Sequence 241 AA;

Query Match 100.0%; Score 753; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCGPGRLLLTGTGDARCCRVHTTRCCRDYPGECCEWDCMCVQPFHCGDPCCCTCRHH 60  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 33 gcgpglllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpfhcgdpccctcrhh 92



QY 61 PCPPGQVQSGKESFGFCIDCASGTFSGGHEGHCCKPWTDCIQFGFLTVPFGNKTHNAV 120  
Db 93 PCPPGGVQSGGKFSFGFCIDCASGTFSGGHEGHCCKPWTDCIQFGFLTVPFGNKTHNAV 152  
QY 121 CV 122  
Db 153 CV 154

Search completed: September 4, 2001, 15:56:23  
Job time: 340 sec



Db 153 cv 154

RESULT 13

AAB47054

ID AAB47054 standard; Protein; 241 AA.

XX AAB47054;

AC AAB47054;

XX 08-MAY-2001 (first entry)

DT Human PRO364.

DE

XX PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor; hGTR; ligand; hGTRL; PRO175; tumour necrosis factor receptor; TNFR; human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; PCF\_2alpha; trauma; cancer; angiogenesis; age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculitides; Reynaud's disease; aneurysm; arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver; fibrosis; neuropathy; rheumatoid arthritis.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH Peptide 1..26

FT /note= "Potential signal peptide"

FT Modified-site 146

FT /note= "N-glycosylated"

FT Domain 162..180

FT /note= "Potential transmembrane domain"

XX

XX WO200103720-A2.

PN 18-JAN-2001.

PD

XX

XX 11-JUL-2000; 2000WO-US18867.

PF

XX 12-JUL-1999; 99US-0143304.

PR

XX (GETH ) GENENTECH INC.

PA

XX Williams PM, Gerritsen ME;

PI

XX WPI: 2001-138257/14.

DR

XX N-PSDB; AAC85433.

DR

XX

XX Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -

PT

XX Claim 1; Fig 1; 76pp; English.

PS

XX This sequence represents PRO364 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor receptor (hGTR). The corresponding ligand (hGTRL), PRO175, is given in AAB47056.

CC PRO364 and PRO175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic agent for the treatment of a cardiovascular, endothelial, angiogenic or angiostatic disorder. The PRO364 cDNA sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was isolated from a library of cDNA fragments derived from human umbilical vein endothelial cells (HUVEC). Administering an effective amount of PRO364 or PRO175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PCF\_2alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering from a tumor or a retinal disorder. PRO364 or PRO175, or their antagonists, are useful for

CC vascular-related drug targeting or as therapeutic targets for the treatment or prevention of atherosclerosis, hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms, arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration, and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis.

XX

SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 22; Length 241;

Best Local Similarity 100.0%; Pred. No. 2.9e-55;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLGTGTARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGDPCCCTTCRHH 60

Db 33 gcgprlllgtgtardccrvhttrccrdypgeecscwcmcvqpefhgdpcccttrhh 92

Qy 61 PCPPGGVQSGGKFSFGFCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVPFGNKTHNAV 120

Db 93 pcppggvgvggkfsfgfcidcasgtfsggheghckpwtcdctqfgfltvpfgnkthnav 152

Qy 121 CV 122

Db 153 cv 154

RESULT 14

AAB50910

ID AAB50910 standard; Protein; 241 AA.

XX AAB50910;

XX 21-MAR-2001 (first entry)

DT Human PRO364 protein.

DE

XX Human; PRO; antiinflammatory; dermatological; antiarthritic; antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid; antidiabetic; nootropic; neuroprotective; hepatotropic; virucide; antiallergic; antiasthmatic; immune related disorder; hepatobiliary disease; autoimmune disease; allergy.

XX Homo sapiens.

OS

XX WO200073452-A2.

PN

XX 07-DEC-2000.

PD

XX 02-JUN-2000; 2000WO-US15264.

PF

XX 02-JUN-1999; 99WO-US12252.

PR 20-JUL-1999; 99US-0144732.

PR 28-JUL-1999; 99US-0144736.

PR 01-SEP-1999; 99US-0146222.

PR 15-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 09-DEC-1999; 99WO-US28634.

PR 09-DEC-1999; 99US-0170262.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04342.

PR 24-FEB-2000; 2000WO-US04414.

PR 15-MAR-2000; 2000WO-US04914.

PR 20-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
immune-mediated renal disease, demyelinating diseases of the central  
and peripheral nervous systems, hepatobiliary diseases, inflammatory  
bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
autoimmune or immune-mediated skin diseases, allergic diseases,  
immunological diseases of the lung, and transplantation associated  
diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAC33414 to AAB33477 represent human PRO polynucleotide and protein  
sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLLTGTDCRCRVHTRCCRDYPGEECCSWDCMCVQPEFHCGDPCCTTCRHH 60  
|||||  
Db 33 gcgpgrrlllgtgdarcrcrvhtrccrdypgeccsewdcmcvqpefhcgdpccctcrhh 92  
Qy 61 PCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVFPGNKTHNAV 120  
|||||  
Db 93 pcppggvqsgkfsfgfcidcasgtfsgghegchkpwtctqfgfltvfpgnkthnav 152  
Qy 121 CV 122  
||  
Db 153 CV 154

RESULT 9  
AAAY95895  
ID AAY95895 standard; Protein; 241 AA.

AC AAY95895;  
XX  
XX 20-NOV-2000 (first entry)  
XX Human tumour necrosis factor receptor-like protein TR1L mutein.

XX TR1L; human; tumour necrosis factor receptor-like protein;  
XX immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
KW mutant.

XX Homo sapiens.  
XX OS  
XX WO200050459-A1.  
XX PN  
XX 31-AUG-2000.  
XX PD  
XX 23-FEB-2000; 2000WO-US04572.  
XX PF  
XX 24-FEB-1999; 99US-0121648.  
XX PR  
XX 13-MAY-1999; 99US-0134172.  
XX PR  
XX 16-JUL-1999; 99US-0144076.  
XX XX  
XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, N1 J;  
XX  
XX WPI; 2000-572072/53.  
XX  
XX Human tumor necrosis factor receptor-like proteins useful for  
PT diagnosis, prevention and treatment of disease states associated with  
PT aberrant cell survival such as autoimmune disease and rheumatoid  
PT arthritis

XX  
XX  
XX Disclosure; 294-295; 278pp; English.  
XX  
XX

CC The present sequence is that of human tumour necrosis factor  
CC receptor-like protein TR1L (see also AAY95879), a novel protein  
CC showing identity to murine glucocorticoid induced tumour necrosis  
CC factor receptor family-related gene. The invention provides  
CC highly conserved TR1L, TR1LSV1 and TR1LSV2 proteins (see AAY95879-81),  
CC as well as vectors, host cells and recombinant methods for their  
CC production. TR1L, TR1LSV1 and/or TR1LSV2 polypeptides are useful  
CC for treating, preventing, prognosis and/or diagnosis of an  
CC immunodeficiency, especially common variable immunodeficiency,  
CC X-linked agammaglobulinemia, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
CC deficiency with hyper IgM. TR1L, TR1LSV1 and/or TR1LSV2  
CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
CC and/or diagnose an autoimmune disease, especially rheumatoid  
CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
CC antibodies can be administered to cells in vitro, ex vivo or in  
CC vivo or to a multicellular organism. Soluble forms of the  
CC polypeptides may also be used. Methods for screening for  
CC agonist/antagonist compounds are also provided.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLLTGTDCRCRVHTRCCRDYPGEECCSWDCMCVQPEFHCGDPCCTTCRHH 60  
|||||  
Db 33 gcgpgrrlllgtgdarcrcrvhtrccrdypgeccsewdcmcvqpefhcgdpccctcrhh 92  
Qy 61 PCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVFPGNKTHNAV 120  
|||||  
Db 93 pcppggvqsgkfsfgfcidcasgtfsgghegchkpwtctqfgfltvfpgnkthnav 152  
Qy 121 CV 122  
||  
Db 153 CV 154

RESULT 10  
AAB24409  
ID AAB24409 standard; Protein; 241 AA.

XX  
XX AAB24409;  
XX  
XX 07-NOV-2000 (first entry)  
XX Human PRO364 protein sequence SEQ ID NO:117.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
KW cytostatic; gene therapy; vaccine.  
XX  
XX Homo sapiens.

XX WO200032221-A2.  
XX PN  
XX 08-JUN-2000.  
XX PD  
XX 30-NOV-1999; 99WO-US28313.  
XX PF  
XX 01-DEC-1998; 98WO-US25108.  
XX PR  
XX 16-DEC-1998; 98US-0112850.  
XX PR  
XX 12-JAN-1999; 99US-0115554.  
XX PR  
XX 08-MAR-1999; 99WO-US05028.  
XX PR  
XX 12-MAR-1999; 99US-0123957.  
XX PR  
XX 28-APR-1999; 99US-0131445.  
XX PR  
XX 14-MAY-1999; 99US-0134287.  
XX PR  
XX 02-JUN-1999; 99WO-US12252.  
XX PR  
XX 23-JUN-1999; 99US-0141037.



PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI: 2000-611444/58.  
 DR N-PSDB; AAA99903.  
 XX  
 XX Novel PRO polypeptides and agonists and antagonists of them, used to  
 PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
 PT  
 XX  
 PS Claim 71; Fig 6; 181pp; English.  
 XX  
 CC The present invention relates to methods for stimulating or inhibiting  
 CC angiogenesis and cardiovascularization. The methods involve the use of  
 CC pharmaceutical compositions based on the following proteins, PRO179,  
 CC PRO338, PRO364, PRO846, PRO1760, PRO205, PRO321, PRO333,  
 CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
 CC proteins were identified by isolating cDNA clones encoding secreted  
 CC proteins. The proteins of the invention may be used to diagnose and  
 CC treat cardiovascular, endothelial or angiogenic disorders. The present  
 CC sequence is one of the proteins of the invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2,9e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPRLLLGTGTDAKCRVHTTRCCRDYPCGEECCSCWDCMCVQPEFHCGDPCCCTCRHH 60  
 |||||  
 Db 33 gcgprlllgtgtdarccrvhttrccrdygcgpcscwdcmcvqpefhcgdpccctcrhh 92  
 |||||  
 QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGHGHCHKRPWTDCTQFGFLTVPPGNKTHNAV 120  
 |||||  
 Db 93 pcppgqgvqsgkfsfgfcidcasgtfsgghghchkpwtcdtqfgfltvpgnkhnav 152  
 |||||  
 QY 121 CV 122  
 Db 153 cv 154

RESULT 8  
 AAB33431  
 ID AAB33431 standard; Protein; 241 AA.  
 XX  
 AC AAB33431;  
 XX  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human PRO364 protein UNQ319 SEQ ID NO:92.  
 XX  
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; neuroprotective;  
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;

graft rejection; graft-versus-host-disease.  
 OS Homo sapiens.  
 XX WO2000053758-A2.  
 PN  
 XX  
 PD 14-SEP-2000.  
 XX  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99US-0128849.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR  
 XX  
 PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

WPI: 2000-572271/53.  
 N-PSDB; AAC58596.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

Claim 33; Fig 36; 309pp; English.

The present invention describes sixty four human PRO proteins which can  
 be used in the treatment of immune related diseases. The human PRO  
 proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 treating and diagnosing immune related disorders. The disorders are  
 selected from systemic lupus erythematosus, rheumatoid arthritis,  
 osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC which affect immunological responses, e.g. autoimmune disorders.

SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 19; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60  
|||||  
DB 33 GCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 92  
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGHGHCCKPWTDCQFGFLTVFPGNKTHNAV 120  
|||||  
DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGHGHCCKPWTDCQFGFLTVFPGNKTHNAV 152

QY 121 CV 122

DB 153 cv 154

RESULT 6

AA05605  
ID AAY06605 standard; Protein; 241 AA.

XX AAY06605;

XX 26-OCT-1999 (first entry)

XX Human TNF receptor homologue PRO364.

XX PRO364; tumour necrosis factor receptor; human; apoptosis;  
KW inflammation; antiinflammatory; NF-KB activation;  
KW autoimmune disease; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /note= "signal peptide"

FT Protein 26..241

FT /note= "mature protein"

FT Modified-site 146

FT /note= "N-glycosylated"

FT Domain 162..180

FT /note= "transmembrane domain"

XX WO9940196-A1.

XX 12-AUG-1999.

XX 09-FEB-1999; 99WO-US02642.

XX 09-FEB-1998; 98US-0024087.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;

PI Pitti RM, Wood WI;

XX WPI: 1999-494296/41.

XX N-PSDB; AAX87670.

XX Tumour necrosis factor receptor homologue - useful for, e.g.

PT modulating apoptosis and NF-KB activation and proinflammatory or

PT autoimmune responses

XX Claim 17; Fig 2A; 104pp; English.

XX The present sequence represents human PRO364, a novel member of the

CC tumour necrosis factor receptor family. The sequence was deduced

CC from a bone marrow cDNA clone (see AAX87670). Methods for the

CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
CC Escherichia coli or yeast host cells, are provided. Claimed  
CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
CC mature protein) and 26-X of the present sequence, where X is any  
CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
CC are useful for modulating apoptosis, NF-KB activation and  
CC proinflammatory or autoimmune responses in mammalian cells  
CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
CC fused to a heterologous sequence such as epitope tag or  
CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
CC assays to identify other proteins or molecules involved in binding  
CC interactions. This is useful for identifying inhibitors or  
CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
CC also be combined with an agent that is cytotoxic, chemotherapeutic  
CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
CC methods, purification methods and also in therapy, e.g. as  
CC inhibitors.

XX SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 20; Length 241;

Best Local Similarity 100.0%; Pred. No. 2.9e-55;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60  
|||||

DB 33 GCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 92  
|||||

QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGHGHCCKPWTDCQFGFLTVFPGNKTHNAV 120  
|||||

DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGHGHCCKPWTDCQFGFLTVFPGNKTHNAV 152  
|||||

QY 121 CV 122

DB 153 cv 154

RESULT 7

AA027651

ID AAB27651 standard; Protein; 241 AA.

XX AAB27651;

XX 26-JAN-2001 (first entry)

XX Human protein PRO364.

XX Cardiovascular; endothelial; angiogenic disorder; PRO179;

XX PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;

XX PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;

XX gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT /label= "signal peptide"

XX WO200053757-A2.

XX 14-SEP-2000.

XX 24-FEB-2000; 2000WO-US05004.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 02-JUN-1999; 99WO-US12252.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 01-SEP-1999; 99WO-US20111.

XX 15-SEP-1999; 99WO-US21090.

XX 30-NOV-1999; 99WO-US28313.

PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
XX  
PS Disclosure: Pages 61-62; 71pp; English.  
XX  
CC This is the amino acid sequence of the truncated human 312C2 T cell  
CC protein from clone A8. The 312C2 proteins are expressed in thymus  
CC cells and are induced on T cells and spleen cells following activation.  
CC Engagement of 312C2 stimulates proliferation of T cell clones,  
CC antigen-specific proliferation and cytokine production by T-cells, and  
CC potentiates T cell expansion or apoptosis. The products can be used  
CC in the treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions.  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX  
SQ Sequence 228 AA;

Query Match 100.0%; Score 737; DB 19; Length 228;  
Best Local Similarity 100.0%; Pred. NO. 4.9e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYFGECCEWDCMCVQPEFHCGDPCTTCAHHPCPPGQGVQSGK 60  
Db 40 darcrrvhttrccrdyfgcceswdcmcvqpfhcgdpcttcrhhpcppggvgsgk 99  
QY 61 FSGFGQICDASGTFSGGHEGCHKPWTCTQFGTLVFPGNKTHNAVCPGSPPAEPLG 119  
Db 100 fsfgqicdasgtfsggheghckpwtctqfgtlvfpgnkthnavcvgpsppaeplg 158

RESULT 2  
ID AAY95879  
XX AAY95879 standard; Protein: 234 AA.  
AC AAY95879;  
XX  
DT 20-NOV-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-like protein TR11.  
XX  
KW TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /label= Signal\_peptide  
FT Protein 26..234  
FT /label= Mature\_protein  
FT Domain 26..162  
FT /label= Extracellular\_domain  
FT Domain 163..179  
FT /label= transmembrane\_domain  
FT Domain 180..234  
FT /label= Intracellular\_domain  
FT Modified-site 146  
FT /note= "N-glycosylated"  
FT Domain 72..81  
FT /note= "conserved domain CD-II"  
FT Domain 84..93  
FT /note= "conserved domain CD-III"  
FT Domain 107..113  
FT /note= "conserved domain CD-IV"  
FT Domain 128..134  
FT /note= "conserved domain CD-V"  
FT Domain 153..160  
FT /note= "conserved domain CD-VI"

FT Domain 176..186  
FT /note= "conserved domain CD-VII"  
FT Domain 204..209  
FT /note= "conserved domain CD-IX"  
FT Domain 224..233  
FT /note= "conserved domain CD-X"  
FT Region 27..36  
FT /note= "epitope-bearing region"  
FT Region 43..51  
FT /note= "epitope-bearing region"  
FT Region 59..67  
FT /note= "epitope-bearing region"  
FT Region 56..64  
FT /note= "epitope-bearing region"  
FT Region 66..71  
FT /note= "epitope-bearing region"  
FT Region 99..107  
FT /note= "epitope-bearing region"  
FT Region 125..133  
FT /note= "epitope-bearing region"  
FT Region 143..151  
FT /note= "epitope-bearing region"  
FT Region 156..164  
FT /note= "epitope-bearing region"  
FT Region 203..211  
FT /note= "epitope-bearing region"  
FT Region 222..230  
FT /note= "epitope-bearing region"  
XX WO200050459-A1.  
PN 31-AUG-2000.  
XX  
PD 23-FEB-2000; 2000WO-US04572.  
XX  
PF 24-FEB-1999; 99US-0121648.  
PR 13-MAY-1999; 99US-0134172.  
PR 16-JUL-1999; 99US-0144076.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, NI J;  
XX  
XX WPI; 2000-572072/53.  
DR N-PSDB; AAA50304.  
XX  
XX Human tumor necrosis factor receptor-like proteins useful for  
PT diagnosis, prevention and treatment of disease states associated with  
PT aberrant cell survival such as autoimmune disease and rheumatoid  
PT arthritis  
XX  
XX Claim 14(c); Fig 1A-B; 278pp; English.  
XX  
CC The present sequence is that of human tumour necrosis factor  
CC receptor-like protein TR11, a novel 25 kDa protein which shows  
CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
CC factor receptor family-related gene. The sequence was deduced from  
CC a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
CC TR11 activated NF-kappaB through a TRAF2-mediated mechanism.  
CC Expression is in an endothelial cell line. This suggests that TR11 and  
CC its ligand may be involved in activated T-cell trafficking.  
CC The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
CC (see AAA50304-06) and highly conserved encoded proteins (see  
CC AAY95879-81), as well as vectors, host cells and recombinant methods for  
CC their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
CC for treating, preventing, prognosis and/or diagnosis of an  
CC immunodeficiency, especially common variable immunodeficiency,  
CC x-linked agammaglobulinemia, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich syndrome or x-linked immunoglobulin  
CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
CC and/or diagnose an autoimmune disease, especially rheumatoid



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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:23 ; Search time 126.12 Seconds  
(without alignments)  
57.202 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DARCCRVHTTRCCRDYPGEE.....GNKTHNAVCPGSPAPLEPLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	737	100.0	228	19 AAW37840	Truncated human 31
2	737	100.0	234	21 AAY95879	Human tumour necro
3	737	100.0	234	21 AAY52158	Tumour necrosis fa
4	737	100.0	235	21 AAY44825	Human molecule ass
5	737	100.0	241	19 AAW37839	Amino acid sequenc
6	737	100.0	241	20 AAY05605	Human TNF receptor
7	737	100.0	241	21 AAB27651	Human protein PRO3
8	737	100.0	241	21 AAB33431	Human PRO364 prote
9	737	100.0	241	21 AAY95895	Human tumour necro
10	737	100.0	241	21 AAB24409	Human PRO364 prote
11	737	100.0	241	21 AAY71467	Human PRO364 prote

12 737 100.0 241 22 AAB20115 Human immunostimul  
13 737 100.0 241 22 AAB47054 Human PRO364. Hom  
14 737 100.0 241 22 AAB50910 Human PRO364 prote  
15 737 100.0 241 22 AAB50982 Human PRO364 prote  
16 737 100.0 241 22 AAB53090 Human angiogenesis  
17 737 100.0 311 19 AAW37842 Human 312C2 protei  
18 721 97.8 240 21 AAY95881 Human tumour necro  
19 721 97.8 240 21 AAY52160 TR11SV2 amino acid  
20 636 86.3 241 21 AAY95880 Human tumour necro  
21 636 86.3 241 21 AAY52159 TR11SV1 amino acid  
22 632.5 85.8 316 22 AAB47055 Polypeptide encode  
23 632.5 85.8 317 20 AAY06645 PRO364-related EST  
24 425.5 57.7 222 19 AAW49018 Mouse glucocortico  
25 425.5 57.7 228 19 AAW49016 Mouse glucocortico  
26 425.5 57.7 228 19 AAW37838 Amino acid sequenc  
27 425.5 57.7 294 19 AAW49017 Mouse glucocortico  
28 395 53.6 232 19 AAW37841 Human 312C2 protei  
29 175.5 23.8 89 21 AAY76013 Murine TNF-alpha f  
30 175.5 23.8 89 22 AAB55952 Skin cell protein,  
31 159.5 21.6 255 16 AAR70977 H4-1BB receptor pr  
32 159.5 21.6 255 16 AAR64197 Human 4-1BB polype  
33 159.5 21.6 255 18 AAW26658 Human 4-1BB recept  
34 159.5 21.6 255 20 AAY33214 Human CD137 protei  
35 159.5 21.6 255 20 AAY28688 .Human receptor pro  
36 159.5 21.6 255 22 AAB50521 Human tumour necro  
37 158.5 21.5 219 18 AAW31759 A novel human h4-1  
38 158.5 21.5 219 20 AAW92523 Human h4-1BBSV rec  
39 158 21.4 206 16 AAR81881 Mouse type-II memb  
40 158 21.4 206 19 AAW48977 Mouse OX40 extrace  
41 158 21.4 438 16 AAR81882 Plasmid pDC406/OX4  
42 158 21.4 438 19 AAW48976 OX40/FC mutein. C  
43 154.5 21.0 219 20 AAW92524 Human h4-1BBSV rec  
44 154 20.9 273 20 AAV42185 Human mFLINT #2 pr  
45 154 20.9 277 16 AAR76996 Deduced sequence e

#### ALIGNMENTS

RESULT 1  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX  
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
OS Homo sapiens.  
XX  
XX  
PN W09806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 14-AUG-1997; 97WO-US19331.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM, Randall TD, Zlotnik A;  
XX  
DR WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PT Isolated 312C2 T cell gene - used to develop products for treating,

FT FT /label= Signature\_sequence  
 FT 68..96  
 FT /label= Signature\_sequence  
 FT 109..147  
 FT /label= Signature\_sequence  
 FT 122..129  
 FT /label= Signature\_sequence  
 FT 157..175  
 FT /label= Signature\_sequence  
 FT 165..186  
 FT /label= Signature\_sequence  
 FT 37  
 FT /note= "Potential phosphorylation site"  
 FT 48  
 FT /note= "Potential phosphorylation site"  
 FT 62  
 FT /note= "Potential phosphorylation site"  
 FT 82  
 FT /note= "Potential phosphorylation site"  
 FT 205  
 FT /note= "Potential phosphorylation site"  
 FT 223  
 FT /note= "Potential phosphorylation site"  
 FT 140  
 FT /note= "N-glycosylated"  
 FT XX  
 PN W020005374-A2.  
 XX  
 XX 03-FEB-2000.  
 XX  
 XX 21-JUL-1999; 99WO-US16637.  
 XX  
 XX 22-JUL-1998; 98US-0093827.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 XX  
 XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 XX  
 XX WPI; 2000-182699/16.  
 DR N-PSDB; AA449948.  
 XX  
 XX Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 XX  
 PS Claim 1; Pages 64-65; 67pp; English.  
 XX  
 CC The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from incyte clone 2809903 isolated from TLYMN0706  
 CC cDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
 CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antitumor,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 XX Sequence 235 AA;

Query Match 100.0%; Score 737; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-54;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGQGVQSGK 60  
 DB 40 darccrvhtrccrdypgeccsewdcmcvqpefhcgdpcttcrhpcppgqgvsgk 99  
 QY 61 FSGFGQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVPGNKTHNAVVCVPSPPAEPLG 119  
 DB 106 fsgfgqidcasgtfsgghegchkpwtctgfgfltvfgpnkthnavcvpsppaeplg 164

Db 100 fsgfgqidcasgtfsgghegchkpwtctgfgfltvfgpnkthnavcvpsppaeplg 158

RESULT 5  
 AAW37839  
 ID AAW37839 standard; Protein; 241 AA.  
 XX  
 AC AAW37839;  
 XX  
 DT 28-JUL-1998 (first entry)  
 XX  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /\*tag= a  
 FT /product= "human 312C2 protein"  
 FT XX  
 PN W09806842-A1.  
 XX  
 PD 19-FEB-1998.  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 XX  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 XX (SCHE ) SCHERING CORP.  
 XX  
 XX Gorman DM, Randall TD, Zlotnik A;  
 XX  
 DR WPI; 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 XX  
 PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 XX  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 XX Sequence 241 AA;

Query Match 100.0%; Score 737; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGQGVQSGK 60  
 DB 46 darccrvhtrccrdypgeccsewdcmcvqpefhcgdpcttcrhpcppgqgvsgk 105  
 QY 61 FSGFGQCIDCASGTFSGGHEGCHKPWTDCQFGFLTVPGNKTHNAVVCVPSPPAEPLG 119  
 DB 106 fsgfgqidcasgtfsgghegchkpwtctgfgfltvfgpnkthnavcvpsppaeplg 164



Qy	1	DARECRVHTTCCRDYFGEECCSWDCMCVQPBHCGDPCCTTCRHHHPCPPGGVGSQ GK	60
Db	46	darcrcvhttrccrdyfgceccswdcmcvqpefhcgdpctctrhpcpgpgvgvsgqk	105
Qy	61	FSFGQCIDCASGTFSGSGHEGCHKPWTDCQFGFLTVFPGNKNHNAVCPGSPAEPLG	119
Db	106	fsfgqicidcasqtfsgqhegchckpwtcdctqfglrvpknkthnavcvpspsaeplq	164

Query Match	100.0%;	Score 737;	DB 21;	Length 241;
Best Local Similarity	100.0%;	Pred. No. 5.2e-54;		
Matches 119;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

RESULT 6  
ID AAY06605  
XX AAY06605 standard; Protein; 241 AA.  
AC AAY06605;  
XX 26-OCT-1999 (first entry)  
DT Human TNF receptor homologue PRO364.  
DE PRO364; tumour necrosis factor receptor; human; apoptosis;  
KW inflammation; antiinflammatory; NF-KB activation;  
KW autoimmune disease; therapy.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..25  
FT /note= "signal peptide"  
FT Protein 26..241  
FT /note= "mature protein"  
FT Modified-site 146  
FT /note= "N-glycosylated"  
FT Domain 162..180  
FT /note= "transmembrane domain"  
XX WO9940196-A1.  
XX 12-AUG-1999.  
XX 09-FEB-1999; 99WO-US02642.  
XX 09-FEB-1998; 98US-0024087.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
PI Pitti RM, Wood WI;  
XX WPI; 1999-494296/41.  
DR N-PSDB; AAX87670.  
XX Tumour necrosis factor receptor homologue - useful for, e.g.  
PT modulating apoptosis and NF-KB activation and proinflammatory or  
PT autoimmune responses  
XX Claim 17; Fig 2A; 104pp; English.  
XX The present sequence represents human PRO364, a novel member of the  
CC tumour necrosis factor receptor family. The sequence was deduced  
CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
CC Escherichia coli or yeast host cells, are provided. Claimed  
CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
CC mature protein) and 26-X of the present sequence, where X is any  
CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
CC are useful for modulating apoptosis, NF-KB activation and  
CC proinflammatory or autoimmune responses in mammalian cells  
CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
CC fused to a heterologous sequence such as epitope tag or  
CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
CC assays to identify other proteins or molecules involved in binding  
CC interactions. This is useful for identifying inhibitors or  
CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
CC also be combined with an agent that is cytotoxic, chemotherapeutic  
CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
CC methods, purification methods and also in therapy, e.g. as  
XX inhibitors.  
XX Sequence 241 AA;

Query Match 100.0%; Score 737; DB 20; Length 241;  
Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPCCTTCRRHHPGPGGVQSQGK 60  
|||||  
Db 46 darccrvhttrccrdypgeccsewdcmcvqpefhcgdpccctcrhhpcppggvqsggk 105  
|||||  
QY 61 FSFGFCIDCASGTFSGGHGHCKPWTDCQTQFGFLTVPGNKTHNAVCPSPPEPLG 119  
|||||  
Db 106 fsfgfcidcasgtfsghghckpwtddctqfgfltvpgnkthnavcvgpppaeplg 164  
|||||  
RESULT 7  
AAB27651  
ID AAB27651 standard; Protein; 241 AA.  
XX AAB27651;  
AC AAB27651;  
XX 26-JAN-2001 (first entry)  
DT Human protein PRO364.  
DE Human protein PRO364.  
XX Cardiovascular; endothelial; angiogenic disorder; PRO179;  
KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
KW gene therapy.  
XX Homo sapiens.  
XX OS  
XX Key Location/Qualifiers  
FH Peptide 1..25  
FT /label= "Signal peptide"  
XX WO200053757-A2.  
XX 14-SEP-2000.  
XX 24-FEB-2000; 2000WO-US05004.  
XX 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gertschen ME;  
PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
PI Watanabe CK, Williams PM, Wood WI;  
XX WPI; 2000-611444/58.  
DR N-PSDB; AAA99903.  
XX Novel PRO polypeptides and agonists and antagonists of them, used to  
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
PT -  
XX Claim 71; Fig 6; 181pp; English.  
XX The present invention relates to methods for stimulating or inhibiting  
CC angiogenesis and cardiovascularization. The methods involve the use of  
CC pharmaceutical compositions based on the following proteins, PRO179,  
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,

CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
CC the exemplification of the present invention.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 737; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DARCCRVHTTRCCRDYDGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCCPGQGVQSGK 60  
Db 46 darccrvhttrccrdydgccsewdcmcvqpefhcgdpccctcrhhpcppggvgsgk 105  
QY 61 FSGFGQICDASGTFSGGHEGCHKPWTDCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 119  
Db 106 fsfgqicdcasgtfsggheghckpwtcdctqfgfltvfpgnkthnavcvpsppaeplg 164

RESULT 11  
AAV71467  
ID AAY71467 standard; Protein; 241 AA.  
AC AAY71467;  
DT 08-NOV-2000 (first entry)  
XX Human PRO364 protein.  
XX  
XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;  
KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;  
KW tumour necrosis factor receptor; GTR protein homologue.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..25 /label= Signal\_peptide  
FT Modified-site 5..11 /note= "N-myristoylation site"  
FT Modified-site 8..14 /note= "N-myristoylation site"  
FT Modified-site 25..31 /note= "N-myristoylation site"  
FT Protein 26..241 /note= "Mature\_PRO364\_protein"  
FT Modified-site 30..36 /note= "N-myristoylation site"  
FT Modified-site 33..39 /note= "N-myristoylation site"  
FT Modified-site 118..124 /note= "N-myristoylation site"  
FT Modified-site 122..128 /note= "N-myristoylation site"  
FT Modified-site 146..150 /note= "Asn is N-glycosylated"  
FT Modified-site 156..162 /note= "N-myristoylation site"  
FT Domain 163..183 /label= Transmembrane\_domain  
FT Binding-site 166..177 /note= "Prokaryotic membrane lipoprotein lipid attachment site"  
FT Region 171..193 /note= "Leucine zipper pattern"  
XX  
XX W0200032778-A2.  
XX  
XX  
PD 08-JUN-2000.  
XX

PF 30-NOV-1999; 99WO-US28409.  
XX  
PR 01-DEC-1998; 98WO-US25108.  
PR 16-DEC-1998; 98US-0112850.  
PR 22-DEC-1998; 98US-0113296.  
PR 20-JUL-1999; 99US-0144758.  
XX 26-JUL-1999; 99US-0145698.  
PA (GETH ) GENENTECH INC.  
XX  
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
XX WPI; 2000-412325/35.  
DR N-ESDB; AAD01240.  
XX  
XX New composition useful for inhibiting neoplastic cell growth and for  
PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
PT their antagonists -  
XX  
XX Claim 31; Fig 4; 108pp; English.  
XX  
XX The present sequence is the human PRO364 protein, encoded by the cDNA  
CC clone, designated as DNA47365-1206. It is isolated from human small  
CC intestine tissue cDNA library, identified using probes based on the  
CC consensus sequence DNA4825, relative to the Incyte expressed sequence  
CC tag (EST) 3003460. This EST has homology to tumour necrosis factor  
CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows  
CC homology to members of the TNFR family and mouse GTR protein.  
CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as  
CC a neoplastic cell growth inhibitor and is used for treating tumours,  
CC using an effective amount of PRO655, PRO364 and PRO344. This composition  
CC is especially useful for treatment of human cancers such as breast,  
XX prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 737; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DARCCRVHTTRCCRDYDGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCCPGQGVQSGK 60  
Db 46 darccrvhttrccrdydgccsewdcmcvqpefhcgdpccctcrhhpcppggvgsgk 105  
QY 61 FSGFGQICDASGTFSGGHEGCHKPWTDCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 119  
Db 106 fsfgqicdcasgtfsggheghckpwtcdctqfgfltvfpgnkthnavcvpsppaeplg 164  
RESULT 12  
AAB20115  
ID AAB20115 standard; Protein; 241 AA.  
XX  
XX AAB20115;  
DT 30-APR-2001 (first entry)  
XX  
DE Human immunostimulant PRO364.  
XX  
XX PRO364; UNQ319; human; immune disease; autoimmune disease;  
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipsoriatic;  
KW antiasthmatic; antiallergic; immunostimulant.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..25 /label= Signal\_peptide  
FT Protein 26..241 /label= Mature\_protein  
FT

```
RESULT 9
AAY95895
ID AAY95895 standard; Protein: 241 AA.
XX
AC AAY95895;
XX
DT 20-NOV-2000 (first entry)
XX
DE Human tumour necrosis factor receptor-like protein TR11 mutelin.
XX
KW TR11; human; tumour necrosis factor receptor-like protein;
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;
KW dermatological; antiinflammatory; therapy; diagnosis; mutelin;
KW mutant.
XX
OS Homo sapiens.
XX
PN WO200050459-A1.
XX
PD 31-AUG-2000.
XX
PF 23-FEB-2000; 200WO-US04572.
XX
PR 24-FEB-1999; 99US-0121648.
PR 13-MAY-1999; 99US-0134172.
PR 16-JUL-1999; 99US-0144076.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, NI J;
XX
DR WPI; 2000-572072/53.
XX
PT Human tumor necrosis factor receptor-like proteins useful for
PT diagnosis, prevention and treatment of disease states associated with
PT aberrant cell survival such as autoimmune disease and rheumatoid
PT arthritis.
XX
PS Disclosure; 294-295; 278pp; English.
XX
CC The present sequence is that of human tumor necrosis factor
CC receptor-like protein Tr11 (see also AAY95879), a novel protein
CC showing identity to murine glucocorticoid induced tumour necrosis
CC factor receptor family-related gene. The invention provides
CC highly conserved Tr11, Tr11SV1 and Tr11SV2 proteins (see AAY95879-81),
CC as well as vectors, host cells and recombinant methods for their
CC production. Tr11, Tr11SV1 and/or Tr11SV2 polypeptides are useful
CC for treating, preventing, prognosis and/or diagnosis of an
CC immunodeficiency, especially common variable immunodeficiency,
CC X-linked agammaglobulinemia, severe combined immunodeficiency,
CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin
CC deficiency with hyper IgM. Tr11, Tr11SV1 and/or Tr11SV2
CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis
CC and/or diagnose an autoimmune disease, especially rheumatoid
CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura
CC or IgA nephropathy. The polypeptides, polynucleotides and/or
CC antibodies can be administered to cells in vitro, ex vivo or in
CC vivo or to a multicellular organism. Soluble forms of the
CC polypeptides may also be used. Methods for screening for
CC agonist/antagonist compounds are also provided.
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 737; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.2e-54;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DARCRVHTTRCCRDYPPGEECCSEWDCMCVQPFHCGDPCCTTCRHHPCPPGGVGSQGK 60
DB ||||||
46 darcrvhttrccrdyppgeccsewdcmcvqpfhcgdpcccttrhhpcppggvgsqgk 105

Oy 61 PSFGFCIDCASGTFSGHGHCXKPKWTDOFGELTVFPGNKTHNAVCPGSPPAEPLG 119
DB ||||||
106 fsfgfcidcasgtfsgghgchckpwtctqfgltvfpgnkthnavcvpsppaeplg 164

RESULT 10
AAB24409
ID AAB24409 standard; Protein: 241 AA.
XX
AC AAB24409;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human PRO364 protein sequence SEQ ID NO:117.
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US28313.
XX
PR 01-DEC-1998; 98WO-US25108.
PR 16-DEC-1998; 98US-0112850.
PR 12-JAN-1999; 99US-0115554.
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
PI Watanabe CK, Williams PM, Wood WI;
XX
WPI; 2000-412154/35.
N-PSDB; AAA77604.
XX
Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating diagnosing a cardiovascular, endothelial or
PT angiogenic disorders in mammals -
XX
Claim 72; Fig 44; 315pp; English.
XX
CC The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating diagnosing a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PRO expression such as cardiovascular, endothelial or
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
```





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 FT Modified-site /note= "N-myristoylation site"  
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 FT Modified-site /note= "N-myristoylation site"  
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 FT Modified-site /note= "N-myristoylation site"  
 FT 122..128  
 FT Modified-site /note= "N-myristoylation site"  
 FT 156..162  
 FT Modified-site /note= "N-myristoylation site"  
 FT 146..150  
 FT Modified-site /note= "Asn is N-glycosylated"  
 FT 166..177  
 FT Peptide /note= "prokaryotic membrane lipoprotein lipid attachment site"  
 FT 171..193  
 FT Peptide /note= "leucine zipper pattern"  
 FT WO200105972-A1.  
 PN 25-JAN-2001.  
 PD 15-MAR-2000; 2000WO-US06884.  
 PP 20-JUL-1999; 99US-0144758.  
 PR (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
 PI Wood WL;  
 XX WPI: 2001-103149/11.  
 DR N-PSDB; AAF30057.  
 CC New PRO polypeptides, nucleic acids and (ant)agonists.\*useful for  
 CC diagnosing and treating immune-related disorders, such as multiple  
 CC sclerosis, rheumatoid arthritis and diabetes -  
 CC Claim 20; Fig 16; 127pp; English.  
 CC The present sequence is that of novel human immunomodulator PRO364  
 CC (UNQ319), as deduced from cDNA (see AAF30057) isolated from a  
 CC small intestine library. PRO364 (26 kDa, pI 6.34) shows sequence  
 CC homology to mouse G1PR protein and may be its human counterpart.  
 CC The invention provides polynucleotides (see AAF30050-62) encoding  
 CC novel human PRO proteins (see AAB20108-20) including PRO364.  
 CC Claimed compositions comprising these proteins or their agonists  
 CC are useful for increasing infiltration of inflammatory cells into  
 CC a tissue of a mammal, stimulating or enhancing an immune  
 CC response, or increasing the proliferation of T-lymphocytes in a  
 CC mammal in response to an antigen. Claimed compositions comprising  
 CC a PRO polypeptide or its antagonist have the opposite effect. A  
 CC claimed method for treating an immune related disorder, such as a T  
 CC cell disorder, involves administering a PRO polypeptide, an agonist  
 CC antibody or an antagonist antibody. The disorder is selected from  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated  
 CC renal disease, demyelinated diseases (such as multiple sclerosis),  
 CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
 CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
 CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive

CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
 CC (such as bullous skin disease, erythema multiforme and psoriasis),  
 CC allergic diseases (such as asthma, allergic rhinitis, atopic  
 CC dermatitis, food hypersensitivity and urticaria), immunologic  
 CC diseases of the lung and transplantation associated diseases (such  
 CC as graft rejection and graft-versus-host disease) (all claimed).  
 CC Claimed methods of diagnosing these disorders comprise detecting  
 CC the level of expression of the PRO gene. Also claimed are a method  
 CC of identifying a compound capable of inhibiting the expression or  
 CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
 CC and a method of stimulating the proliferation of T lymphocytes  
 CC using PRO364.  
 XX  
 SQ Sequence 241 AA;  
 Query Match 100.0%; Score 737; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. NO. 5.2e-54;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 46 darcrcrvhttrccrdypgeccsewdcmcvqpefhgcpcttcrrhhpcppgqvsgsk 105  
 QY 61 FSGFGQCIDCASGTFSGGHEGHCXKRWTDCTQFGFLTVPNGKTHNAVCPGSPPAEPLG 119  
 Db 106 fsfgfqcidasgtfsggheghckpwtcdtqfgfltvpngkthnavcvp9spaeplg 164  
 RESULT 13  
 AAB47054  
 ID AAB47054 standard; Protein: 241 AA.  
 XX  
 AC AAB47054;  
 XX  
 DT 08-MAY-2001 (first entry)  
 DE Human PRO364.  
 XX  
 KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
 KW hG1TR; ligand; hG1TRL; PRO175; tumour necrosis factor receptor; TNFR;  
 KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
 KW myocardial infarction; PGF-2alpha; trauma; cancer; angiogenesis;  
 KW age-related macular degeneration; antibody; periodontal disease;  
 KW vascular-related drug targeting; atherosclerosis; hypertension;  
 KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
 KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
 KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /note= "Potential signal peptide"  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "Potential transmembrane domain"  
 XX  
 WO200103720-A2.  
 PN 18-JAN-2001.  
 PD 11-JUL-2000; 2000WO-US18867.  
 PF 12-JUL-1999; 99US-0143304.  
 PR (GETH ) GENENTECH INC.  
 PA Williams PM, Gerritsen ME;  
 XX WPI: 2001-138257/14.  
 DR N-PSDB; AAC85433.  
 DR

---

Db 46 darcrrvhttrccrdypgeccsewcmcvqpfhcgdpccctcrhpcppggvsgqgk 105  
QY 61 FSFGQCIDCASGTFSGGHEGCHKPWTDTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 119  
Db 106 fsfgqcidcasgtfsgghegchckpwtctqfgfltvfpgnkthnavcvpgspapleplg 164

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ID AAB50982 standard; Protein; 241 AA.  
XX  
AC AAB50982;  
XX  
XX 21-MAR-2001 (first entry)  
XX Human PRO364 protein.  
XX Human; PRO: cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
KW vulnery; antianginal; gene therapy; cardiovascular disease;  
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
KW wound healing.  
XX  
OS Homo sapiens.  
XX  
XX WO200073445-A2.  
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XX 07-DEC-2000.  
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XX PF 17-MAY-2000; 2000WO-US13705.  
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XX PR 02-JUN-1999; 99WO-US12252.  
XX PR 23-JUN-1999; 99US-0141037.  
XX PR 20-JUL-1999; 99US-0144758.  
XX PR 26-JUL-1999; 99US-0145698.  
XX PR 28-JUL-1999; 99US-0146222.  
XX PR 01-SEP-1999; 99WO-US20111.  
XX PR 30-NOV-1999; 99WO-US28313.  
XX PR 30-NOV-1999; 99WO-US28409.  
XX PR 02-DEC-1999; 99WO-US28565.  
XX PR 16-DEC-1999; 99WO-US30095.  
XX PR 11-FEB-2000; 2000WO-US03565.  
XX PR 18-FEB-2000; 2000WO-US04341.  
XX PR 18-FEB-2000; 2000WO-US04342.  
XX PR 24-FEB-2000; 2000WO-US05004.  
XX PR 02-MAR-2000; 2000WO-US05841.  
XX PR 10-MAR-2000; 2000WO-US06319.  
XX PR 15-MAR-2000; 2000WO-US06884.  
XX PR 21-MAR-2000; 2000WO-US07532.  
XX PR 30-MAR-2000; 2000WO-US08439.  
XX  
XX PA (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
XX WPI; 2001-025251/03.  
XX  
XX N-PSDB; AAC90566.  
XX  
XX Seventeen nucleic acids encoding PRO polypeptides which are useful in  
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
PT disorders in a mammal -  
XX  
XX Claim 71; Fig 8; 182pp; English.  
XX  
XX The present sequence is one of seventeen novel PRO polypeptides. The PRO  
CC nucleic acids, polypeptides, agonists and antagonists are useful for  
CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial

CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
CC antagonists are also used to prevent tumour angiogenesis and for treating  
CC periodontal diseases. They are also used to stimulate wound healing and  
CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder.  
XX  
SQ Sequence 241 AA;  
  
Query Match 100.0%; Score 737; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 46 darcrrvhttrccrdypgeccsewcmcvqpfhcgdpccctcrhpcppggvsgqgk 105  
  
QY 61 FSFGQCIDCASGTFSGGHEGCHKPWTDTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 119  
Db 106 fsfgqcidcasgtfsgghegchckpwtctqfgfltvfpgnkthnavcvpgspapleplg 164

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 XX 31-AUG-2000.  
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 XX 23-FEB-2000; 2000WO-US04572.  
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 PR 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, NI J;  
 XX  
 XX WPI; 2000-572072/53.  
 DR N-PSDB; AAA50304.  
 XX  
 XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -  
 XX  
 PS Claim 14(c); Fig 1A-B; 278pp; English.  
 XX  
 CC The present sequence is that of human tumor necrosis factor  
 CC receptor-like protein TR11, a novel 25 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
 CC TR11 activated NF-kappaB through a TRAF2-mediated mechanism.  
 CC Expression is activation-inducible. The TR11 ligand is constitutively  
 CC expressed in an endothelial cell line. This suggests that TR11 and  
 CC its ligand may be involved in activated T-cell trafficking.  
 CC The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
 CC (see AAA50304-06) and highly conserved encoded proteins (see  
 CC IAY95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an

CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognose  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
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 Query Match 100.0%; Score 979; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-70;  
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 Qy 61 YPGEECCSEWDCMCVQPFHCGDPCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 Db 61 ypgeeccsewdcmcvqpfhcgdpcttcrhhpcppgqgvqsgkfsfgqcidcasgtf 120  
 Qy 121 SGGHEGCHKPWTDCTQFGFLTVPGNKTHNAVCPGSPPAEPLG 164  
 Db 121 sgghegchkpwtcdtqfgfltvpgnknthnavcvpgspapeplg 164  
 RESULT 2  
 RAY52158  
 ID AAY52158 standard; Protein; 234 AA.  
 XX AC AAY52158;  
 XX  
 DT 01-FEB-2000 (first entry)  
 XX  
 DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.  
 KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;  
 KW G1TR; growth; differentiation; cell death; immune deficiency disorder;  
 KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
 KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW inflammatory condition.  
 OS Homo sapiens.  
 XX  
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 FT Protein 26..234  
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 FT Domain 163..179  
 FT /note= "Transmembrane domain"  
 FT Domain 180..234  
 FT /note= "Intracellular domain"  
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 XX 29-APR-1999.  
 XX  
 XX 21-OCT-1998; 98WO-US22085.  
 XX  
 XX 21-OCT-1997; 97US-0063212.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:24 ; Search time 126.12 Seconds  
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Title: US-09-512-363-2\_COPY\_1\_164

Perfect score: 979

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Post-processing: Minimum Match 0%

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3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	979	100.0	234	21 AAY95879 Human tumour necro
2	979	100.0	234	21 AAY52158 Tumour necrosis fa
3	979	100.0	241	19 AAW37839 Amino acid sequenc
4	979	100.0	241	20 AAY06605 Human TNF receptor
5	979	100.0	241	21 AAB27651 Human protein PRO3
6	979	100.0	241	21 AAB33431 Human PRO364 prote
7	979	100.0	241	21 AAY95895 Human tumour necro
8	979	100.0	241	21 AAB24409 Human PRO364 prote
9	979	100.0	241	21 AAY71467 Human PRO364 prote
10	979	100.0	241	22 AAB20115 Human immunostimul
11	979	100.0	241	22 AAB47054 Human PRO364. Hom

12	979	100.0	241	22 AAB50910 Human PRO364 prote
13	979	100.0	241	22 AAB50982 Human angio genesis
14	979	100.0	241	22 AAB53090 Truncated human 31
15	947	96.7	228	19 AAW37840 Human molecule ass
16	947	96.7	235	21 AAY44825 Human 312C2 protei
17	947	96.7	311	19 AAW37842 Human tumour necro
18	931	95.1	240	21 AAY95881 TR11SV2 amino acid
19	931	95.1	240	21 AAY52160 PRO364-related EST
20	842.5	86.1	317	20 AAY06645 Polypeptide encode
21	837.5	85.5	316	22 AAB47055 Human tumour necro
22	649	66.3	241	21 AAY95880 TR11SV1 amino acid
23	649	66.3	241	21 AAY52159 Human 312C2 protei
24	605	61.8	232	19 AAW37841 Mouse glucocorticoid
25	510	52.1	222	19 AAW49018 Amino acid sequenc
26	510	52.1	228	19 AAW49016 Mouse glucocorticoid
27	510	52.1	228	19 AAW37838 Amino acid sequenc
28	510	52.1	294	19 AAW49017 Murine TNF-alpha f
29	255	26.0	89	21 AAY76013 Skin cell protein,
30	255	26.0	89	22 AAB55952 Mouse type-II memb
31	166.5	17.0	206	16 AAR81881 Mouse OX40 extrac
32	166.5	17.0	206	19 AAW48977 Plasmid pDC406/OX4
33	166.5	17.0	438	16 AAR81882 OX40/Fc mutein. C
34	166.5	17.0	438	19 AAW48976 Deduced sequence e
35	166	16.5	277	16 AAR76996 ACT-4 cell surface
36	162	16.5	277	16 AAR74737 ACT-4-h-1 receptor
37	162	16.5	277	16 AAB35329 Human OX40 protein
38	162	16.5	277	22 AAB50522 Human tumour necro
39	162	16.5	277	22 AAB70977 H4-1BB receptor pr
40	160.5	16.4	255	16 AAR64197 Human 4-1BB polype
41	160.5	16.4	255	18 AAW26658 Human 4-1BB recept
42	160.5	16.4	255	20 AAY33214 Human CD137 protei
43	160.5	16.4	255	20 AAY28688 Human receptor pro
44	160.5	16.4	255	20 AAY28688 Human tumour necro
45	160.5	16.4	255	22 AAB50521

#### ALIGNMENTS

RESULT 1  
AAY95879 standard; Protein; 234 AA.  
ID AAY95879 standard; Protein; 234 AA.  
XX AC AC  
XX AAY95879;  
DT 20-NOV-2000 (first entry)  
XX Human tumour necrosis factor receptor-like protein TR11.  
DE TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis.  
XX Homo sapiens.  
XX OS  
XX  
FH Key Location/Qualifiers  
FT Peptide /label= Signal\_peptide  
FT Protein /label= Mature\_protein  
FT Domain /label= Extracellular\_domain  
FT Domain /label= Transmembrane\_domain  
FT Domain /label= Intracellular\_domain  
FT Modified-site /note= "N-glycosylated"  
FT Domain /note= "conserved domain CD-II"  
FT Domain /note= "conserved domain CD-III"

26-OCT-1999 (first entry)  
Human TNF receptor homologue PRO364.  
PRO364; tumour necrosis factor receptor; human: apoptosis;  
inflammation; antiinflammatory; NF-KB activation;  
autoimmune disease; therapy.  
Homo sapiens.

XX FH Key Location/Qualifiers  
XX FT Peptide 1..25  
XX FT Protein /note= "signal peptide"  
XX FT Protein 26..241  
XX FT Modified-site 146 /note= "mature protein"  
XX FT /note= "N-glycosylated"  
XX FT Domain 162..180  
XX FT /note= "transmembrane domain"

XX WO9940196-A1.  
XX PN Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
XX PI Pitti RM, Wood WI;  
XX DR WPI: 1999-494296/41.  
XX DR N-PSDB; AAX87670.

XX TT Tumour necrosis factor receptor homologue - useful for, e.g.  
XX PT modulating apoptosis and NF-KB activation and proinflammatory or  
XX PT autoimmune responses

XX PS Claim 17; Fig 2a; 104pp; English.

XX CC The present sequence represents human PRO364, a novel member of the  
XX CC tumour necrosis factor receptor family. The sequence was deduced  
XX CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
XX CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
XX CC Escherichia coli or yeast host cells, are provided. Claimed  
XX CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
XX CC mature protein) and 26-X of the present sequence, where X is any  
XX CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
XX CC are useful for modulating apoptosis, NF-KB activation and  
XX CC proinflammatory or autoimmune responses in mammalian cells  
XX CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
XX CC fused to a heterologous sequence such as epitope tag or  
XX CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
XX CC assays to identify other proteins or molecules involved in binding  
XX CC interactions. This is useful for identifying inhibitors or  
XX CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
XX CC also be combined with an agent that is cytotoxic, chemotherapeutic  
XX CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
XX CC methods, purification methods and also in therapy, e.g. as  
XX CC inhibitors.

XX SQ Sequence 241 AA;

Query Match 100.0%; Score 979; DB 20; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qj 1 MAQHGANGAFRALGCLALLCALSLGQRTGGPGCGPGLLLGTGTDAKCCRVHTTRCCRD 60  
Db 1 maqhgangafralcgllalcalslgqrtygpgcgprlllgtgtdarccrvhttrccrd 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
Db 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppgqgvsgkfsfgqcidcasgtf 120

QY 121 SGHGHGCKPWTDCQFGFLTVFPGNKTINAVCVPGSPPAEPLG 164  
Db 121 sggheghckpwtcdtqfgfltvfpgnktinavcvpgsppeep.lg 164

RESULT 5  
AAB27651  
ID AAB27651 standard; Protein: 241 AA.  
XX AC AAB27651;  
XX DT 26-JAN-2001 (first entry)  
XX DE Human protein PRO364.  
XX KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
XX KW PRO338; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
XX KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
XX KW gene therapy.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..25  
XX FT /label= "Signal peptide"  
XX PN WO200053757-A2.  
XX PD 14-SEP-2000.  
XX PF 24-FEB-2000; 2000WO-US05004.  
XX PR 08-MAR-1999; 99WO-US05028.  
XX PR 12-MAR-1999; 99US-0123957.  
XX PR 02-JUN-1999; 99WO-US12252.  
XX PR 20-JUL-1999; 99US-0144758.  
XX PR 26-JUL-1999; 99US-0145698.  
XX PR 01-SEP-1999; 99WO-US20111.  
XX PR 15-SEP-1999; 99WO-US21090.  
XX PR 30-NOV-1999; 99WO-US28313.  
XX PR 30-NOV-1999; 99WO-US28409.  
XX PR 02-DEC-1999; 99WO-US28565.  
XX PR 18-FEB-2000; 2000WO-US04342.  
XX PR 22-FEB-2000; 2000WO-US04414.  
XX PA (GETH ) GENENTECH INC.  
XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
XX PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
XX PI Watanabe CK, Williams PM, Wood WI;  
XX DR WPI: 2000-611444/58.  
XX DR N-PSDB; AAA99903.  
XX PT Novel PRO polypeptides and agonists and antagonists of them, used to  
XX PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
XX PS Claim 71; Fig 6; 181pp; English.  
XX CC The present invention relates to methods for stimulating or inhibiting  
XX CC angiogenesis and cardiovascularization. The methods involve the use of  
XX CC pharmaceutical compositions based on the following proteins, PRO179,  
XX CC PRO338, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,  
XX CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
XX CC proteins were identified by isolating cDNA clones encoding secreted  
XX CC proteins. The proteins of the invention may be used to diagnose and  
XX CC treat cardiovascular, endothelial or angiogenic disorders. The present

XX Ni J, Ruben SM;  
PI  
XX  
XX WPI; 2000-061922/05.  
DR N-PSDB; AA237762.  
XX  
XX New tumour necrosis factor receptor-like polypeptides used to, e.g.  
PT treat Digeorge syndrome -  
XX  
XX Claim 14; Fig 1; 167pp; English.  
XX  
XX This is the amino acid sequence of the human tumour necrosis factor  
CC receptor-like protein (Trll receptor). The invention relates to Trll and  
CC two splice variants TrllSV1 and TrllSV2. The nucleotide sequences were  
CC determined by sequencing cloned cDNAs AA237765-237766. The Trll receptor  
CC and its splice variants show homology to the murine glucocorticoid  
CC induced tumour necrosis factor receptor family-related gene (GTRF).  
CC Trll, TrllSV1 and TrllSV2 polypeptides may be involved in the regulation  
CC of cell-type specific receptor-mediated cell growth, differentiation,  
CC and ultimately, cell death. They can be used for screening for  
CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
CC used for treating a disease state associated with aberrant cell  
CC survival. They can be used for treating immune deficiency disorders,  
CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
CC platelet disorders or wounds resulting from trauma or surgery. They can  
CC also be used to treat heart attacks, strokes, Addison's disease,  
CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
CC hypersensitivity to an antigenic molecule, organ rejection or graft  
CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
CC disease, hyperproliferative disorders, or infections. They can also be  
CC used to repair, replace, or protect tissue damaged by congenital  
CC defects, trauma, age, disease, surgery, including cosmetic plastic  
CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
CC detection, diagnosis and prognosis.  
XX Sequence 234 AA;  
SQ  
Query Match 100.0%; Score 979; DB 21; Length 234;  
Best Local Similarity 100.0%; Pred. No. 3.9e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGMAGAFRALCGLLCALSLGQRTGGPGCGPGRLLLTGTDCRCRVRHTTCRCD 60  
DB 1 maqhgmgafrafcgllalcalsglrptggpgcgprlllgtgdarccrvhttrcd 60  
QY 61 YPGEECCSEWDCMVCQPEFHCGDPCTTCRHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
DB 61 YPGEECCSEWDCMVCQPEFHCGDPCTTCRHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
QY 121 SGGHEGCHKPWTDCQFGFLTVFPGNKTHNAVCPVPGSPAPPLG 164  
DB 121 sgghegchckpwtcdqfgfltvfpgnkthnavcvpgspapplg 164  
RESULT 3  
AAW37839  
ID AAW37839 standard; Protein; 241 AA.  
XX  
XX AAW37839;  
XX  
XX 28-JUL-1998 (first entry)  
XX  
XX DE; Amino acid sequence of the human 312C2 T cell protein.

XX Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT CDS 1..726  
FT /\*tag= a  
FT /product= "human 312C2 protein"  
XX  
XX WC9806842-A1.  
XX 19-FEB-1998.  
XX 14-AUG-1997; 97WO-US13931.  
XX 07-OCT-1996; 96US-0027901.  
XX 16-AUG-1996; 96US-0689943.  
XX (SCHE ) SCHERING CORP.  
XX Gorman DM, Randall TD, Zlotnik A;  
XX WPI; 1998-159534/14.  
XX N-PSDB; AAV19153.  
XX  
XX Isolated 312C2 T cell gene - used to develop products for treating,  
PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
XX  
XX Claim 2; Pages 59-60; 71pp; English.  
XX  
XX This is the amino acid sequence encoding the human 312C2 T cell  
CC protein. The 312C2 proteins are expressed in thymus cells and are  
CC induced on T cells and spleen cells following activation. Engagement  
CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
CC proliferation and cytokine production by T-cells, and potentiates T  
CC cell expansion or apoptosis. The products can be used in the  
CC treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX  
XX Sequence 241 AA;  
SQ  
Query Match 100.0%; Score 979; DB 19; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGMAGAFRALCGLLCALSLGQRTGGPGCGPGRLLLTGTDCRCRVRHTTCRCD 60  
DB 1 maqhgmgafrafcgllalcalsglrptggpgcgprlllgtgdarccrvhttrcd 60  
QY 61 YPGEECCSEWDCMVCQPEFHCGDPCTTCRHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
DB 61 YPGEECCSEWDCMVCQPEFHCGDPCTTCRHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
QY 121 SGGHEGCHKPWTDCQFGFLTVFPGNKTHNAVCPVPGSPAPPLG 164  
DB 121 sgghegchckpwtcdqfgfltvfpgnkthnavcvpgspapplg 164  
RESULT 4  
AAW06605  
ID AAW06605 standard; Protein; 241 AA.  
XX  
XX AAW06605;  
XX  
XX

Db 121 sgghgchckpwtcdctqfgyflvfpnknthnavcvgpppaeplg 164  
 |||

RESULT 7  
 AAY95895  
 ID AAY95895 standard; Protein; 241 AA.  
 XX  
 AC AAY95895;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-like protein TR11 mutin.

XX TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antirheumatic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutin;  
 KW mutant.

XX Homo sapiens.  
 OS  
 XX  
 PN WO200050459-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 23-FEB-2000; 2000WO-US04572.  
 XX  
 PR 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, N1 J;

PI WPI; 2000-572072/53.

XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -

PS Disclosure; 294-295; 278pp; English.

XX The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.

XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4e-70;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFAALCALCALSLGQRTGGGCGGPRLLLTGTDTARCCRVHTTRCCRD 60  
 |||  
 Db 1 maqhgamafralcgllallcalslgqrptgpgcgprllltgttdarccrvhttrccrd 60  
 |||  
 QY 61 YPGECCSEWDGCMVQPEFHCDCPCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
 |||  
 Db 61 ypgeccsewdgcmvqpefchcdpcttcrrhhpcppgqgvqsggkfsfgfcldcasgtf 120  
 |||  
 QY 121 SGGHEGHCCKPWTCDCTQFGFLTVFPGNKNTHNAVVCVPGSPPAEPLG 164  
 |||  
 Db 121 sgghgchckpwtcdctqfgyflvfpnknthnavcvgpppaeplg 164  
 |||

RESULT 8

AAB24409

ID AAB24409 standard; Protein; 241 AA.

XX AAB24409;

DT 07-NOV-2000 (first entry)

DE Human PRO364 protein sequence SEQ ID NO:117.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.

OS Homo sapiens.

XX WO2000032221-A2.

PD 08-JUN-2000.

PF 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1998; 98WO-US25108.

PR 16-DEC-1998; 98US-0112850.

PR 12-JAN-1999; 99US-0115554.

PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0144758.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 29-OCT-1999; 99US-0162506.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;

PI Godowski FJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;

PI Watanabe CK, Williams PM, Wood WI;

DR WPI; 2000-412154/35.

DR N-PSDB; AAA77604.

XX Nucleic acids encoding PRO polypeptides useful for preventing,

PT diagnosing and treating disorders in mammals -

PT angioleptic disorders in mammals -

XX Claim 72; Fig 44; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides

CC useful for preventing, diagnosing and treating disorders in mammals by

CC cardiovascular, endothelial or angiogenic disorder in mammals by



CC sequence is one of the proteins of the invention.

SQ Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALLCALSLGQRPTGGCGPGRLLLTGTDCRCRVHTTRCCRD 60  
|||||  
DB 1 maqhgamafralcgallcalslgqrptggcgprlllgtgdarcrcrvhttrccrd 60  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGQGVQSQGKFSFGQCIDCASGTF 120  
|||||  
DB 61 ypgeccsewdcmcvqpefhcgdpcccttcrrhpcppgqgvsgkfsfgqcidcasgtf 120  
QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPILG 164  
|||||  
DB 121 sgghegchkpwtctqfgfltvfpgnkthnavcvpgspppaepilg 164

# RESULT 6

AAB33431

ID AAB33431 standard; Protein: 241 AA.

XX AAB33431;

XX 29-JAN-2001 (first entry)

XX Human PRO364 protein UNQ319 SEQ ID NO:92.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
KW antianemic; hepatotropic; virucide; antiposoriatic; antiallergic;  
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease.

XX Homo sapiens.

XX WO200053758-A2.

XX 14-SEP-2000.

PD 02-MAR-2000; 2000WO-US05841.

PF 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99US-0123618.

PR 12-MAR-1999; 99US-0123957.

PR 23-MAR-1999; 99US-0125775.

PR 12-APR-1999; 99US-0128849.

PR 20-APR-1999; 99WO-US08615.

PR 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.  
PR 03-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
XX  
PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.

DR N-PSDB; AAC58596.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of

PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

XX Claim 33; Fig 36; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can

CC be used in the treatment of immune related diseases. The human PRO

CC proteins, anti-PRO antibodies, agonists and antagonists are useful for

CC treating and diagnosing immune related disorders. The disorders are

CC selected from systemic lupus erythematosus, rheumatoid arthritis,

CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,

CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems, hepatobiliary diseases, inflammatory

CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,

CC autoimmune or immune-mediated skin diseases, allergic diseases,

CC immunological diseases of the lung, and transplantation associated

CC diseases including graft rejection and graft-versus-host-disease.

CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and

CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;

Best Local Similarity 100.0%; Pred. No. 4e-70;

Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALLCALSLGQRPTGGCGPGRLLLTGTDCRCRVHTTRCCRD 60

|||||

DB 1 maqhgamafralcgallcalslgqrptggcgprlllgtgdarcrcrvhttrccrd 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGQGVQSQGKFSFGQCIDCASGTF 120

|||||

DB 61 ypgeccsewdcmcvqpefhcgdpcccttcrrhpcppgqgvsgkfsfgqcidcasgtf 120

QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPILG 164



CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
 CC and for identifying agonists and antagonists of these processes. The  
 CC nucleic acids and the proteins they encode may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PRO expression such as cardiovascular, endothelial or  
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and  
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors  
 CC containing them and the PRO polypeptide may be used to treat disorders  
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
 CC the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4e-70;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALGGLALLCALSLGQRPTGGCGPGRLLLTGTDTARCCRVHTTRCCRD 60  
 Db 1 maqhgamgafralcglallcalslgrptggpgcgprlllgtgtarccrvhttrccrd 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGGVQSGKFSFGQCIDCASGTF 120  
 Db 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppggvgvsgkfsfgqcidcasgtf 120

QY 121 SGGHEGCHKPWTDCQFGTLTFPPGNKTNNAVCPGSPPAEPLG 164  
 Db 121 sggheghckpwtcdctqfgtltfvpgnknthnavcvpsppaeplg 164

RESULT 9

AA71467  
 ID AA71467 standard; Protein; 241 AA.

AC AA71467;

DT 08-NOV-2000 (first entry)

DE Human PRO364 protein.

XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;  
 KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
 KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
 KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;  
 KW tumour necrosis factor receptor; GTR protein homologue.

XX Homo sapiens.

OS Key Location/Qualifiers  
 XX Peptide 1..25 /label= Signal\_peptide  
 FT Modified-site 5..11 /note= "N-myristoylation site"  
 FT Modified-site 8..14 /note= "N-myristoylation site"  
 FT Modified-site 25..31 /note= "N-myristoylation site"  
 FT Protein 26..241 /label= Mature\_PRO364\_protein  
 FT Modified-site 30..36 /note= "N-myristoylation site"  
 FT Modified-site 33..39 /note= "N-myristoylation site"  
 FT Modified-site 118..124 /note= "N-myristoylation site"  
 FT Modified-site 122..128 /note= "N-myristoylation site"  
 FT Modified-site 146..150 /note= "N-myristoylation site"  
 FT Modified-site 156..162 /note= "Asn is N-glycosylated"  
 FT Modified-site /note= "N-myristoylation site"

FT Domain 163..183  
 FT /label= Transmembrane\_domain  
 FT Binding-site 166..177  
 FT /note= "Prokaryotic membrane lipoprotein lipid  
 FT attachment site"  
 FT Region 171..193  
 FT /note= "Leucine zipper pattern"  
 XX WO200032778-A2.  
 PN 08-JUN-2000.  
 PD 30-NOV-1999; 99WO-US28409.  
 PF 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 22-DEC-1998; 98US-0113296.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 XX (GETH ) GENENTECH INC.  
 PA Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
 XX WPI: 2000-412325/35.  
 DR N-PSDB; AAD01240.  
 XX New composition useful for inhibiting neoplastic cell growth and for  
 PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
 PT their antagonists -  
 PS Claim 31; Fig 4; 108pp; English.

XX The present sequence is the human PRO364 protein, encoded by the cDNA  
 CC clone, designated as DNA47365-1206. It is isolated from human small  
 CC intestine tissue cDNA library, identified using probes based on the  
 CC consensus sequence DNA44825, relative to the incyte expressed sequence  
 CC tag (EST) 3003460. This EST has homology to tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows  
 CC homology to members of the TNFR family and mouse GTR protein.  
 CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as  
 CC a neoplastic cell growth inhibitor and is used for treating tumours,  
 CC using an effective amount of PRO655, PRO364 and PRO344. This composition  
 CC is especially useful for treatment of human cancers such as breast,  
 CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.  
 XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4e-70;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALGGLALLCALSLGQRPTGGCGPGRLLLTGTDTARCCRVHTTRCCRD 60  
 Db 1 maqhgamgafralcglallcalslgrptggpgcgprlllgtgtarccrvhttrccrd 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGGVQSGKFSFGQCIDCASGTF 120  
 Db 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppggvgvsgkfsfgqcidcasgtf 120

QY 121 SGGHEGCHKPWTDCQFGTLTFPPGNKTNNAVCPGSPPAEPLG 164  
 Db 121 sggheghckpwtcdctqfgtltfvpgnknthnavcvpsppaeplg 164

RESULT 10

AAB20115  
 ID AAB20115 standard; Protein; 241 AA.

XX AAB20115;

XX 30-APR-2001 (first entry)

CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 979; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALLCALSIGQRTGPGCGPGRLLLTGTDCRCRVRTTCRRD 60  
DB 1 maqhgamgafralcgllalcalcslgqrptgpgcgprlllgtgdarcrcrvhtrccrd 60  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
DB 61 ypgeccsewdcmcvqpefhcgdpccctcrhhpcppgpgvgvsgkfsfgfcidcasgtf 120  
QY 121 SGGHEGCHKPMTDCTQFGFLTFVPGNKNTHNAVCPGSPAPPLG 164  
DB 121 sggheghckpwtcdtqfgfltfvpgnknthnavcvgpsppaeplg 164

RESULT 13  
AAB50982

ID AAB50982 standard; Protein; 241 AA.

AC AAB50982;

DT 21-MAR-2001 (first entry)

XX Human PRO364 protein.

XX Human; PRO: cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;  
KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
KW vulnary; antianginal; gene therapy; cardiovascular disease;  
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
KW wound healing.

OS Homo sapiens.

XX WO200073445-A2.

XX 07-DEC-2000.

XX 17-MAY-2000; 2000WO-US13705.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 01-SEP-1999; 99WO-US20111.

XX 30-NOV-1999; 99WO-US28313.

XX 02-DEC-1999; 99WO-US28409.

XX 16-DEC-1999; 99WO-US28565.

XX 11-FEB-2000; 99WO-US30095.

XX 18-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
XX (GETH ) GENENTECH INC.  
PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX WPI; 2001-025251/03.  
DR N-PSDB; AAC90566.  
XX  
PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
PT disorders in a mammal -  
XX  
PS Claim 71; Fig 8; 182pp; English.

CC The present sequence is one of seventeen novel PRO polypeptides. The PRO  
CC nucleic acids, polypeptides, agonists and antagonists are useful for  
CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
CC antagonists are also used to prevent tumour angiogenesis and for treating  
CC periodontal diseases. They are also used to stimulate wound healing and  
CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 979; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALLCALSIGQRTGPGCGPGRLLLTGTDCRCRVRTTCRRD 60  
DB 1 maqhgamgafralcgllalcalcslgqrptgpgcgprlllgtgdarcrcrvhtrccrd 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
DB 61 ypgeccsewdcmcvqpefhcgdpccctcrhhpcppgpgvgvsgkfsfgfcidcasgtf 120

QY 121 SGGHEGCHKPMTDCTQFGFLTFVPGNKNTHNAVCPGSPAPPLG 164

DB 121 sggheghckpwtcdtqfgfltfvpgnknthnavcvgpsppaeplg 164

RESULT 14

AAB53090

ID AAB53090 standard; Protein; 241 AA.

XX AAB53090;

XX 28-FEB-2001 (first entry)

XX Human angiogenesis-associated protein PRO364, SEQ ID NO:142.

XX Human; angiogenesis-associated protein; PRO: endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.

XX

FT Modified-site /note= "Potential signal peptide"  
 FT 146  
 FT /note= "N-glycosylated"  
 FT 162..180  
 FT Domain /note= "Potential transmembrane domain"  
 FT 162..180  
 PN WO200103720-A2.  
 XX 18-JAN-2001.  
 XX 11-JUL-2000; 2000WO-US18867.  
 XX 12-JUL-1999; 99US-0143304.  
 XX (GETH ) GENENTECH INC.  
 XX Williams PM, Gerritsen ME;  
 XX WPI: 2001-138257/14.  
 DR N-PSDB; AAC85433.  
 XX  
 XX Composition for diagnosing and treating cardiovascular, endothelial and  
 XX angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -  
 XX  
 XX Claim 1; Fig 1; 76pp; English.  
 XX  
 XX This sequence represents PRO364 polypeptide, which is a human gluco-  
 XX corticoid-induced tumor necrosis factor receptor (hcITR). The  
 XX corresponding ligand (hcITR), PRO175, is given in AAB47056.  
 XX PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
 XX endothelial, angiogenic or angiostatic agent for the treatment of a  
 XX cardiovascular, endothelial, angiogenic or angiostatic disorder. The  
 XX PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)  
 XX database as having homology to members of the tumour necrosis factor  
 XX receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
 XX isolated from a library of cDNA fragments derived from human umbilical  
 XX vein endothelial cells (HUVBC). Administering an effective amount of  
 XX PRO364 or PRO175 or their antagonists is useful for treating cardiac  
 XX hypertrophy (which is initiated by myocardial infarction and  
 XX characterized by the presence of an elevated level of PGF<sub>2</sub>alpha),  
 XX trauma, a cancer, or age-related macular degeneration in a human.  
 XX Administering a therapeutically effective amount of an antibody that  
 XX binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
 XX by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
 XX disorder. PRO364 or PRO175, or their antagonists, are useful for  
 XX vascular-related drug targeting or as therapeutic targets for the  
 XX treatment or prevention of atherosclerosis, hypertension, inflammatory  
 XX vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
 XX thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
 XX and treatment of lung or liver fibrosis, periodontal diseases,  
 XX attraction of bone-forming cells, central and peripheral nervous  
 XX system disease and neuropathies and rheumatoid arthritis.  
 XX  
 XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4e-70; Indels 0; Gaps 0;  
 Matches 164; Conservative 0; Mismatches 0;

QY 1 MAQHGAAGAFALCGIALCALSLGQRPTGGCGGRLLLGTGTARCCRVHTTCRCD 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 maqhgaagafalcgialcalslgrptggcggrlllggttdarccrvhttrccrd 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 YPGEECCSEWDCMCVQPEFHCGPCCTTCRHHPCPGQGVQSGCKFSFGQCIDCASGTF 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 ypgeecscsewdcmcvqpefhcgpccttcrrhpcpgqgvqsggkfsfgqcidcasgtf 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 SGHEGHCPRWTDCTQFGILTVPFGKNTNNAVCPGSPPAEPLG 164  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 sgghedhcxpwtcdtqfgiltvfpgnktnnavcvpgspppaeplg 164  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 12  
 AAB50910  
 ID AAB50910 standard; Protein; 241 AA.  
 XX  
 XX AAB50910;  
 AC  
 DT 21-MAR-2001 (first entry).  
 XX  
 XX Human PRO364 protein.  
 DE  
 DE  
 XX  
 XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
 KW antiallergic; antiasthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200073452-A2.  
 PN  
 XX  
 XX 07-DEC-2000.  
 PD  
 XX  
 XX 02-JUN-2000; 2000WO-US15264.  
 PF  
 XX  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 13-SEP-1999; 99WO-US21547.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX  
 XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tamas D, Watanabe CK;  
 PI Wood WI;  
 XX  
 XX WPI: 2001-025253/03.  
 DR  
 DR N-PSDB; AAC91469.  
 XX  
 XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 58; Fig 18; 218pp; English.  
 XX  
 XX The present sequence is one of thirty three novel PRO polypeptides.  
 CC The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

Query Match 96.7%; Score 947; DB 19; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.3e-67;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	7	MGAFRALGGLALLCALSLGQRPTGGGCGPGRLLLGTTDARCCRVHTTRCCRDYPGEEC	66
Db	1	mgafralcglallcalslgrptgpgcgprllllgttdarccrvhttrccrdypgeec	60
Qy	67	CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGQVQSQKFSFGQCIDCASGTFSGGHEG	126
Db	61	csewdcmcvqpefhcgpccctcrhhpcppgggvgqgkfsfgqcidcasgtfsggheg	120
Qy	127	HCKPWTDTQTQGFLLTVFPGNKTHNAVCPGSPPAEPLG	164
Db	121	hckpwtddtqfgfltvfpgnkthnavcvpgspppaeplg	158

Search completed: September 4, 2001, 15:56:25  
Job time: 342 sec

OS Homo sapiens.  
XX WO200053753-A2.  
XX 14-SEP-2000.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 08-MAR-1999; 99WO-US050208.  
XX 12-MAR-1999; 99US-0123957.  
XX 14-MAY-1999; 99US-0134287.  
XX 02-JUN-1999; 99WO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 20-JUL-1999; 99US-0144758.  
XX 26-JUL-1999; 99US-0145698.  
XX 01-SEP-1999; 99WO-US20111.  
XX 08-SEP-1999; 99WO-US20594.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21347.  
XX 05-OCT-1999; 99WO-US23089.  
XX 30-NOV-1999; 99WO-US28313.  
XX 30-NOV-1999; 99WO-US28409.  
XX 02-DEC-1999; 99WO-US28564.  
XX 02-DEC-1999; 99WO-US28565.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoletti NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX WPI: 2001-090793/10.  
XX N-PSDB; AAC9479.  
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX Claim 69; Fig 54; 293pp; English.  
XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AA853064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
XX invention.  
XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGMGAFRALCGIALCALSLGQRPTGGPGCGRLLLTGTGTARCCRVHTTRCCRD 60  
DB 1 maqhgamafralcgialcalslgqrptggpgcgrrlllgtgtardccrvhttrccrd 60  
QY 61 YPGEECCSEWDCMCVQPEFHGCDPCTTCRRHPCPPGGGVOSQGFSGFCIDCASGTF 120  
DB 61 ypgeeccsewdcmcvqpefhcgdpcttcrhpcppggvgvsgqkfsfgicdcasgtf 120  
QY 121 SGGHEGHCKPMTDCTQFGFLTVPFGKNTNNAVCVPGSPAPPLG 164  
DB 121 sggheghckpwtddctqfgfltvfpngkthnavcvpgspapaelg 164  
RESULT 15  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX AC AAW37840;  
XX DT 28-JUL-1998 (first entry)  
XX DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
XX KW antigen-specific T cell proliferation; cytokine production by T-cell;  
XX KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
XX KW autoimmune disorders.  
XX OS Homo sapiens.  
XX PN WO9806842-A1.  
XX PD 19-FEB-1998.  
XX PF 14-AUG-1997; 97WO-US13931.  
XX PR 07-OCT-1996; 96US-0027901.  
XX PR 16-AUG-1996; 96US-0689943.  
XX PA (SCHE ) SCHERING CORP.  
XX Gorman DM, Randall TD, Zlotnik A;  
XX WPI: 1998-159534/14.  
XX N-PSDB; AAV19154.  
XX Isolated 312C2 T cell gene - used to develop products for treating,  
PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
XX Disclosure; Pages 61-62; 71pp; English.  
XX This is the amino acid sequence of the truncated human 312C2 T cell  
CC protein from clone\_A8. The 312C2 proteins are expressed in thymus  
CC cells and are induced on T cells and spleen cells following activation.  
CC Engagement of 312C2 stimulates proliferation of T cell clones,  
CC antigen-specific proliferation and cytokine production by T-cells, and  
CC potentiates T cell expansion or apoptosis. The products can be used  
CC in the treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX Sequence 228 AA;

Db 26 qrtggpgcpgrrlllgtgtarccrvhttrccrdypgeccsewcmcvqpefhcgdp 85  
Qy 61 CTTCTRHHPCCPPGQVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTDCQTQGF 114  
Db 86 cttcrhhpcppggvggqkfsfgfcidcasgtfsggheghckpwtcdctqfgf 139

RESULT 15  
AAB50982  
ID AAB50982 standard; Protein; 241 AA.  
XX AC AAB50982;  
XX DT 21-MAR-2001 (first entry)  
XX DE Human PRO364 protein.  
XX KW Human; PRO: cardiatic; antiangiogenic; antiarteriosclerotic; hypotensive;  
KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
KW vulnery; antianginal; gene therapy; cardiovascular disease;  
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
KW wound healing.  
XX OS Homo sapiens.  
XX PN WO200073445-A2.  
XX PD 07-DEC-2000.  
XX PF 17-MAY-2000; 2000WO-US13705.  
XX PR 02-JUN-1999; 99WO-US12252.  
XX PR 23-JUN-1999; 99US-0141037.  
XX PR 20-JUL-1999; 99US-0144758.  
XX PR 26-JUL-1999; 99US-0145698.  
XX PR 28-JUL-1999; 99US-0146222.  
XX PR 01-SEP-1999; 99WO-US20111.  
XX PR 30-NOV-1999; 99WO-US28313.  
XX PR 30-NOV-1999; 99WO-US28409.  
XX PR 02-DEC-1999; 99WO-US28565.  
XX PR 16-DEC-1999; 99WO-US30095.  
XX PR 11-FEB-2000; 2000WO-US03565.  
XX PR 18-FEB-2000; 2000WO-US04341.  
XX PR 18-FEB-2000; 2000WO-US04342.  
XX PR 24-FEB-2000; 2000WO-US05004.  
XX PR 02-MAR-2000; 2000WO-US05841.  
XX PR 10-MAR-2000; 2000WO-US06319.  
XX PR 15-MAR-2000; 2000WO-US06884.  
XX PR 21-MAR-2000; 2000WO-US07532.  
XX PR 30-MAR-2000; 2000WO-US08439.  
XX PA (GETH ) GENENTECH INC.  
XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pictl RM, Watanabe CK, Williams PM, Wood WI;  
XX DR WPI; 2001-025251/03.  
XX DR N-PSDB; AAC90566.  
XX PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
XX PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
XX PT disorders in a mammal -  
XX PS Claim 71; Fig 8; 182pp; English.  
XX CC The present sequence is one of seventeen novel PRO polypeptides. The PRO  
XX CC nucleic acids, polypeptides, agonists and antagonists are useful for  
XX CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
XX CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
XX CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
XX CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial

CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
CC antagonists are also used to prevent tumour angiogenesis and for treating  
CC periodontal diseases. They are also used to stimulate wound healing and  
CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder.  
XX SQ Sequence 241 AA;  
Query Match 100.0%; Score 711; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QRPTGGPGCGPGRLLLTGTGTARCCRVHTTRCCRDYEGECCSEWCMCVQPEFHCGDPC 60  
DB 26 qrptggpgcpgrrlllgtgtarccrvhttrccrdypgeccsewcmcvqpefhcgdp 85  
QY 61 CTTCTRHHPCCPPGQVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTDCQTQGF 114  
DB 86 cttcrhhpcppggvggqkfsfgfcidcasgtfsggheghckpwtcdctqfgf 139

Search completed: September 4, 2001, 15:56:23  
Job time: 340 sec



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XX Composition for diagnosing and treating cardiovascular, endothelial and  
PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -  
PS Claim 1; Fig 1; 76pp; English.  
XX This sequence represents PRO364 polypeptide, which is a human gluco-  
CC corticoid-induced tumor necrosis factor receptor (hGTR). The  
CC corresponding ligand (hGTRL), PRO175, is given in ABA47056.  
CC PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
CC endothelial, angiogenic or angiotatic agent for the treatment of a  
CC cardiovascular, endothelial, angiogenic or angiotatic disorder. The  
CC PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)  
CC database as having homology to members of the tumor necrosis factor  
CC receptor (TNF) family of polypeptides. The PRO175 cDNA sequence was  
CC isolated from a library of cDNA fragments derived from human umbilical  
CC vein endothelial cells (HUEVC). Administering an effective amount of  
CC PRO364 or PRO175 or their antagonists is useful for treating cardiac  
CC hypertrophy (which is initiated by myocardial infarction and  
CC characterized by the presence of an elevated level of PGF<sub>2</sub>alpha),  
CC trauma, a cancer, or age-related macular degeneration in a human.  
CC Administering a therapeutically effective amount of an antibody that  
CC binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
CC by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
CC disorder. PRO364 or PRO175, or their antagonists, are useful for  
CC vascular-related drug targeting or as therapeutic targets for the  
CC treatment or prevention of atherosclerosis, hypertension, inflammatory  
CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
CC and treatment of lung or liver fibrosis, periodontal diseases,  
CC attraction of bone-forming cells, central and peripheral nervous  
CC system disease and neuropathies and rheumatoid arthritis.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 711; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QRPTGGGCGPGRLLLTGTDCRCRVHTTRCCRDYPGECSEWDCMCVQPFHCGDPC 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
26 qrptggpgcgprlllgtgtdcrcrvhttrccrdypgeccsewdcmcvqpfhcgdp 85  
Oy 61 CTTCRHPCPPGGQSGKFSFGQICDASGTFSGHGHCKPWTDCTQFG 114  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
86 cttcrhpcppggvsgqkfsfgqicdcaagtfsghgchckpwtctqf 139

RESULT 14  
AAB50910  
ID AAB50910 standard; Protein; 241 AA.

XX AC AAB50910;  
XX DT 21-MAR-2001 (first entry)  
XX DE Human PRO364 protein.  
XX KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
KW antiinflammatory; cardiant; antianaemic; immunosuppressive; antithyroid;  
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antiasthmatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy.  
XX OS Homo sapiens.

XX WO200073452-A2.  
XX PD 07-DEC-2000.

XX 02-JUN-2000; 2000WO-US15264.

PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144732.  
PR 20-JUL-1999; 99US-0144758.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 09-DEC-1999; 99US-0170262.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
XX  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
XX Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
XX Wood WI;  
XX WPI; 2001-025253/03.  
XX N-PSDB; AAC91469.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
PT in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -

XX Claim 58; Fig 18; 218pp; English.

XX The present sequence is one of thirty three novel PRO polypeptides.  
CC The PRO polypeptides, anti-PRO antibodies, agonists and  
CC antagonists are useful for treating and diagnosing immune related  
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.

XX Sequence 241 AA;

Query Match 100.0%; Score 711; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QRPTGGGCGPGRLLLTGTDCRCRVHTTRCCRDYPGECSEWDCMCVQPFHCGDPC 60





RESULT 6  
AA06605  
ID AAY06605 standard; Protein; 241 AA.  
XX  
AC AAY06605;  
XX  
DT 26-OCT-1999 (first entry)  
XX  
DE Human TNF receptor homologue PRO364.  
XX  
KW PRO364; tumour necrosis factor receptor; human; apoptosis;  
inflammation; antiinflammatory; NF-KB activation;  
KW autoimmune disease; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT Protein /note= "signal peptide"  
FT Protein 26..241  
FT Modified-site /note= "mature protein"  
FT 146  
FT Domain /note= "N-glycosylated"  
FT 162..180  
FT /note= "transmembrane domain"  
XX  
PN WO9940196-A1.  
XX  
PD 12-AUG-1999.  
XX  
PF 09-FEB-1999; 99WO-US02642.  
XX  
PR 09-FEB-1998; 98US-0024087.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
PI Pitti RM, Wood WI;  
XX  
XX WPI: 1999-494296/41.  
DR N-PSDB; AAX87670.  
XX  
XX Tumour necrosis factor receptor homologue - useful for, e.g.  
PT modulating apoptosis and NF-KB activation and proinflammatory or  
PT autoimmune responses  
XX  
XX Claim 17; Fig 2A; 104pp; English.  
XX  
XX The present sequence represents human PRO364, a novel member of the  
CC tumour necrosis factor receptor family. The sequence was deduced  
CC from a bone marrow cDNA-clone (see AAX87670). Methods for the  
CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
CC Escherichia coli or yeast host cells, are provided. Claimed  
CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
CC mature protein) and 26-X of the present sequence, where X is any  
CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
CC are useful for modulating apoptosis, NF-KB activation and  
CC proinflammatory or autoimmune responses in mammalian cells  
CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
CC fused to a heterologous sequence such as epitope tag or  
CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
CC assays to identify other proteins or molecules involved in binding  
CC interactions. This is useful for identifying inhibitors or  
CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
CC also be combined with an agent that is cytotoxic, chemotherapeutic  
CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
CC methods, purification methods and also in therapy, e.g. as  
XX inhibitors.  
SQ Sequence 241 AA;

Query Match 100.0%; Score 711; DB 20; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QRTGPGCGGRLLLGTGTDAKCRVHTRCRDYDPGEECCSEWDCMCVQPFHCGDPC 60  
|||||  
DB 26 qrtgpgcggrlllgtgttdarccrvhttrccrdypgeccsewdcmcvqpfhcgdpc 85  
QY 61 CTTCRHPCPPGGVQSGKFSFGFCIDCASGTFSGHGHCKPWTDTQGF 114  
|||||  
DB 86 cttcrhpcppggvgvsggkfsfgfcidcasgtfsgghghckpwtddtqgf 139  
RESULT 7  
AAB27651  
ID AAB27651 standard; Protein; 241 AA.  
XX  
AC AAB27651;  
XX  
DT 26-JAN-2001 (first entry)  
XX  
DE Human protein PRO364.  
XX  
KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
KW PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /label= "Signal peptide"  
XX  
PN WO200053757-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 24-FEB-2000; 2000WO-US05004.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
PI Watanabe CK, Williams PM, Wood WI;  
XX  
XX WPI: 2000-611444/58.  
DR N-PSDB; AAA99903.  
XX  
XX Novel PRO polypeptides and agonists and antagonists of them, used to  
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
XX  
XX Claim 71; Fig 6; 181pp; English.  
XX  
XX The present invention relates to methods for stimulating or inhibiting  
CC angiogenesis and cardiovascularization. The methods involve the use of  
CC pharmaceutical compositions based on the following proteins, PRO179,  
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,

CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
 CC proteins were identified by isolating cDNA clones encoding secreted  
 CC proteins. The proteins of the invention may be used to diagnose and  
 CC treat cardiovascular, endothelial or angiogenic disorders. The present  
 CC sequence is one of the proteins of the invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 711; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRTGGPGCGPGLLLGTGTDAACRCRVHTTRCCRDYDGECCSEWDCMCVQPEFHCGDPC 60  
 Db 26 qrtggpgcgprlllgtgtddarccrvhttrccrdydpgeccsewdcmcvqpefhcgdp 85  
 QY 61 CTTCRHPCPPGGVGSQGFSGFCIDCASGTFSGHGHCKPWTDCQTFG 114  
 Db 86 cttcrhpcppggvgvsgqkfsgfqcldcasgtfsgghghckpwtcdctqf 139

RESULT 8  
 AAB33431  
 ID AAB33431 standard; Protein; 241 AA.  
 XX AAB33431;  
 AC AAB33431;  
 DT 29-JAN-2001 (first entry)  
 DE Human PRO364 protein UNQ319 SEQ ID NO:92.  
 XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200053758-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 02-MAR-2000; 2000WO-US05841.  
 XX  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 11-FEB-2000; 2000WO-US00376.  
 PR 18-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX  
 DR WPI: 2000-572271/53.  
 DR N-PSDB: AAC58596.  
 XX

Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 Claim 33; Fig 36; 309pp; English.

The present invention describes sixty four human PRO proteins which can  
 be used in the treatment of immune related diseases. The human PRO  
 proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 treating and diagnosing immune related disorders. The disorders are  
 selected from systemic lupus erythematosus, rheumatoid arthritis,  
 osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
 systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 immune-mediated renal disease, demyelinating diseases of the central  
 and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 autoimmune or immune-mediated skin diseases, allergic diseases,  
 immunological diseases of the lung, and transplantation associated  
 diseases including graft rejection and graft-versus-host-disease.  
 AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 sequences given in the exemplification of the present invention.

Sequence 241 AA;

Query Match 100.0%; Score 711; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGLLLGTGTDAACRCRVHTTRCCRDYDGECCSEWDCMCVQPEFHCGDPC 60  
 Db 26 qrtggpgcgprlllgtgtddarccrvhttrccrdydpgeccsewdcmcvqpefhcgdp 85  
 QY 61 CTTCRHPCPPGGVGSQGFSGFCIDCASGTFSGHGHCKPWTDCQTFG 114  
 Db 86 cttcrhpcppggvgvsgqkfsgfqcldcasgtfsgghghckpwtcdctqf 139

This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (Trll receptor). The invention relates to Trll and two splice variants TrllSV1 and TrllSV2. The nucleotide sequences were determined by sequencing cloned cDNAs AAZ37765-237766. The Trll receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GTR). Trll, TrllSV1 and TrllSV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, George syndrome, HIV infection, severe combined immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, Ischemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for detection, diagnosis and prognosis.



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 FT 122..129  
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 FT 37  
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 FT Modified-site /note= "Potential phosphorylation site"  
 FT 62  
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 FT 82  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 205  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 223  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 140  
 FT Modified-site /note= "N-glycosylated"  
 FT XX  
 PN WO20005374-A2.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 21-JUL-1999; 99WO-US16637.  
 XX  
 PR 22-JUL-1998; 98US-0093827.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 XX  
 DR WPI; 2000-182699/16.  
 DR N-PSDB; AAZ49948.  
 XX  
 PT Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 XX  
 PS Claim 1; Pages 64-65; 67pp; English.  
 XX  
 CC The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06  
 CC cDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
 CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 SQ Sequence 235 AA;

Query Match 100.0%; Score 711; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGRLLLGTGTARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPC 60  
 |||||  
 Db 20 qrtggpgcgprlllgtgtardccrvhttrccrdypgeccsewdcmcvqpefhcgdpc 79  
 |||||  
 QY 61 CTTCTRHHPCCPGGQVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 114  
 |||||

Db 80 cttcrhhpcppgqvgqskfsfgfcidcasgtfsggheghckpwtcdctqfgf 133

RESULT 5  
 AAW37839  
 ID AAW37839 standard; Protein; 241 AA.  
 XX  
 AC AAW37839;  
 XX  
 DT 28-JUL-1998 (first entry)  
 XX  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /\*tag= a  
 FT /product= "human 312C2 protein"  
 FT XX  
 PN WO9806842-A1.  
 XX  
 PD 19-FEB-1998.  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 XX  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Gorman DM, Randall TD, Zlotnik A;  
 XX  
 DR WPI; 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 XX  
 PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, autoimmune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 XX  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 711; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGRLLLGTGTARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPC 60  
 |||||  
 Db 26 qrtggpgcgprlllgtgtardccrvhttrccrdypgeccsewdcmcvqpefhcgdpc 85  
 |||||  
 QY 61 CTTCTRHHPCCPGGQVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 114  
 |||||  
 Db 86 cttcrhhpcppgqvgqskfsfgfcidcasgtfsggheghckpwtcdctqfgf 139

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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:22 ; Search time 136.12 Seconds  
(without alignments)  
54.798 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_139

Perfect score: 711

Sequence: 1 QRPTGPGCGPCGRLLLTGT.....FSGHEGHCKPWTDTQFGF 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	228	19 AAW37840	Truncated human 31
2	711	100.0	234	21 AAY95879	Human tumour necro
3	711	100.0	234	21 AAY52158	Tumour necrosis fa
4	711	100.0	235	21 AAY44825	Human molecule ass
5	711	100.0	241	19 AAW37839	Amino acid sequenc
6	711	100.0	241	20 AAY06605	Human TNF receptor
7	711	100.0	241	21 AAB27651	Human protein PRO3
8	711	100.0	241	21 AAB33431	Human PRO364 prote
9	711	100.0	241	21 AAY95895	Human tumour necro
10	711	100.0	241	21 AAB24409	Human PRO364 prote
11	711	100.0	241	21 AAY71467	Human PRO364 prote

12	711	100.0	241	22 AAB20115	Human immunostimul
13	711	100.0	241	22 AAB47054	Human PRO364. Hom
14	711	100.0	241	22 AAB50910	Human PRO364 prote
15	711	100.0	241	22 AAB50982	Human PRO364 prote
16	711	100.0	241	22 AAB53090	Human anglogenesis
17	711	100.0	311	19 AAW37842	Human 312C2 protei
18	711	100.0	316	22 AAB47055	Polypeptide encode
19	711	100.0	317	20 AAY06645	PRO364-related EST
20	695	97.7	240	21 AAY95881	Human tumour necro
21	695	97.7	240	21 AAY52160	TR11SV2 amino acid
22	509	71.6	232	19 AAW37841	Human 312C2 protei
23	502	70.6	241	21 AAY95880	Human tumour necro
24	502	70.6	241	21 AAY52159	TR11SV1 amino acid
25	373.5	52.5	222	19 AAW49018	Mouse glucocortic
26	373.5	52.5	228	19 AAW49016	Mouse glucocortic
27	373.5	52.5	228	19 AAW37838	Amino acid sequenc
28	373.5	52.5	294	19 AAW49017	Mouse glucocortic
29	219.5	30.9	89	21 AAY76013	Murine TNF-alpha f
30	219.5	30.9	89	22 AAB55952	Skin cell protein,
31	147.5	20.7	206	16 AAR81881	Mouse type-II memb
32	147.5	20.7	206	19 AAW48977	Mouse OX40 extrac
33	147.5	20.7	438	16 AAR81882	Plasmid pDC406/OX4
34	147.5	20.7	438	19 AAW48976	OX40/Fc mutain. C
35	141	19.8	205	22 AAB66985	41bb protein. Uni
36	140	19.7	191	22 AAB66986	41bb protein. Uni
37	140	19.7	256	16 AAR70978	4-1BB receptor pro
38	140	19.7	256	16 AAR64199	Murine 4-1BB poly
39	140	19.7	256	17 AAW04173	Mouse receptor 4-1
40	140	19.7	256	18 AAW26659	Mouse 4-1BB recept
41	140	19.7	256	20 AAY33215	Murine CD137 prote
42	140	19.7	256	20 AAY28687	Mouse Receptor 4-1
43	135.5	19.1	255	16 AAR70977	H4-1BB receptor pr
44	135.5	19.1	255	16 AAR64197	Human 4-1BB poly
45	135.5	19.1	255	18 AAW26658	Human 4-1BB recept

#### ALIGNMENTS

RESULT 1  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
DE Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX Homo sapiens.  
XX  
PN WO9806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 14-AUG-1997; 97WO-US13931.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM, Randall TD, Zlotnik A;  
XX  
DR WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PT Isolated 312C2 T cell gene - used to develop products for treating,

PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
PS Disclosure; Pages 61-62; 71pp; English.  
XX  
CC This is the amino acid sequence of the truncated human 312C2 T cell  
CC protein from clone A8. The 312C2 proteins are expressed in thymus  
CC cells and are induced on T cells and spleen cells following activation.  
CC Engagement of 312C2 stimulates proliferation of T cell clones, and  
CC antigen-specific proliferation and cytokine production by T-cells, and  
CC potentiates T cell expansion or apoptosis. The products can be used  
CC in the treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX  
SQ Sequence 228 AA;

Query Match 100.0%; Score 711; DB 19; Length 228;  
Best Local Similarity 100.0%; Pred. NO. 2.8e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGPGCGPGRLLIGTGDARCRVHTTRCCRDYPCGECSEWDCMCVOPFHCgDPC 60  
Db 20 qrtgpgcgprlllgtgdarcrrvhttrccrdypgeccsewdcmcvopfhcgDpc 79  
QY 61 CTTCTRHHPGPPGQGVQSGQKFSFGFCIDCASGTFSGHEGHCkPWTdCTQGF 114  
Db 80 cttcrhhpcppgqvsgqkfsfgfcldcasgtfsgghegchekpwtcdtqfg 133

RESULT 2  
AAY95879  
ID AAY95879 standard; Protein; 234 AA.  
AC AAY95879;  
XX  
DT 20-NOV-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-like protein TR11.  
XX  
KW TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX

Key Location/Qualifiers  
FH Peptide 1..25  
FT /label= Signal\_peptide  
FT Protein 26..234  
FT /label= Mature\_protein  
FT Domain 26..162  
FT /label= Extracellular\_domain  
FT Domain 163..179  
FT /label= Transmembrane\_domain  
FT Domain 180..234  
FT /label= Intracellular\_domain  
FT Modified-site 146  
FT /note= "N-glycosylated"  
FT Domain 72..81  
FT /note= "conserved domain CD-II"  
FT Domain 84..93  
FT /note= "conserved domain CD-III"  
FT Domain 107..113  
FT /note= "conserved domain CD-IV"  
FT Domain 128..134  
FT /note= "conserved domain CD-V"  
FT Domain 153..160  
FT /note= "conserved domain CD-VI"

Domain 176..186  
FT /note= "conserved domain CD-VII"  
FT Domain 204..209  
FT /note= "conserved domain CD-IX"  
FT Domain 224..233  
FT /note= "conserved domain CD-X"  
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FT /note= "epitope-bearing region"  
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FT Region 59..67  
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FT /note= "epitope-bearing region"  
FT Region 203..211  
FT /note= "epitope-bearing region"  
FT Region 222..230  
FT /note= "epitope-bearing region"  
XX WO200050459-A1.  
XX 31-AUG-2000.  
XX  
XX 23-FEB-2000; 2000WO-US04572.  
XX  
XX 24-FEB-1999; 99US-0121648.  
XX 13-MAY-1999; 99US-0134172.  
XX 16-JUL-1999; 99US-0144076.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, NI J;  
XX  
XX WPI; 2000-572072/53.  
XX N-PSDB; AAA50304.  
XX  
XX Human tumor necrosis factor receptor-like proteins useful for  
XX diagnosis, prevention and treatment of disease states associated with  
XX aberrant cell survival such as autoimmune disease and rheumatoid  
XX arthritis  
XX  
XX Claim 14(c); Fig 1A-B; 278pp; English.  
XX  
XX The present sequence is that of human tumour necrosis factor  
XX receptor-like protein TR11, a novel 25 kDa protein which shows  
XX 58.6% identity to murine glucocorticoid induced tumour necrosis  
XX factor receptor family-related gene. The sequence was deduced from  
XX a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
XX TR11 activated NF-kappaB through a TRAF2-mediated mechanism.  
XX Expression is activation-inducible. The TR11 ligand is constitutively  
XX expressed in an endothelial cell line. This suggests that TR11 and  
XX its ligand may be involved in activated T-cell trafficking.  
XX The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
XX (see AAA50304-06) and highly conserved encoded proteins (see  
XX AAY95879-81), as well as vectors, host cells and recombinant methods for  
XX their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
XX for treating, preventing, prognosis and/or diagnosis of an  
XX immunodeficiency, especially common variable immunodeficiency,  
XX X-linked agammaglobulinemia, severe combined immunodeficiency  
XX (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
XX deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
XX antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
XX and/or diagnose an autoimmune disease, especially rheumatoid

CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent,  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or in  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.

XX Sequence 234 AA;

Query Match 100.0%; Score 841; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRPFGGCGGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60  
 DB 26 qrpfggpgcgprlllgtgtgdarccrvhttrccrdypgeecscwdcmcvqpefhcgdpc 85  
 QY 61 CTTCTRHHPGCGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVFP 120  
 DB 86 cttctrhpcpggvgqgkfsfgfcidcasgtfsgghedhckpwtcdctqfgfltvfp 145

QY 121 NKTHNAVCPGSPPAEP 137

DB 146 nkthnavcpgsppaep 162

#### RESULT 3

AAV52158

ID AAY52158 standard; Protein; 234 AA.

XX AC AAY52158;

DT 01-FEB-2000 (first entry)

XX Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.

XX Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;  
 KW GTR; growth; differentiation; cell death; immune deficiency disorder;  
 KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
 KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; Huntingdon's disease;  
 KW inflammatory condition.

XX Homo sapiens.

OS Location/Qualifiers  
 FH 1..25  
 FT /label= Signal\_peptide  
 FT 26..234  
 FT /label= TR11  
 FT 26..162  
 FT /note= "Extracellular domain"  
 FT 163..179  
 FT /note= "Transmembrane domain"  
 FT 180..234  
 FT /note= "Intracellular domain"

XX WQ920758-A1.

XX 29-APR-1999.

XX 21-OCT-1998; 98WO-US22085.

XX 21-OCT-1997; 97US-0063212.

XX (HUMA-) HUMAN GENOME SCI INC.

XX N1 J, Ruben SM;

XX

DR WPI; 2000-061922/05.

XX N-PSDB; AAZ37762.

PT New tumour necrosis factor receptor-like polypeptides used to, e.g.

PT treat Digeorge syndrome -

PS Claim 14; Fig 1; 167pp; English.

XX

CC This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor-like protein (TR11 receptor). The invention relates to TR11 and  
 CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
 CC determined by sequencing cloned cDNAs AAZ37765-237766. The TR11 receptor  
 CC and its splice variants show homology to the murine glucocorticoid  
 CC induced tumour necrosis factor receptor family-related gene (GTR).

CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation  
 CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for

CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell

CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency,

CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can

CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's

CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent

CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft

CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or

CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be

CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic

CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's

CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for

CC detection, diagnosis and prognosis.

XX Sequence 234 AA;

Query Match 100.0%; Score 841; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.8e-60;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRPFGGCGGRLLLGTGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60

DB 26 qrpfggpgcgprlllgtgtgdarccrvhttrccrdypgeecscwdcmcvqpefhcgdpc 85

QY 61 CTTCTRHHPGCGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVFP 120

DB 86 cttctrhpcpggvgqgkfsfgfcidcasgtfsgghedhckpwtcdctqfgfltvfp 145

QY 121 NKTHNAVCPGSPPAEP 137

DB 146 nkthnavcpgsppaep 162

#### RESULT 4

AAV44825

ID AAY44825 standard; Protein; 235 AA.

XX AC AAY44825;

DT 18-MAY-2000 (first entry)

XX Human molecule associated with cell proliferation, MACP-5.

XX Human; molecule associated with cell proliferation; MACP-5;



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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:22 ; Search time 126.12 Seconds  
(without alignments)  
65.854 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162

Perfect score: 841

Sequence: 1 QPRTGPGCGPGRLLGTCT.....FPGKTHNAVCPGPPAEP 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries.

#### Database :

A\_Geneseq\_0601:\*

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- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:\*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT:\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT:\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT:\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT:\*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT:\*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT:\*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT:\*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT:\*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT:\*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT:\*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT:\*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT:\*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT:\*
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- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT:\*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT:\*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT:\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	841	100.0	228	19 AAW37840	Truncated human 31
2	841	100.0	234	21 AAY95879	Human tumour necro
3	841	100.0	234	21 AAY52158	Tumour necrosis fa
4	841	100.0	235	21 AAY44825	Human molecule ass
5	841	100.0	241	19 AAW37839	Amino acid sequenc
6	841	100.0	241	20 AAY06605	Human TNF receptor
7	841	100.0	241	21 AAB27651	Human protein PRO3
8	841	100.0	241	21 AAB33431	Human PRO364 prote
9	841	100.0	241	21 AAY95895	Human tumour necro
10	841	100.0	241	21 AAB24409	Human PRO364 prote
11	841	100.0	241	21 AAY71467	Human PRO364 prote

12	841	100.0	241	22 AAB20115	Human immunostimul
13	841	100.0	241	22 AAB47054	Human PRO364. Hom
14	841	100.0	241	22 AAB50910	Human PRO364 prote
15	841	100.0	241	22 AAB50982	Human PRO364 prote
16	841	100.0	241	22 AAB53090	Human angiogenesis
17	841	100.0	311	19 AAW37842	Human 312C2 protei
18	825	98.1	240	21 AAY95881	Human tumour necro
19	825	98.1	240	21 AAY52160	Human 312C2 protei
20	746.5	88.8	316	22 AAB47055	Mouse glucocortico
21	746.5	88.8	317	20 AAV06645	Polypeptide encode
22	632	75.1	241	21 AAY95880	PRO364-related EST
23	632	75.1	241	21 AAY52159	Human tumour necro
24	509	60.5	232	19 AAW37841	TRILSVI amino acid
25	465.5	55.4	222	19 AAW49018	Human 312C2 protei
26	465.5	55.4	228	19 AAW49016	Mouse glucocortico
27	465.5	55.4	228	19 AAW37838	Mouse glucocortico
28	465.5	55.4	294	19 AAW49017	Amino acid sequenc
29	219.5	26.1	89	21 AAY76013	Mouse glucocortico
30	219.5	26.1	89	22 AAB55952	Murine TNF-alpha f
31	166.5	19.8	206	16 AAR81881	Skin cell protein,
32	166.5	19.8	206	19 AAW48977	Mouse type-II memb
33	166.5	19.8	438	16 AAR81882	Mouse OX40 extrace
34	166.5	19.8	438	19 AAW48976	Plasmid pDC406/OX4
35	162.5	19.3	277	16 AAR76996	Deduced sequence e
36	160.5	19.1	255	16 AAR70977	H4-1BB receptor pr
37	160.5	19.1	255	16 AAR64197	Human 4-1BB polype
38	160.5	19.1	255	18 AAW26658	Human 4-1BB recept
39	160.5	19.1	255	20 AAY32214	Human CD137 protei
40	160.5	19.1	255	20 AAY28688	Human receptor pro
41	160.5	19.1	255	22 AAB50521	Human tumour necro
42	158.5	18.8	219	18 AAW31759	A novel human h4-1
43	158.5	18.8	219	20 AAW92523	Human h4-1BBSV rec
44	158.5	18.8	277	16 AAR74737	ACT-4 cell surface
45	158.5	18.8	277	16 AAR79904	ACT-4-h-1 receptor

#### ALIGNMENTS

#### RESULT 1

AAW37840  
ID AAW37840 standard; Protein; 228 AA.

XX AC AAW37840;

XX DT 28-JUL-1998 (first entry)

XX DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.

XX KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;

XX KW antigen-specific T cell proliferation; cytokine production by T-cell;

XX KW apoptosis; cancer; haematopoietic cells; lymphoid cell;

XX KW autoimmune disorders.

XX OS Homo sapiens.

XX PN WO9806842-A1.

XX PD 19-FEB-1998.

XX PF 14-AUG-1997; 97WO-US13931.

XX PR 07-OCT-1996; 96US-0027901.

XX PR 16-AUG-1996; 96US-0689943.

XX PA (SCHE ) SCHERING CORP.

XX PI Gorman DM, Randall TD, Zlotnik A;

XX XX WPI; 1998-159534/14.

XX DR N-PSDB; AAV19154.

XX PT Isolated 312C2 T cell gene - used to develop products for treating,

PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX other T cell disorders  
 PS Disclosure; Pages 61-62; 71pp; English.  
 XX This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX Sequence 228 AA;  
 SQ

Query Match 100.0%; Score 841; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPTGPGCGPGRLLIGTGDARCCRVHTTRCCRDYDPEECCSEWDCMCVQPEPHCGDPC 60  
 Db 20 qrtgpgcgpggrlligtgdarccrvhttrccrdydpccsewdcmcvqpephcgdp 79  
 QY 61 CTTCRHHPGPPGQGVQSGQSFQFCIDCASGTFSGHEGHCCKPWTDCQFGFLTVPFG 120  
 Db 80 cttcrhhpcpgpgvqsgqkfsgfcidcasgtfsgheghckpwtcdctqfgfltpfg 139  
 QY 121 NKTHNAVCPGSPAP 137  
 Db 140 nkthnavcpgspap 156

RESULT 2  
 AAY95879  
 ID AAY95879 standard; Protein; 234 AA.  
 AC AAY95879;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-like protein TR11.  
 KW TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Signal\_peptide  
 FT Protein 26..234  
 FT /label= Mature\_protein  
 FT Domain 26..162  
 FT /label= Extracellular\_domain  
 FT Domain 163..179  
 FT /label= Transmembrane\_domain  
 FT Domain 180..234  
 FT /label= Intracellular\_domain  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 72..81  
 FT /note= "conserved domain CD-II"  
 FT Domain 84..93  
 FT /note= "conserved domain CD-III"  
 FT Domain 107..113  
 FT /note= "conserved domain CD-IV"

FT Domain 128..134  
 FT /note= "conserved domain CD-V"  
 FT Domain 153..160  
 FT /note= "conserved domain CD-VI"  
 FT Domain 176..186  
 FT /note= "conserved domain CD-VII"  
 FT Domain 204..209  
 FT /note= "conserved domain CD-IX"  
 FT Domain 224..233  
 FT /note= "conserved domain CD-X"  
 FT Region 27..36  
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 FT Region 59..67  
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 FT /note= "epitope-bearing region"  
 FT Region 143..151  
 FT /note= "epitope-bearing region"  
 FT Region 156..164  
 FT /note= "epitope-bearing region"  
 FT Region 203..211  
 FT /note= "epitope-bearing region"  
 FT Region 222..230  
 FT /note= "epitope-bearing region"  
 XX WO200050459-A1.  
 XX  
 XX 31-AUG-2000.  
 XX  
 XX 23-FEB-2000; 2000WO-US04572.  
 XX  
 XX 24-FEB-1999; 99US-0121648.  
 XX 13-MAY-1999; 99US-0134172.  
 XX 16-JUL-1999; 99US-0144076.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Ni J;  
 XX  
 XX WPI: 2000-572072/53.  
 XX N-PSDB: AAA50304.  
 XX  
 XX Human tumor necrosis factor receptor-like proteins useful for  
 XX diagnosis, prevention and treatment of disease states associated with  
 XX aberrant cell survival such as autoimmune disease and rheumatoid  
 XX arthritis -  
 XX  
 XX Claim 14(c): Fig 1A-B; 278pp; English.  
 XX  
 XX The present sequence is that of human tumour necrosis factor  
 XX receptor-like protein TR11, a novel 25 kDa protein which shows  
 XX 58.6% identity to murine glucocorticoid induced tumour necrosis  
 XX factor receptor family-related gene. The sequence was deduced from  
 XX a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
 XX TR11 activated NF-kappaB through a TRAF2-mediated mechanism.  
 XX Expression is activation-inducible. The TR11 ligand is constitutively  
 XX expressed in an endothelial cell line. This suggests that TR11 and  
 XX its ligand may be involved in activated T-cell trafficking.  
 XX The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
 XX (see AAA50304-06) and highly conserved encoded proteins (see  
 XX AAY95879-81), as well as vectors, host cells and recombinant methods for  
 XX their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 XX for treating, preventing, prognosis and/or diagnosis of an  
 XX immunodeficiency, especially common variable immunodeficiency,  
 XX X-linked agammaglobulinemia, severe combined immunodeficiency

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PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX WPI: 2001-025253/03.
DR N-PSDB; AAC91469.
XX
XX Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX
PS Claim 58; Fig 18; 218pp; English.
XX
CC The present sequence is one of thirty three novel PRO polypeptides.
CC The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 841; DB 22; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGPRLLLTGTGDARCCRVHTTRCCRDYPGEECCSWDCMCVQPEFHCGDPC 60
Db 26 qrptggpgcgprlllgtgdarccrvhttrccrdypgeccsewdcmcvqpefhcgdp 85

QY 61 CTTCRHPCPPGCGVQSQGKFSFGQICDASGTFSGGHEGHCCKPWTDCQGFGLTVFPG 120
Db 86 cttcrhhpcppggvqsgkfsfgqicdasgtfsgghgchckpwtcdtqgfgltvfpg 145

QY 121 NKTHNAVCPGSPPAEP 137
Db 146 nkthnavcpgpspapep 162

RESULT 15
AAB50982
ID AAB50982 standard; Protein; 241 AA.
XX
AC AAB50982;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO364 protein.

```

Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulvurary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; angiogenic disorder; cancer; periodontal disease; wound healing.

Homo sapiens.

WO200073445-A2.

07-DEC-2000.

17-MAY-2000; 2000WO-US13705.

02-JUN-1999; 99WO-US12252.

23-JUN-1999; 99US-0141037.

20-JUL-1999; 99US-0144758.

26-JUL-1999; 99US-0145698.

28-JUL-1999; 99US-0146222.

01-SEP-1999; 99WO-US20111.

30-NOV-1999; 99WO-US28313.

30-NOV-1999; 99WO-US28409.

02-DEC-1999; 99WO-US28565.

16-DEC-1999; 99WO-US30095.

11-FEB-2000; 2000WO-US03565.

18-FEB-2000; 2000WO-US04341.

18-FEB-2000; 2000WO-US04342.

24-FEB-2000; 2000WO-US05004.

02-MAR-2000; 2000WO-US05841.

10-MAR-2000; 2000WO-US06319.

15-MAR-2000; 2000WO-US06884.

21-MAR-2000; 2000WO-US07532.

30-MAR-2000; 2000WO-US08439.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA; Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

WPI: 2001-025251/03.

N-PSDB; AAC90566.

Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic disorders in a mammal -

Claim 71; Fig 8; 182pp; English.

The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.

Sequence 241 AA;

Query Match 100.0%; Score 841; DB 22; Length 241; Best Local Similarity 100.0%; Pred. No. 1.9e-60; Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGPRLLLTGTGDARCCRVHTTRCCRDYPGEECCSWDCMCVQPEFHCGDPC 60  
|||||  
Db 26 qrptggpgcgprlllgtgdarccrvhttrccrdypgeccsewdcmcvqpefhcgdp 85  
|||||

QY 61 CTTCRHPCPPGCGVQSQGKFSFGQICDASGTFSGGHEGHCCKPWTDCQGFGLTVFPG 120  
|||||  
Db 86 cttcrhhpcppggvqsgkfsfgqicdasgtfsgghgchckpwtcdtqgfgltvfpg 145  
|||||

QY 121 NKTHNAVCPGSPPAEP 137  
|||||  
Db 146 nkthnavcpgpspapep 162  
|||||

RESULT 15  
AAB50982  
ID AAB50982 standard; Protein; 241 AA.  
XX  
AC AAB50982;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Human PRO364 protein.



Search completed: September 4, 2001, 15:56:22  
Job time: 339 sec

XX SQ Sequence 241 AA;

Query Match 100.0%; Score 841; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPRTGGPGCGRLLIGTGTDCARCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60  
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Db 26 qrtpgpgcgprlllgtgttdarccrvhttrccrdypgeecscsewdcmcvqpefhcgdp 85  
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QY 61 CTTCRHHPCCPGGVSQGSFQFCIDCASGTFSGGHEGHCXKPTWDTQGFGLTVFPG 120  
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Db 86 cttcrhhpcppggvgsgkfsgfqcicdcsgrtfgghegchckpwtcdtqgfglvfp 145  
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QY 121 NKTHNAVCPGSPPAEP 137  
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Db 146 nkthnavcpvspaep 162  
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RESULT 12  
AAB20115  
ID AAB20115 standard; Protein; 241 AA.  
AC AAB20115;  
XX  
XX 30-APR-2001 (first entry)  
XX  
XX Human immunostimulant PRO364.  
XX  
XX PRO364; UNQ319; human; immune disease; autoimmune disease;  
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipsoriatic;  
KW antiasthmatic; antiallergic; immunostimulant.  
XX  
XX Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /label= Signal\_peptide  
FT Protein 26..241  
FT /label= Mature\_protein  
FT Domain 163..183  
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FT Modified-site 30..36  
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FT Modified-site 122..128  
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FT Modified-site 146..150  
FT /note= "Asn is N-glycosylated"  
FT Peptide 166..177  
FT /note= "prokaryotic membrane lipoprotein lipid attachment site"  
FT Peptide 171..193  
FT /note= "leucine zipper pattern"

XX  
XX WO200105972-A1.  
XX  
XX 25-JAN-2001.  
XX PD

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DB 146 nkthnavcvpgspap 162
|||||
RESULT 13
AAB47054
ID AAB47054 standard; Protein; 241 AA.
XX
XX AAB47054;
XX
XX 08-MAY-2001 (first entry)
XX
XX Human PRO364.
XX
KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
KW HGTR; ligand; HGTR; PRO175; tumour necrosis factor receptor; TNFR;
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
KW myocardial infarction; PGF_2alpha; trauma; cancer; angiogenesis;
KW age-related macular degeneration; antibody; periodontal disease;
KW vascular-related drug targeting; atherosclerosis; hypertension;
KW inflammatory vasculitis; Reynaud's disease; aneurysm;
KW arterial restenosis; thrombophlebitis; tumour angiogenesis;
KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..26 "Potential signal peptide"
XX Modified-site 146 /note= "N-glycosylated"
XX Domain 162..180 /note= "Potential transmembrane domain"
XX
XX WO200103720-A2.
XX
XX 18-JAN-2001.
XX
XX 11-JUL-2000; 2000WO-US18867.
XX
XX 12-JUL-1999; 99US-0143304.
XX
XX (GETH ) GENENTECH INC.
XX
XX Williams PM, Gerritsen ME;
XX
XX WPI; 2001-138257/14.
XX
XX N-PSDB; AAC85433.
XX
XX Composition for diagnosing and treating cardiovascular, endothelial and
XX angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -
XX
XX Claim 1; Fig 1; 76pp; English.
XX
XX This sequence represents PRO364 polypeptide, which is a human gluco-
XX corticoid-induced tumor necrosis factor receptor (HGTR). The
XX corresponding ligand (HGTR), PRO175, is given in AAB47056.
XX PRO364 and PRO175 may be used in a mixture with a cardiovascular,
XX endothelial, angiogenic or angiostatic agent for the treatment of a
XX cardiovascular, endothelial, angiogenic or angiostatic disorder. The
XX PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)
XX database as having homology to members of the tumour necrosis factor
XX receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was
XX isolated from a library of cDNA fragments derived from human umbilical
XX vein endothelial cells (HUVEC). Administering an effective amount of
XX PRO364 or PRO175 or their antagonists is useful for treating cardiac
XX hypertrophy (which is initiated by myocardial infarction and
XX characterized by the presence of an elevated level of pGF-2alpha),
XX trauma, a cancer, or age-related macular degeneration in a human.
XX Administering a therapeutically effective amount of an antibody that
XX binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced
XX by PRO364 or PRO175 in a human suffering from a tumor or a retinal
XX disorder. PRO364 or PRO175, or their antagonists, are useful for
XX
```

```
CC vascular-related drug targeting or as therapeutic targets for the
CC treatment or prevention of atherosclerosis, hypertension, inflammatory
CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,
CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration
CC and treatment of lung or liver fibrosis, periodontal diseases,
CC attraction of bone-forming cells, central and peripheral nervous
CC system disease and neuropathies and rheumatoid arthritis.
XX
XX Sequence 241 AA;
XX
XX Query Match 100.0%; Score 841; DB 22; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-60;
XX Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ORPTGGPGGGRLLLTGTDAARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
XX Db |||||||
XX QY 26 grtpgpgcgprlllgtgtardccrvhttrccrdygeccsewdcmcvqpefhcgopc 85
XX Db |||||||
XX QY 61 CTTCTRHHPCCPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCTQFGFLTVPFG 120
XX Db |||||||
XX QY 86 cttcrhhpcpgpgvgvsgkfsfgfcidcasgtfsggheghckpwtcdtqfgltvfp 145
XX
XX QY 121 NKTHNAVCPGSPAP 137
XX Db |||||||
XX 146 nkthnavcvpgspap 162
XX
XX RESULT 14
XX AAB50910
XX ID AAB50910 standard; Protein; 241 AA.
XX
XX AC AAB50910;
XX
XX XX 21-MAR-2001 (first entry)
XX
XX DE Human PRO364 protein.
XX
XX KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
XX KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
XX KW antiidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
XX KW antiallergic; antiasthmatic; immune related disorder;
XX KW hepatobiliary disease; autoimmune disease; allergy.
XX
XX OS Homo sapiens.
XX
XX XX WO200073452-A2.
XX
XX XX 07-DEC-2000.
XX
XX PF 02-JUN-2000; 2000WO-US15264.
XX
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 20-JUL-1999; 99US-0144732.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 28-JUL-1999; 99US-0146222.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 25-SEP-1999; 99WO-US21547.
XX PR 29-OCT-1999; 99US-0162506.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 01-DEC-1999; 99WO-US28634.
XX PR 09-DEC-1999; 99US-0170262.
XX PR 20-DEC-1999; 99WO-US30911.
XX PR 05-JAN-2000; 2000WO-US00219.
XX PR 06-JAN-2000; 2000WO-US00376.
XX PR 11-FEB-2000; 2000WO-US03565.
XX PR 18-FEB-2000; 2000WO-US04341.
XX PR 22-FEB-2000; 2000WO-US04342.
XX PR 24-FEB-2000; 2000WO-US04414.
XX PR 25-FEB-2000; 2000WO-US04914.
XX PR 15-MAR-2000; 2000WO-US06884.
XX PR 20-MAR-2000; 2000WO-US07377.
XX
```

CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 XX Sequence 241 AA;

Query Match 100.0%; Score 841; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYFGECCEWDCMCVQPEFHCGDPC 60  
 |||||  
 Db 26 qrtgpgpgcgprlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdp 85  
 QY 61 CTTCTRRHPCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGFLTVPFG 120  
 |||||  
 Db 86 cttcrhhpcppggvgqgkfsfgfcidcasgtfsgghegchkpwtcdctqfgltvfp 145  
 QY 121 NKTHNAVCPGSPPAEP 137  
 |||||  
 Db 146 nkthnavcpgspap 162

RESULT 9  
 AAY95895  
 ID AAY95895 standard; Protein; 241 AA.  
 AC AAY95895;  
 XX  
 XX 20-NOV-2000 (first entry)  
 XX Human tumour necrosis factor receptor-like protein TR11 mutein.  
 XX

KW TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
 KW mutant.

XX Homo sapiens.  
 XX WO200050459-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 XX 23-FEB-2000; 2000WO-US04572.  
 XX  
 XX 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J;  
 PI WPI; 2000-572072/53.  
 DR  
 XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -  
 XX  
 XX Disclosure; 294-295; 278pp; English.  
 PS  
 XX

CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 XX Sequence 241 AA;

Query Match 100.0%; Score 841; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYFGECCEWDCMCVQPEFHCGDPC 60  
 |||||  
 Db 26 qrtgpgpgcgprlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdp 85  
 QY 61 CTTCTRRHPCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGFLTVPFG 120  
 |||||  
 Db 86 cttcrhhpcppggvgqgkfsfgfcidcasgtfsgghegchkpwtcdctqfgltvfp 145  
 QY 121 NKTHNAVCPGSPPAEP 137  
 |||||  
 Db 146 nkthnavcpgspap 162

RESULT 10  
 AAB24409  
 ID AAB24409 standard; Protein; 241 AA.  
 AC AAB24409;  
 XX  
 XX 07-NOV-2000 (first entry)  
 XX Human PRO364 protein sequence SEQ ID NO:117.  
 XX  
 XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200032221-A2.  
 XX  
 XX 08-JUN-2000.  
 XX  
 XX 30-NOV-1999; 99WO-US28313.  
 XX  
 XX 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.

```
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
PI Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2000-412154/35.
DR N-PSDB; AAA77604.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating disorders in mammals -
PT angiogenic disorders in mammals -
XX
XX Claim 72; Fig 44; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating disorders in mammals
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PRO expression such as cardiovascular, endothelial or
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 841; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QRPTGGCGGRLLLGTGTDAKRCRVHTRCRRYPGEECCSEWDCMCVQPEFHCGDPC 60
Db 26 qrptggcggrlllgtgtdarccrvhtrccrdypgeecscwdcmcvqpefhcgdp 85
Qy 61 CTTCRHHPCPPGQVQSGKFSFGQCIDCASGTFSGHGHCKPWTCTQFGFLTVPFG 120
Db 86 cttcrhhpcppgqvqsggkfsfgqcidcasgtfsghghegkcpwtcdtqfgfltvpg 145
Qy 121 NKTHNAVCPGSPPAEP 137
Db 146 nkthnavcvpsppaep 162
RESULT 11
AAAY71467
ID AA71467 standard; Protein; 241 AA.
XX
XX AAAY71467;
AC
XX
DT 08-NOV-2000 (first entry)
XX
XX Human PRO364 protein.
XX
XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
TW breast; prostate; colon; lung; renal; ovarian; central nervous system;
```

```
KW CNS: leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
KW tumour necrosis factor receptor; G1FR protein homologue.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..25 /label= Signal_peptide
XX Modified-site 5..11 /note= "N-myristoylation site"
XX Modified-site 8..14 /note= "N-myristoylation site"
XX Modified-site 25..31 /note= "N-myristoylation site"
XX Modified-site 26..241 /note= "N-myristoylation site"
XX Protein /label= Mature_PRO364_protein
XX Modified-site 30..36 /note= "N-myristoylation site"
XX Modified-site 33..39 /note= "N-myristoylation site"
XX Modified-site 118..124 /note= "N-myristoylation site"
XX Modified-site 122..128 /note= "N-myristoylation site"
XX Modified-site 146..150 /note= "N-myristoylation site"
XX Modified-site 156..162 /note= "Asn is N-glycosylated"
XX Domain 163..183 /note= "N-myristoylation site"
XX Binding-site 166..177 /label= Transmembrane_domain
XX Region 171..193 /note= "Prokaryotic membrane lipoprotein lipid attachment site"
XX W0200032778-AA2.
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US28409.
XX
XX 01-DEC-1998; 98WO-US25108.
XX 16-DEC-1998; 98US-0112850.
XX 22-DEC-1998; 98US-0113296.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
PI WPI; 2000-412325/35.
DR N-PSDB; AAD01240.
XX
XX New composition useful for inhibiting neoplastic cell growth and for
PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
PT their antagonists -
XX
XX Claim 31; Fig 4; 108pp; English.
XX
XX The present sequence is the human PRO364 protein, encoded by the cDNA
CC clone, designated as DNA47365-1206. It is isolated from human small
CC intestine tissue cDNA library, identified using probes based on the
CC consensus sequence DNA44825, relative to the Incyte expressed sequence
CC tag (EST) 3003460. This EST has homology to tumour necrosis factor
CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows
CC homology to members of the TNFR family and mouse G1FR protein.
CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as
CC a neoplastic cell growth inhibitor and is used for treating tumours,
CC using an effective amount of PRO655, PRO364 and PRO344. This composition
CC is especially useful for treatment of human cancers such as breast,
CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
CC
```

CC which affect immunological responses, e.g. autoimmune disorders.

XX Sequence 241 AA;

Query Match 100.0%; Score 841; DB 19; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.9e-60;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRPTEGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEPHCGDPC 60

Db 26 qrpTgpgcgpggrlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdp 85

QY 61 CTTCTRRHPCPPGGVQSGKFSGFCIDCASGTFSGHGHCKPWTDCQFGFLTVPFG 120

Db 86 cttcrhpcppggvgqgkfsgfcldcasgtfsgghghckpwtcdctqfgfltvfp 145

QY 121 NKTHNAVCPGSPPAEP 137

Db 146 nkthnavcvpgsppaep 162

RESULT 6

AAY06605

ID AAY06605 standard; Protein; 241 AA.

XX AAY06605;

AC AAY06605;

XX 26-OCT-1999 (first entry)

DT Human TNF receptor homologue PRO364.

DE PRO364; tumour necrosis factor receptor; human; apoptosis;

XX inflammation; antiinflammatory; NF-KB activation;

KW autoimmune disease; therapy.

KW Homo sapiens.

XX Key

FT Peptide

FT 1..25

FT /note= "signal peptide"

FT Protein

FT 26..241

FT /note= "mature protein"

FT Modified-site

FT 146

FT /note= "N-glycosylated"

FT 162..180

FT /note= "transmembrane domain"

FT XX

PN W09940196-A1.

XX 12-AUG-1999.

XX 09-FEB-1999; 99WO-US02642.

XX 09-FEB-1998; 98US-0024087.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;

PI Pitti RM, Wood WI;

XX WPI: 1999-494296/41.

XX N-PSDB; AAX87670.

DR Tumour necrosis factor receptor homologue - useful for, e.g.

XX modulating apoptosis and NF-KB activation and proinflammatory or

PT autoimmune responses

XX Claim 17; Fig 2A; 104pp; English.

PS The present sequence represents human PRO364, a novel member of the

XX tumour necrosis factor receptor family. The sequence was deduced

CC from a bone marrow cDNA clone (see AAX87670). Methods for the

CC

CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or  
 CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.

XX Sequence 241 AA;

Query Match 100.0%; Score 841; DB 20; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.9e-60;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRPTEGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEPHCGDPC 60

Db 26 qrpTgpgcgpggrlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdp 85

QY 61 CTTCTRRHPCPPGGVQSGKFSGFCIDCASGTFSGHGHCKPWTDCQFGFLTVPFG 120

Db 86 cttcrhpcppggvgqgkfsgfcldcasgtfsgghghckpwtcdctqfgfltvfp 145

QY 121 NKTHNAVCPGSPPAEP 137

Db 146 nkthnavcvpgsppaep 162

RESULT 7

AAB27651

ID AAB27651 standard; Protein; 241 AA.

XX AAB27651;

AC AAB27651;

XX 26-JAN-2001 (first entry)

DT Human protein PRO364.

DE Cardiovascular; endothelial; angiogenic disorder; PRO179;

XX PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;

KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;

XX gene therapy.

XX Homo sapiens.

OS Key

FT Peptide

FT 1..25

FT /label= "signal peptide"

XX WO200053757-A2.

XX 14-SEP-2000.

XX 24-FEB-2000; 2000WO-US05004.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 02-JUN-1999; 99WO-US12252.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 01-SEP-1999; 99WO-US20111.

XX 15-SEP-1999; 99WO-US21090.

XX 30-NOV-1999; 99WO-US28313.



OS Homo sapiens.  
PN WO200053753-A2.  
XX 14-SEP-2000.  
PD  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
FA (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2001-090793/10.  
XX N-PSDB; AAC97479.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
PS  
PS Claim 69; Fig 54; 293pp; English.  
XX  
XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
XX invention.  
XX  
XX Sequence 241 AA;

Query Match 100.0%; Score 969; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGMGAFRALCGLALLCALSLGQRPTGGPGCGRLLLTGTGDARCCRVHTTRCCRD 60  
Db 1 maghgamafralcgllallcalslgqrptgpgcgprlllgtgdarccrvhttrccrd 60  
QY 61 YPGECECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
Db 61 ypgeecceccsewdcmcvqpefhcgdpcccttcrrhhpcppgqgvsggkfsfgqcidcasgtf 120  
QY 121 SGGHEGCKPWTDCQTQFGFTLVFPGNKTHNAVCPVGPSPPAEP 162  
Db 121 sggheghckpwtcdtqfgftlvfpgnkthnavcvgvsgppaep 162  
RESULT 15  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX  
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX  
OS Homo sapiens.  
XX  
PN WO9806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 14-AUG-1997; 97WO-US13931.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM, Randall TD, Zlotnik A;  
XX  
DR WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PS Isolated 312C2 T cell gene - used to develop products for treating,  
XX e.g. cancers, auto-immune disorders, transplantation rejection and  
XX other T cell disorders  
XX Disclosure; Pages 61-62; 71pp; English.  
XX  
XX This is the amino acid sequence of the truncated human 312C2 T cell  
XX protein from clone\_A8. The 312C2 proteins are expressed in thymus  
XX cells and are induced on T cells and spleen cells following activation.  
XX Engagement of 312C2 stimulates proliferation of T cell clones,  
XX antigen-specific proliferation and cytokine production by T-cells, and  
XX potentiates T cell expansion or apoptosis. The products can be used  
XX in the treatment of conditions associated with abnormal physiology or  
XX development, including abnormal proliferation, e.g. cancerous  
XX conditions or degenerative conditions. They can be used in the  
XX regulation or development of haematopoietic cells, e.g. lymphoid cells  
XX which affect immunological responses, e.g. autoimmune disorders.  
XX  
XX Sequence 228 AA;



```
Query Match      96.78; Score 937; DB 19; Length 228;
Best Local Similarity 100.0%; Pred. NO. 4.3e-67;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGLALLCALSLGQRPTGGPGCGRLLILGTGTARCCRVHTTRCCRDYPGEEC 66
    |||||||
Db 1 mgafralcglallcalslgqrptggpgcgprlllgtgtardccrvhttrccrdypgeec 60
    |||||||

QY 67 CSEWDCMCVQPEFHCGDPCCCTTCRHHPCPCGQVOSQKFSFGQCIDCASGTFSGGHEG 126
    |||||||
Db 61 csewdcmcvqpefhcgdpcccttcrrhhpcppgvgqgkfsfgqcidcasgtfsggheg 120
    |||||||

QY 127 HCKPWTDTQFGFLTVPFGNKTNAVCPGSPPAEP 162
    |||||||
Db 121 hckpwtddtdgflitvfpgnkthnavcvpgsppaep 156
    |||||||
```

Search completed: September 4, 2001, 15:56:22  
Job time: 339 sec



CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantion associated diseases  
XX including graft rejection and graft-versus-host diseases.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 969; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALCALSLGQRTGPGCGPGRLLILGTGTDCRCRVTHTTCCRD 60  
DB 1 maqhgamafralcglalcalcslgqrtpgpgcgprllilgtgtdarcrcrvhttrccrd 60  
QY 61 YPGEECCSEWDCMCVQPFHCGDPCCTTCRHHPCPGQGVQSGKFSFGQIDCASGTF 120  
DB 61 ypgeecscswdcmcvqpfhcgdpccctcrhhpcpgpgvgvsgkfsfgqdcasgtf 120  
QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEP 162  
DB 121 sggheghckpwtctqfgfltvfpgnknthnavcvpgspppaep 162

## RESULT 13

AAB50982  
ID AAB50982 standard; Protein; 241 AA.

XX AC AAB50982;

DT 21-MAR-2001 (first entry)

XX DE Human PRO364 protein.

KW Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
KW vasotrophic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
KW vulnerary; antianginal; gene therapy; cardiovascular disease;  
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
KW wound healing.

XX OS Homo sapiens.

XX PN W0200073445-A2.

XX PD 07-DEC-2000.

XX PF 17-MAY-2000; 2000WO-US13705.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 23-JUN-1999; 99US-0141037.

XX PR 20-JUL-1999; 99US-0144758.

XX PR 26-JUL-1999; 99US-0145698.

XX PR 28-JUL-1999; 99US-0146222.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 30-NOV-1999; 99WO-US28409.

XX PR 02-DEC-1999; 99WO-US28565.

XX PR 16-DEC-1999; 99WO-US30095.

XX PR 11-FEB-2000; 2000WO-US03565.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 18-FEB-2000; 2000WO-US04342.

PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;

XX Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;

XX Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2001-025251/03.

XX DR N-PSDB; AAC90566.

XX Seventeen nucleic acids encoding PRO polypeptides which are useful in  
XX diagnosis and treatment of cardiovascular, endothelial or angiogenic  
XX disorders in a mammal -

XX Claim 71; Fig 8; 182pp; English.

XX The present sequence is one of seventeen novel PRO polypeptides. The PRO  
XX nucleic acids, polypeptides, agonists and antagonists are useful for  
XX treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
XX Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
XX age-related macular degeneration, atherosclerosis, hypertension, arterial  
XX restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
XX infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
XX antagonists are also used to prevent tumour angiogenesis and for treating  
XX periodontal diseases. They are also used to stimulate wound healing and  
XX tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
XX antibodies are useful for diagnosing a cardiovascular, endothelial or  
XX angiogenic disorder.

XX SQ Sequence 241 AA;

Query Match 100.0%; Score 969; DB 22; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.3e-69;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALCALSLGQRTGPGCGPGRLLILGTGTDCRCRVTHTTCCRD 60  
DB 1 maqhgamafralcglalcalcslgqrtpgpgcgprllilgtgtdarcrcrvhttrccrd 60

QY 61 YPGEECCSEWDCMCVQPFHCGDPCCTTCRHHPCPGQGVQSGKFSFGQIDCASGTF 120

DB 61 ypgeecscswdcmcvqpfhcgdpccctcrhhpcpgpgvgvsgkfsfgqdcasgtf 120

QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEP 162

DB 121 sggheghckpwtctqfgfltvfpgnknthnavcvpgspppaep 162

## RESULT 14

AAB53090

ID AAB53090 standard; Protein; 241 AA.

XX AC AAB53090;

XX DT 28-FEB-2001 (first entry)

XX DE Human angiogenesis-associated protein PRO364, SEQ ID NO:142.

KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.

XX

modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.

Sequence 241 AA;

Query Match 100.0%; Score 969; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGALLCALSLGQRTGGCGPGRLLLTGTDAACRVRHTTRCCRD 60  
|||||  
Db 1 maqhgamgafRALCGALLCALSLGQRTGGCGPGRLLLTGTDAACRVRHTTRCCRD 60  
QY 61 YPGEECCSEWDCMVCQPEPHCGDPCTTCRHHPCPPGGVQSGKFSFGQCIDCASGTF 120  
|||||  
Db 61 ypgeeccsewdcmvcqpefhcgdpcttcrhhpcppggvgvsggkfsfgqcidcasgtf 120  
QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTNAVCPGSPPAEP 162  
|||||  
Db 121 sgghegchkpwtctqfgfltvfpgnktnavcvpgsppaep 162

RESULT 9

AA771467  
ID AA771467 standard; Protein; 241 AA.

AC AA771467;

DT 08-NOV-2000 (first entry)

XX Human PRO364 protein.

XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;  
KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;  
KW tumour necrosis factor receptor; GITR protein homologue.

XX Homo sapiens.

XX Location/Qualifiers

Key Peptide 1..25 /label= Signal\_peptide  
FT Modified-site 5..11 /note= "N-myristoylation site"  
FT Modified-site 8..14 /note= "N-myristoylation site"  
FT Modified-site 25..31 /note= "N-myristoylation site"  
FT Protein 26..241 /label= Mature\_PRO364\_protein  
FT Modified-site 30..36 /note= "N-myristoylation site"  
FT Modified-site 33..39 /note= "N-myristoylation site"  
FT Modified-site 118..124 /note= "N-myristoylation site"  
FT Modified-site 122..128 /note= "N-myristoylation site"  
FT Modified-site 146..150 /note= "N-myristoylation site"  
FT Modified-site 156..162 /note= "Asn is N-glycosylated"  
FT Modified-site /note= "N-myristoylation site"

FT Domain 163..183 /label= Transmembrane\_domain  
FT Binding-site 166..177 /note= "Prokaryotic membrane lipoprotein lipid attachment site"  
FT Region 171..193 /note= "Leucine zipper pattern"

XX WO200032778-A2.

PN 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28409.

XX 01-DEC-1998; 98WO-US25108.

PR 16-DEC-1998; 98US-0112850.

PR 22-DEC-1998; 98US-0113296.

PR 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

PA (GETH ) GENENTECH INC.

XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;

XX WPI; 2000-412325/35.

DR N-PSDB; AAD01240.

XX New composition useful for inhibiting neoplastic cell growth and for treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their antagonists -

PS Claim 31; Fig 4; 108pp; English.

XX The present sequence is the human PRO364 protein, encoded by the cDNA clone, designated as DNA47365-1206. It is isolated from human small intestine tissue cDNA library, identified using probes based on the consensus sequence DNA44825, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TNFR) family of polypeptides. PRO364 sequence also shows homology to members of the TNFR family and mouse GITR protein.  
CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, CC using an effective amount of PRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.

XX Sequence 241 AA;

Query Match 100.0%; Score 969; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGALLCALSLGQRTGGCGPGRLLLTGTDAACRVRHTTRCCRD 60  
|||||

Db 1 maqhgamgafRALCGALLCALSLGQRTGGCGPGRLLLTGTDAACRVRHTTRCCRD 60  
|||||

QY 61 YPGEECCSEWDCMVCQPEPHCGDPCTTCRHHPCPPGGVQSGKFSFGQCIDCASGTF 120  
|||||

Db 61 ypgeeccsewdcmvcqpefhcgdpcttcrhhpcppggvgvsgkfsfgqcidcasgtf 120  
|||||

QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTNAVCPGSPPAEP 162  
|||||

Db 121 sgghegchkpwtctqfgfltvfpgnktnavcvpgsppaep 162  
|||||

RESULT 10

AAB20115

ID AAB20115 standard; Protein; 241 AA.

XX AAB20115;

XX 30-APR-2001 (first entry)



PK T3-SEP-69; 06017700-0000

QV 121 SSGHEGHCKPWTDCCTOFGELTVFPGNKTHNAVCPVGSPPAEP 162

Db 121 sgghegckpwtcdtqfglftvfpnknthnavcvpsppaep 162  
|||||

RESULT 7  
AA95895  
ID AAY95895 standard; Protein; 241 AA.  
XX  
AC AAY95895;  
XX  
XX 20-NOV-2000 (first entry)  
DT  
XX Human tumour necrosis factor receptor-like protein TR11 mutein.  
DE  
XX  
XX TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
KW mutant.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200050459-A1.  
PN  
XX  
XX 31-AUG-2000.  
PD  
XX  
XX 23-FEB-2000; 2000WO-US04572.  
PF  
XX  
XX 24-FEB-1999; 99US-0121648.  
PR  
XX 13-MAY-1999; 99US-0134172.  
PR  
XX 16-JUL-1999; 99US-0144076.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Ruben SM, Ni J;  
PI  
XX  
XX WPI; 2000-572072/53.  
DR  
XX  
XX Human tumor necrosis factor receptor-like proteins useful for  
PT diagnosis, prevention and treatment of disease states associated with  
PT aberrant cell survival such as autoimmune disease and rheumatoid  
PT arthritis -  
PT  
XX Disclosure; 294-295; 278pp; English.  
PS  
XX

The present sequence is that of human tumour necrosis factor receptor-like protein TR11 (see also AAY95895), a novel protein showing identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The invention provides highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95895-81), as well as vectors, host cells and recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2 antagonists (e.g. antibodies) are used to treat, prevent, prognosis and/or diagnose an autoimmune disease, especially rheumatoid arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.

Sequence 241 AA;

Query Match 100.0%; Score 969; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAAGAFRALCGIALCALSLGCRPTGGCGPGRLLLTGTGTCRCRVHTTRCCRD 60  
Db |||||  
1 maqhgaagafralcglalcalslgcrptggcgpgrrlllgtgtdarccrvhttrccrd 60  
QY 61 YPGECCSEWDCMCVQPEPHCGDPCCTTCRHHPCPPGOGVQSGKFSFGFCIDCASGTF 120  
Db |||||  
61 ypgeccsewdcmcvqpephcgdpcccttcrrhhpcppggvgvsggkfsfgfcidcasgtf 120  
QY 121 SGGHEGCKPWTCDTQFGELTVFPGNKTHNAVCVPSPPAEP 162  
Db |||||  
121 sgghegckpwtcdtqfglftvfpnknthnavcvpsppaep 162  
RESULT 8  
AAB24409  
ID AAB24409 standard; Protein; 241 AA.  
XX  
AC AAB24409;  
XX  
DT 07-NOV-2000 (first entry)  
DE Human PRO364 protein sequence SEQ ID NO:117.  
XX  
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
KW cytostatic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
XX WO200032221-A2.  
PN  
XX  
XX 08-JUN-2000.  
PD  
XX  
XX 30-NOV-1999; 99WO-US28313.  
PF  
XX  
XX 01-DEC-1998; 98WO-US25108.  
PR  
XX 16-DEC-1998; 98US-0112850.  
PR  
XX 12-JAN-1999; 99US-0115554.  
PR  
XX 08-MAR-1999; 99WO-US05028.  
PR  
XX 12-MAR-1999; 99US-0123957.  
PR  
XX 28-APR-1999; 99US-0131445.  
PR  
XX 14-MAY-1999; 99US-0134287.  
PR  
XX 02-JUN-1999; 99WO-US12252.  
PR  
XX 23-JUN-1999; 99US-0141037.  
PR  
XX 20-JUL-1999; 99US-0144758.  
PR  
XX 26-JUL-1999; 99US-0145698.  
PR  
XX 01-SEP-1999; 99WO-US20111.  
PR  
XX 08-SEP-1999; 99WO-US20594.  
PR  
XX 13-SEP-1999; 99WO-US20944.  
PR  
XX 15-SEP-1999; 99WO-US21090.  
PR  
XX 15-SEP-1999; 99WO-US21547.  
PR  
XX 05-OCT-1999; 99WO-US23089.  
PR  
XX 29-OCT-1999; 99US-0162506.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
PI Watanabe CK, Williams PM, Wood WI;  
XX  
XX WPI; 2000-412154/35.  
DR  
XX N-PSDB; AAA77604.  
XX  
XX Nucleic acids encoding PRO polypeptides useful for preventing,  
PT diagnosing and treating diagnosing a cardiovascular, endothelial or  
PT angiogenic disorders in mammals -  
XX  
XX Claim 72; Fig 44; 315pp; English.  
PS  
XX  
XX The present invention describes nucleic acids encoding PRO polypeptides  
CC useful for preventing, diagnosing and treating diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder in mammals by

XX N1 J, Ruben SM;  
 XX WPI: 2000-061922/05.  
 DR N-PSDB; AAZ37762.  
 XX  
 PT New tumour necrosis factor receptor-like polypeptides used to, e.g.  
 PT treat Digeorge syndrome -  
 XX  
 PS Claim 14; Fig 1; 167pp; English.  
 XX  
 CC This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor-like protein (TR11 receptor). The invention relates to TR11 and  
 CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
 CC determined by sequencing cloned cDNAs AAZ37765-237766. The TR11 receptor  
 CC and its splice variants show homology to the murine glucocorticoid  
 CC induced tumour necrosis factor receptor family-related gene (GIRF).  
 CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation  
 CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease, Grave's  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.  
 XX  
 SQ Sequence 234 AA;

Query Match 100.0%; Score 969; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAQHGMAGFALCGIALCALSLGQRPTGGPGCGPRLLLGTGTARCCRVHTTCCRD 60  
 DB 1 maqhgmagfalcgialcalslgrptggpgcgprllllgtgtarccrvhttrccrd 60  
 QY 61 YPGEECCSEWDCMCVQPEFHCGDPCTTCRRHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
 DB 61 ypgeeccewdcmcvqpefhcgdpcttcrhpcppgqgvsgkfsfgfcidcasgtf 120  
 QY 121 SGGHEGCHKPWTDCQTQFGFLTVPFGNKTNAVCPVPSPPAEP 162  
 DB 121 sggheghckpwtcdctqfgfltvpfgnktnavcvpsppaep 162

RESULT 3  
 AAW37839  
 XX AAW37839 standard; Protein; 241 AA.  
 AC AAW37839;  
 XX  
 DT 28-JUL-1998 (first entry)  
 XX  
 DE Amino acid sequence of the human 312C2 T cell protein.

XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..726  
 FT CDS /\*tag= a  
 FT /product= "human 312C2 protein"  
 XX  
 PN WO9806842-A1.  
 PD 19-FEB-1998.  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 XX  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Gorman DM, Randall TD, Zlotnik A;  
 XX  
 DR WPI: 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 XX  
 PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 XX  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 969; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAQHGMAGFALCGIALCALSLGQRPTGGPGCGPRLLLGTGTARCCRVHTTCCRD 60  
 DB 1 maqhgmagfalcgialcalslgrptggpgcgprllllgtgtarccrvhttrccrd 60  
 QY 61 YPGEECCSEWDCMCVQPEFHCGDPCTTCRRHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
 DB 61 ypgeeccewdcmcvqpefhcgdpcttcrhpcppgqgvsgkfsfgfcidcasgtf 120  
 QY 121 SGGHEGCHKPWTDCQTQFGFLTVPFGNKTNAVCPVPSPPAEP 162  
 DB 121 sggheghckpwtcdctqfgfltvpfgnktnavcvpsppaep 162

RESULT 4  
 AAY06605  
 ID AAY06605 standard; Protein; 241 AA.  
 XX  
 AC AAY06605;  
 XX



DT	26-OCT-1999	(first entry)
XX		
XX	Human TNF receptor homologue PRO364.	
XX		
KW	PRO364; tumour necrosis factor receptor; human; apoptosis;	
KW	inflammation; antiinflammatory; NF-KB activation;	
KW	autoimmune disease; therapy.	
XX		
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
PH	Peptide	1..25
FT		/note= "signal peptide"
FT	Protein	26..241
FT		/note= "mature protein"
FT	Modified-site	146
FT		/note= "N-glycosylated"
FT	Domain	162..180
FT		/note= "transmembrane domain"
XX		
XX	W09940196-A1.	
PN		
XX		
PD	12-AUG-1999.	
XX		
XX	09-FEB-1999;	99WO-US02642.
PF		
XX		
PR	09-FEB-1998;	98US-0024087.
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;	
PI	Pitti RM, Wood WI;	
XX		
XX	WPI: 1999-494296/41.	
DR	N-PSDB; AAX87670.	
DR		
XX		
PT	Tumour necrosis factor receptor homologue - useful for, e.g.	
PT	modulating apoptosis and NF-KB activation and proinflammatory or	
PT	autoimmune responses	
XX		
PS	Claim 17; Fig 2A; 104pp; English.	
XX		
CC	The present sequence represents human PRO364, a novel member of the	
CC	tumour necrosis factor receptor family. The sequence was deduced	
CC	from a bone marrow cDNA clone (see AAX87670). Methods for the	
CC	recombinant production of PRO364 polypeptides, e.g. in CHO,	
CC	Escherichia coli or yeast host cells, are provided. Claimed	
CC	polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the	
CC	mature protein) and 26-X of the present sequence, where X is any	
CC	one of amino acid residues 157-167 of PRO364. PRO364 polypeptides	
CC	are useful for modulating apoptosis, NF-KB activation and	
CC	proinflammatory or autoimmune responses in mammalian cells	
CC	(claimed). Chimeric molecules comprising a PRO364 polypeptide	
CC	fused to a heterologous sequence such as epitope tag or	
CC	immunoglobulin Fc region are also claimed. PRO364 can be used in	
CC	assays to identify other proteins or molecules involved in binding	
CC	interactions. This is useful for identifying inhibitors or	
CC	agonists of receptor/ligand binding. The PRO364 polypeptides may	
CC	also be combined with an agent that is cytotoxic, chemotherapeutic	
CC	or a growth inhibitor. PRO364 antibodies are useful in diagnostic	
CC	methods, purification methods and also in therapy, e.g. as	
CC	inhibitors.	
XX		
SQ	Sequence	241 AA;
	Query Match	100.0%; Score 969; DB 20; Length 241;
	Best Local Similarity	100.0%; Pred. No. 1.3e-69;
	Matches 162; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MAQHGANGAFRALCGLALLCALSIGQRTGPGCGPGRLLLTGTDARCCRVHTRCRCD 60
Db	1	maqhganqafrcalcgallcalslqqrptgpgcgpglllqtdgdcrcrvhtrccrd 60

Qy	61	YPGECCSEWDCMCVQPEFHGCDPCTTCRRHHPCPPGGVSGQKFSFGQICDASGTF	120
Db	61	ypgeccsewdcmcvqpefhgdpctctrrhhpcppggvsgqkfsfgqicdca	120
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Db	121	sggheghckpwtcdtqfgflrvfpgnkthnavcvgpspae	162
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AA	AAB27651		
ID	AAB27651 standard; Protein; 241 AA.		
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AC	AAB27651;		
XX			
DT	26-JAN-2001 (first entry)		
XX			
DE	Human protein PRO364.		
XX			
KW	Cardiovascular; endothelial; angiogenic disorder; PRO179;		
KW	PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;		
KW	PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;		
KW	gene therapy.		
XX			
OS	Homo sapiens.		
XX			
FH	Key		
FT	Peptide		
FT	1..25		
FT	/label= "Signal peptide"		
XX			
PN	WO200053757-A2.		
XX			
PD	14-SEP-2000.		
XX			
PF	24-FEB-2000; 2000WO-US05004.		
XX			
PR	08-MAR-1999; 99WO-US05028.		
PR	12-MAR-1999; 99US-0123957.		
PR	02-JUN-1999; 99WO-US12252.		
PR	20-JUL-1999; 99US-0144758.		
PR	26-JUL-1999; 99US-0145698.		
PR	01-SEP-1999; 99WO-US20111.		
PR	15-SEP-1999; 99WO-US21090.		
PR	30-NOV-1999; 99WO-US28313.		
PR	30-NOV-1999; 99WO-US28409.		
PR	02-DEC-1999; 99WO-US28565.		
PR	18-FEB-2000; 2000WO-US04342.		
PR	22-FEB-2000; 2000WO-US04414.		
XX			
PA	(GETH ) GENENTECH INC.		
XX			
PI	Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;		
PI	Goddard A, Gurney AL, Hillan KU, Marsters SA, Paoni NF, Pitti RM;		
PI	Watanabe CK, Williams PM, Wood WI;		
XX			
DR	WPI: 2000-611444/58.		
XX			
XX	N-PSDB: AAA99903.		
XX			
PT	Novel PRO polypeptides and agonists and antagonists of them, used to		
PT	diagnose and treat cardiovascular, endothelial and angiogenic disorders		
XX			
PS	Claim 71; Fig 6; 181pp; English.		
XX			
CC	The present invention relates to methods for stimulating or inhibiting		
CC	angiogenesis and cardiovascularization. The methods involve the use of		
CC	pharmaceutical compositions based on the following proteins, PRO179,		
CC	PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,		
CC	PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These		
CC	proteins were identified by isolating cDNA clones encoding secreted		
CC	proteins. The proteins of the invention may be used to diagnose and		
CC	treat cardiovascular, endothelial or angiogenic disorders. The present		

GenCore version 4.5  
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OK protein - protein search, using sw model

Run on: September 4, 2001, 15:56:21 ; Search time 126.12 Seconds  
(without alignments)  
77.871 Million cell updates/sec

Title: US-09-512-363-2-copy\_1\_162

Perfect score: 969  
Sequence: 1 MACHGAMGAFRALCGLALC.....FPGNKTHNAVCPGSPPAEP 162

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	969	100.0	234	21	Human tumour necro
2	969	100.0	234	21	Tumour necrosis fa
3	969	100.0	241	19	Amino acid sequenc
4	969	100.0	241	20	Human TNF receptor
5	969	100.0	241	21	Human protein PRO3
6	969	100.0	241	21	Human PRO364 prote
7	969	100.0	241	21	Human tumour necro
8	969	100.0	241	21	Human PRO364 prote
9	969	100.0	241	21	Human PRO364 prote
10	969	100.0	241	22	Human immunostimul
11	969	100.0	241	22	Human PRO364. Hom

12	969	100.0	241	22	AAB50910	Human PRO364 prote
13	969	100.0	241	22	AAB50982	Human PRO364 prote
14	969	100.0	241	22	AAB53090	Human angiogenesis
15	937	96.7	228	19	AAW37840	Truncated human 31
16	937	96.7	235	21	AAW44825	Human molecule ass
17	937	96.7	311	19	AAW37842	Human 312C2 protei
18	921	95.0	240	21	AAW5881	Human tumour necro
19	921	95.0	240	21	AAW52160	TR11SV2 amino acid
20	842.5	86.9	317	20	AAW06645	PRO364-related EST
21	837.5	86.4	316	22	AAW47055	Polypeptide encode
22	639	65.9	241	21	AAW5880	Human tumour necro
23	639	65.9	241	21	AAW52159	TR11SV1 amino acid
24	605	62.4	232	19	AAW37841	Human 312C2 protei
25	506	52.2	222	19	AAW49018	Mouse glucocorticoid
26	506	52.2	228	19	AAW49016	Mouse glucocorticoid
27	506	52.2	228	19	AAW37838	Amino acid sequenc
28	506	52.2	294	19	AAW49017	Mouse glucocorticoid
29	255	26.3	89	21	AAW6013	Murine TNF-alpha f
30	255	26.3	89	22	AAW5952	Skin cell protein,
31	166.5	17.2	206	16	AAW81881	Mouse type-II memb
32	166.5	17.2	206	19	AAW48977	Mouse type-II memb
33	166.5	17.2	438	16	AAW81882	Mouse OX40 extrace
34	166.5	17.2	438	19	AAW48976	Plasmid pOC406/OX4
35	166	17.1	277	16	AAW76996	Deduced sequence e
36	162	16.7	277	16	AAW74737	ACT-4 cell surface
37	162	16.7	277	16	AAW79904	ACT-4-h-1 receptor
38	162	16.7	277	22	AAW35329	Human OX40 protein
39	162	16.7	277	22	AAW50522	Human tumour necro
40	160.5	16.6	255	16	AAW70977	H4-1BB receptor pr
41	160.5	16.6	255	16	AAW64197	Human 4-1BB polype
42	160.5	16.6	255	18	AAW26658	Human 4-1BB recept
43	160.5	16.6	255	20	AAW33214	Human CD137 protei
44	160.5	16.6	255	20	AAW28688	Human receptor pro
45	160.5	16.6	255	22	AAB50521	Human tumour necro

ALIGNMENTS

RESULT 1  
AAW95879  
ID AAY95879 standard; Protein; 234 AA.  
XX  
AC AAY95879;  
XX  
DT 20-NOV-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-like protein TR11.  
XX  
KW TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25 /label= Signal\_peptide  
FT Protein 26..234 /label= Mature\_protein  
FT Domain 26..162 /label= Extracellular\_domain  
FT Domain 163..179 /label= Transmembrane\_domain  
FT Domain 180..234 /label= Intracellular\_domain  
FT Modified-site 146 /note= "N-glycosylated"  
FT Domain 72..81 /note= "conserved domain CD-II"  
FT Domain 84..93 /note= "conserved domain CD-III"

FT Domain 107..113 /note= "conserved domain CD-IV"

FT Domain 128..134 /note= "conserved domain CD-V"

FT Domain 153..160 /note= "conserved domain CD-VI"

FT Domain 176..186 /note= "conserved domain CD-VII"

FT Domain 204..209 /note= "conserved domain CD-IX"

FT Domain 224..233 /note= "conserved domain CD-X"

FT Region 27..36 /note= "epitope-bearing region"

FT Region 43..51 /note= "epitope-bearing region"

FT Region 59..67 /note= "epitope-bearing region"

FT Region 56..64 /note= "epitope-bearing region"

FT Region 66..71 /note= "epitope-bearing region"

FT Region 99..107 /note= "epitope-bearing region"

FT Region 125..133 /note= "epitope-bearing region"

FT Region 143..151 /note= "epitope-bearing region"

FT Region 156..164 /note= "epitope-bearing region"

FT Region 203..211 /note= "epitope-bearing region"

FT Region 222..230 /note= "epitope-bearing region"

FT Region 222..230 /note= "epitope-bearing region"

XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J;

XX WPI; 2000-572072/53.

XX N-PSDB; AAA50304.

XX Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis -

XX Claim 14(c); Fig 1A-B; 278pp; English.

XX The present sequence is that of human tumour necrosis factor receptor-like protein TR11, a novel 25 kDa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The sequence was deduced from a cDNA clone (see AAA50304) discovered in a T-helper cell library. TR11 activated NF-kappaB through a TRAF2-mediated mechanism. Expression is activation-inducible. The TR11 ligand is constitutively expressed in an endothelial cell line. This suggests that TR11 and its ligand may be involved in activated T-cell trafficking. The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AAY95879-81), as well as vectors, host cells and recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an

CC immunodeficiency, especially common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2 antagonists (e.g. antibodies) are used to treat, prevent, prognosis and/or diagnose an autoimmune disease, especially rheumatoid arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.

XX Sequence 234 AA;

SQ

Query Match 100.0%; Score 969; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-69;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 maqhgaagafalcalcalgslgrptggpggrlllgtgdarccrvhttrccrd 60  
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Qy 61 YPEEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTF 120  
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Db 61 ypgeecscsewdcmcvqpefhcgdpccctcrhhpcppggvgvsgkfsfgqicdcsgrtf 120  
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Qy 121 SGGHGHGCKPWTDCQFGFLTVFPNGKTHNAVCPGSPPAEP 162  
|||||

Db 121 sggheghckpwtcdtqfgfltvfpngkthnavcvpgspppaep 162  
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RESULT 2

AAAY52158

ID AAY52158 standard; Protein; 234 AA.

XX

AC AAY52158;

DT 01-FEB-2000 (first entry)

XX Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.

XX Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2; GITR; growth; differentiation; cell death; immune deficiency disorder; Digorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntington's disease; inflammatory condition.

XX Homo sapiens.

XX Key Location/Qualifiers

FX Peptide 1..25 /label= Signal\_peptide

FT Protein 26..234 /label= TR11

FT Domain 26..162 /note= "Extracellular domain"

FT Domain 163..179 /note= "Transmembrane domain"

FT Domain 180..234 /note= "Intracellular domain"

XX WO9920758-A1.

XX 29-APR-1999.

XX 21-OCT-1998; 98WO-US22085.

XX 21-OCT-1997; 97US-0063212.

XX (HUMA-) HUMAN GENOME SCI INC.

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	Matches 162;	Conservative	0;	Mismatches	0;	Indels	0;
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Qy	61	YPGECCSEWDCMVQPEHFHCGDPCCCTCRHHPPPGGVGSQGKFSFGFCIDCASGTF	120				
Db	61	YPGECCSEWDCMVQPEHFHCGDPCCCTCRHHPPPGGVGSQGKFSFGFCIDCASGTF	120				
Qy	121	SGGHEGHCKPWTDCTQGFGLTVFPGNKTHNAVCPGSPPAEP	162				
Db	121	SGGHEGHCKPWTDCTQGFGLTVFPGNKTHNAVCPGSPPAEP	162				

RESULT 2  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS

ADDRESS: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-6

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Dd	121	HCKPWTCTCFGLTFVPGNKTHNAVCVPGSPPAEP	156	

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RESULT 3
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: Sequence 8, Application US/08911423
: Patent No. 6111090
: GENERAL INFORMATION:
: APPLICANT: Gorman, Daniel M.
: APPLICANT: Randall, Troy D.
: APPLICANT: Zlotnik, Albert
: TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
: TITLE OF INVENTION: REAGENTS
: NUMBER OF SEQUENCES: 8
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STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match	96.7%	Score 937;	DB 3;	Length 311;
Best Local Similarity	100.0%;	Pred. NO. 4e-74;		
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			Indels	0;
			Gaps	0;

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Qy	67	CSEWDNCVQPEFHCGDPCC	126
Qy		CSEWDNCVQPEFHCGDPCC	126
Db	61	CSEWDNCVQPEFHCGDPCC	120
Db		CSEWDNCVQPEFHCGDPCC	120
Qy	127	HCKPWTICTQFGFLTVP	162
Qy		HCKPWTICTQFGFLTVP	162

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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:34 ; Search time 65.86 Seconds  
(without alignments)  
50.647 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_162

Perfect score: 969

Sequence: 1 MAOHGAMGAFRALCGLALLC.....FPGKNTNNAVCPGSPPAEP 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	605	62.4	232	3	US-08-911-423-7
5	506	52.2	228	3	US-08-911-423-2
6	255	26.3	89	4	US-09-188-930-191
7	166.5	17.2	206	1	US-08-097-827-7
8	166.5	17.2	206	1	US-08-494-574-7
9	166.5	17.2	438	1	US-08-097-827-11
10	166.5	17.2	438	1	US-08-494-574-11
11	162	16.7	277	2	US-08-147-784-2
12	162	16.7	277	4	US-08-195-967-2
13	160.5	16.6	255	1	US-08-236-918A-8
14	160.5	16.6	255	2	US-08-816-605-9
15	160.5	16.6	255	5	PCT-US96-03965-2
16	159.5	16.4	219	2	US-08-816-605-2
17	153	15.8	191	3	US-08-974-022-52
18	153	15.8	256	1	US-08-236-918A-6
19	153	15.8	256	5	PCT-US96-03965-2
20	153	15.8	300	2	US-08-794-796-2
21	151	15.6	205	3	US-08-974-022-51
22	149	15.4	140	4	US-08-477-347-17
23	141.5	14.6	401	3	US-08-974-022-2
24	139.5	14.4	139	2	US-08-219-237B-8
25	139.5	14.4	401	3	US-08-974-022-4
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27	138.5	14.3	451	3	US-08-996-139-4

Query Match 100.0%; Score 969; DB 3; Length 241;

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Sequence 15, Appl  
Sequence 15, Appl  
Sequence 48, Appl  
Sequence 7, Appli  
Sequence 2, Appli  
Patent No. 5395760

28 138.5 14.3 451 4 US-08-995-659-4  
29 138.5 14.3 616 3 US-08-996-139-6  
30 138.5 14.3 616 4 US-08-995-659-6  
31 135.5 14.0 197 3 US-08-974-022-49  
32 135.5 14.0 289 4 US-03-042-785A-11  
33 133 13.7 401 3 US-08-974-022-6  
34 133 13.7 401 4 US-09-042-785A-12  
35 131 13.5 591 3 US-08-996-139-2  
36 131 13.5 591 4 US-08-995-659-2  
37 129.5 13.4 253 4 US-09-042-785A-4  
38 129.5 13.4 605 4 US-09-042-785A-23  
39 129.5 13.4 655 3 US-08-959-382-2  
40 123 12.7 625 3 US-08-996-139-15  
41 123 12.5 625 4 US-08-995-659-15  
42 121 12.5 227 3 US-08-974-022-48  
43 121 12.5 461 4 US-03-042-785A-7  
44 119 12.3 461 1 US-08-385-229-2  
45 119 12.3 461 6 5395760-2

#### ALIGNMENTS

RESULT 1  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chang, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

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; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 89
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-191

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Query Match      26.3%; Score 255; DB 4; Length 89;
Best Local Similarity 46.3%; Pred. No. 1.2e-15;
Matches 44; Conservative 17; Mismatches 26; Indels 8; Gaps 2;

QY      8  GAFRALCGLLALCALSLGQ-RPTGGPGGPGPRLLLGTCTDARCCRVHTTCCRDPYGPBEC 66
      |||  | :||:| | |||  |||||:| :| :||| :|  ||:|
Db      1  GAWANLYGVSMCLVDLILGQSPVEEPGGCGPKGVQNGSGNNTGCCSLYA-----PGKED 53

QY      67  CSEWDCMCVQPEFHCGDFPCCTTCRHHCPPPCGVQ 101
      | :| :||| | :||| | :||| | :||| | :||| |
Db      54  CPKERCICVTPEYHCGDPCKICKHYPCQPGORVE 88

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RESULT 7
US-08-097-827-7
; Sequence 7, Application us/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/097,827
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-097-827-7

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Query Match	17.2%;	Score 166.5;	DB 1;	Length 206;
Best Local Similarity	28.7%;	Pred. No. 1.2e-07;		

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Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;

Qy 26 QRPTGGPGCGRLLLG--TGTDA--CCRVHT----TRCCRD-YPG-----EECCSEWDC 72
      :|||      |||      |||      :|||      |||      |
Db 6 QQPT-----ALLLLGLTLCVTARRLNCVKHTYPSGHKKCCRCQCPGHGMVNRCDHTRDT 58
      :|||      |||      |||      :|||      |||      |
Qy 73 MCVPEFHCGDPC-----CITCRHHP-----CPEGQG 99
      :|||      |||      |||      :|||      |||      |
Db 59 LC-----HPCETGFNEAVNYDTCKQCQTCQNRHSGSELKQNCPTPTQDPTVCRCPGTQ 110
      :|||      |||      |||      :|||      |||      |
Qy 100 VOSGKSFSGQCDCASGTFSGGHEGHCKPWTCTQFGTLVFPGNKTHNAVC 153
      :|||      |||      |||      :|||      |||      |
Db 111 PRQDSGYKLGVDCVPCPPGHPGSPGNQACKPWTNCTLSGKQTRHPASDLSLDAVC 164
      :|||      |||      |||      :|||      |||      |

RESULT 8
US-08-494-574-7
; Sequence 7, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-494-574-7

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Query Match	17.2%	Score 166.5;	DB 1;	Length 206;
Best Local Similarity	28.7%;	pred. No. 1.2e-07;		
Matches	50; Conservative	12; Mismatches	51; Indels	61; Gaps
Qy	26	QRPTGGCGGRLLG--TCTDAR--CCRVHT-----TRCRD-YPG-----EECCSWDC	72	
	:			:
Db	6	QQPT-----ALLGLLTGTARRLCNVKHTVPSGHKKRCQCQPGHVMNRCDHTRDT	58	
Qy	73	MCVPEFHCGDPG-----CITCRHP-----CPGQG	99	
	:			:
Db	59	LC-----HPCETGFYNEAVNYDTCKQTCHNRRSGSELKONCTPQTQTVRCRGRTQ	110	

Db 121 HCKPWTDCQFGFLVFPNGKTHNAVCPGSPPAEP 156  
|||||

RESULT 4  
US-08-911-423-7  
; Sequence 7, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-7

Query Match 62.4%; Score 605; DB 3; Length 232;  
Best Local Similarity 78.1%; Pred. No. 1.6e-45;  
Matches 107; Conservative 5; Mismatches 17; Indels 8; Gaps 3;

Qy 7 MGAFRALCGLALLCALSLGQRTGGPGGGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
Db 1 MGAFRALCGLALLCALSLGQRTGGPGGGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
Qy 67 CSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQGVQSGKFSFGFQCI----DCASGTFSG 122  
Db 61 CSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQGVQSGK----SWRCLWESTQARGSTRAR 117  
Qy 123 GH-EGHCKPWTDCQFG 138  
Db 118 GRARGHRCPARTCGGWG 134

RESULT 5  
US-08-911-423-2

; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-2

Query Match 52.2%; Score 506; DB 3; Length 228;  
Best Local Similarity 54.5%; Pred. No. 5.7e-37;  
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

Qy 7 MGAFRALCGLALLCALSLGQ-RPTGGPGGGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65  
Db 1 MGAWAMLYGVSMCLVLDLQGFVVEEFGCGKGVQSGNNTRCCSLYA-----PGKE 53  
Qy 66 CCSPWDCMCVQPEFHGCDPCTTCRHHPCPPGQGVQSGKFSFGFQCIDCASGTFSGSGHE 125  
Db 54 DCPKERCICVTPEYHCGDPCKICKHYPCQPGQVQSGQDIVFGRCVACAMGTFISAGRD 113  
Qy 126 GHCKPWTDCQFGFLVFPNGKTHNAVCPGSPPAE 161  
Db 114 GHCLWNCVQFGFLVFPNGKTHNAVCIPEPLPTE 149

RESULT 6  
US-09-188-930-191  
; Sequence 191, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,784
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-147-784-2

Query Match 16.7%; Score 162; DB 2; Length 277;
Best Local Similarity 29.7%; Pred. No. 3.9e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGLALLCALSLG-----QRTGGPGCGPGRLLLTGTGDARCCRVHT 54
   || || || || || || || || || || || || || || || || || || || ||
Db 4 GARRLGRGPCAALLLLGLGLSTVTLGHCVGDTPSPNDRCCHECR--PGNGMVSRCSRQN 61
   || || || || || || || || || || || || || || || || || || || ||
QY 55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSGKFSF 108
   || || || || || || || || || || || || || || || || || || || ||
Db 62 TVCRPCGPGFYNDVYSSKPKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKP 121
   || || || || || || || || || || || || || || || || || || || ||
QY 109 GFQCIDCASGTFSGHGHCCKPWTCTQGFGLTVFPGNKTHNAVCPGSPPA 160
   || || || || || || || || || || || || || || || || || || || ||
Db 122 GVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLOPASNSSDAICEDRDPPA 173
   || || || || || || || || || || || || || || || || || || || ||

RESULT 12
US-08-195-967-2
; Sequence 2, Application US/08195967
; Patent No. 6242566
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourle and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-147-784-2
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;
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-195-967-2

Query Match 16.7%; Score 162; DB 4; Length 277;
Best Local Similarity 29.7%; Pred. No. 3.9e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGLALLCALSLG-----QRTGGPGCGPGRLLLTGTGDARCCRVHT 54
   || || || || || || || || || || || || || || || || || || || ||
Db 4 GARRLGRGPCAALLLLGLGLSTVTLGHCVGDTPSPNDRCCHECR--PGNGMVSRCSRQN 61
   || || || || || || || || || || || || || || || || || || || ||
QY 55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSGKFSF 108
   || || || || || || || || || || || || || || || || || || || ||
Db 62 TVCRPCGPGFYNDVYSSKPKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKP 121
   || || || || || || || || || || || || || || || || || || || ||
QY 109 GFQCIDCASGTFSGHGHCCKPWTCTQGFGLTVFPGNKTHNAVCPGSPPA 160
   || || || || || || || || || || || || || || || || || || || ||
Db 122 GVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLOPASNSSDAICEDRDPPA 173
   || || || || || || || || || || || || || || || || || || || ||

RESULT 13
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-236-918A-8
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; APPLICANT: Fanslow, William

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;
; COUNTRY: U
;
; ZIP: 94301

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; COUNTRY: U
; ZIP: 94301

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Search completed: September 4, 2001, 15:57:34  
Job time: 376 sec

0

Query Match 16.6%; Score 160.5; DB 1; Length 255;  
Best Local Similarity 30.9%; Pred. No. 4.9e-07;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTGDARCCRVHTTRCCRDYPG-----ECCS-----EWDGCMVQPFHCGDP 84  
DB 48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKCSSTSNAECDG---TPGFHCLGA 97

QY 85 CCTTCRRHHPGPPGQVQSGKSFQFCIDCASGTFSGGHEGCKPWTCTQFGFLTVFP 144  
DB 98 GCSMC-EQDCKQGQELTKKG-----CKDCFCFTNDQKRGICRPWTNCSLDGKSVLVN 149

QY 145 GNKTHNAVCPG-----SPPA---EP 162  
DB 150 GTKERDVVCGPSPADLSPGASSVTPAPAREP 181

RESULT 14  
US-08-816-605-9  
; Sequence 9, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: NI, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,605  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8512  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-816-605-9

Query Match 16.6%; Score 160.5; DB 2; Length 255;  
Best Local Similarity 30.9%; Pred. No. 4.9e-07;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTGDARCCRVHTTRCCRDYPG-----ECCS-----EWDGCMVQPFHCGDP 84  
DB 48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKCSSTSNAECDG---TPGFHCLGA 97

QY 85 CCTTCRRHHPGPPGQVQSGKSFQFCIDCASGTFSGGHEGCKPWTCTQFGFLTVFP 144  
DB 98 GCSMC-EQDCKQGQELTKKG-----CKDCFCFTNDQKRGICRPWTNCSLDGKSVLVN 149

QY 145 GNKTHNAVCPG-----SPPA---EP 162  
DB 150 GTKERDVVCGPSPADLSPGASSVTPAPAREP 181

RESULT 15  
PCT-US96-03965-8  
; Sequence 8, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuil  
; TITLE OF INVENTION: Monoclonal antibody against human  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KW05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-03965-8

Query Match 16.6%; Score 160.5; DB 5; Length 255;  
Best Local Similarity 30.9%; Pred. No. 4.9e-07;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTGDARCCRVHTTRCCRDYPG-----ECCS-----EWDGCMVQPFHCGDP 84  
DB 48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKCSSTSNAECDG---TPGFHCLGA 97

QY 85 CCTTCRRHHPGPPGQVQSGKSFQFCIDCASGTFSGGHEGCKPWTCTQFGFLTVFP 144  
DB 98 GCSMC-EQDCKQGQELTKKG-----CKDCFCFTNDQKRGICRPWTNCSLDGKSVLVN 149

QY 145 GNKTHNAVCPG-----SPPA---EP 162  
DB 150 GTKERDVVCGPSPADLSPGASSVTPAPAREP 181

SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-8

Query Match 19.1%; Score 160.5; DB 5; Length 255;  
Best Local Similarity 30.9%; Pred. No. 3.8e-07;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

Qy 9 CGPGRLLGTGDARCCRVHTTRCCRDYPG-----ECCS-----EWDCCMCVQPEFHCGDP 59  
Db 48 CPNNSFSAGG--QRTCDI-----CRQKGVTRTRKCSSTSNAECDC---TPGFHCLGA 97  
Qy 60 CTTTCRRHPCPPGQGVQSGKFSFGQICDCASGTFSGGHEGHCRTWTCTQGFGLTVFP 119  
Db 98 GCSMC-EQCKQGGELTKKG-----CKDCGTFNDQKRGICRPWTNCSLDGKSVLVN 149  
Qy 120 GNKTHNAVCPG-----SPPA---EP 137  
Db 150 GTKERDVVCGSPADLSPGASSVTPAPAREP 181

RESULT 14  
US-08-816-605-2  
Sequence 2, Application US/08816605  
Patent No. 5874240  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Gentz, Reiner  
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816.605  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-605-2

Query Match 18.8%; Score 158.5; DB 2; Length 219;  
Best Local Similarity 33.0%; Pred. No. 5e-07;  
Matches 38; Conservative 11; Mismatches 45; Indels 21; Gaps 5;

Qy 33 CRDYPG-----EECS-----EWDCCMCVQPEFHCGDPCCCTTCRHHPCPPGQGVQSGKFS 82

Db 28 CSNCPAGVFRTRKCSSTSNAECDC---TPGFHCLGAGCSMC-EQCKQCGELTKKG--- 80  
Qy 83 FGFQCIDCASGTFSGGHEGHCRTWTCTQGFGLTVFPGNKTHNAVCPVPGSPAPAP 137  
Db 81 ----CKDCGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSP 131

RESULT 15  
US-08-147-784-2  
Sequence 2, Application US/08147784  
Patent No. 5821332  
GENERAL INFORMATION:  
APPLICANT: Godfrey, Wayne  
APPLICANT: Buck, David  
APPLICANT: Engleman, Edgar G.  
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Hourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,784  
FILING DATE: 03-NOV-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 05490A-220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-147-784-2

Query Match 18.8%; Score 158.5; DB 2; Length 277;  
Best Local Similarity 31.6%; Pred. No. 6.2e-07;  
Matches 42; Conservative 10; Mismatches 70; Indels 11; Gaps 4;  
Qy 9 CGPGRLLGTGDARCCRVHTTRCCRDYPG--ECCSSEWDCM-CVQPEFHCGD---PCCT 62  
Db 46 CRP-----GNGMVSRCRSRSONTVCRPCGPGFYNDVSSKPKCKPCTWCNLSRSGSERKQICT 100  
Qy 63 TCRHPCPPGQGVQSGKFSFGQICDCASGTFSGGHEGHCRTWTCTQGFGLTVFPGNK 122  
Db 101 ATQDTVCRCRAGTQPLDSYKPGVDCAPCPGHFSPGDNQACKPWTNCTLAGKHTLQPASN 160  
Qy 123 THNAVCPVPGSPA 135  
Db 161 SSDAICEDRDPPA 173

Search completed: September 4, 2001, 15:57:34  
Job time: 376 sec



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RESULT 9
US-08-097-827-11
; Sequence 11, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-097-827-11

Query Match 19.8%; Score 166.5; DB 1; Length 438;
Best Local Similarity 28.7%; Pred. No. 1.9e-07;
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;

Qy 1 QRTGGPGCGPGRLLLG--TGTDA--CCRVHT---TRCCRD--YPG-----ECCSEWDC 47
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 6 QQPT-----ALLLLGLTGLVTARRLNCVKHTYPSGHKCCRCQPGHGMVNRCDHTRDT 58
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 48 MCVOPEFHCGDPC-----CTTCRHHP-----CPPGQG 74
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 59 LC-----HPCETGFYNEAVNYDTCKQCTCNHRSGSELKQNCPTQDTCRCRPGTQ 110
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 75 VOSQKRFSGFCIDCASGTFSGGHEGHCKPWTDCQFGFLTFPPGNKTHNAV 128
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 111 PRQDSGYKLGVDVCPGPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 10
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

Query Match 19.8%; Score 166.5; DB 1; Length 438;
Best Local Similarity 28.7%; Pred. No. 1.9e-07;
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;

Qy 1 QRTGGPGCGPGRLLLG--TGTDA--CCRVHT---TRCCRD--YPG-----ECCSEWDC 47
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 6 QQPT-----ALLLLGLTGLVTARRLNCVKHTYPSGHKCCRCQPGHGMVNRCDHTRDT 58
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 48 MCVOPEFHCGDPC-----CTTCRHHP-----CPPGQG 74
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 59 LC-----HPCETGFYNEAVNYDTCKQCTCNHRSGSELKQNCPTQDTCRCRGTQ 110
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 75 VOSQKRFSGFCIDCASGTFSGGHEGHCKPWTDCQFGFLTFPPGNKTHNAV 128
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 111 PRQDSGYKLGVDVCPGPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 11
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
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; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-816-605-9

Query Match 19.1%; Score 160.5; DB 2; Length 255;
Best Local Similarity 30.9%; Pred. No. 3.8e-07;
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps

QY 9 CGPRLLLGTGDARCCRVHTTRCCRDYPG-----EECCS----EWDCCMCVQPERHCGDP 59
Db 48 CPNPSFSSAGG--QRTCDI-----CQCKGVFTRECSSTNAECDC---TPGFHCLGA 97
QY 60 CCTTCRRHPHCPGGQVQSOGKSFQGCIDCASGTFSGGHEGCKPWTCTQGFGLTVFP 119
Db 98 GCSMC-EQDCKQQLTKKG-----CKDCCFGTENDQKRGICRPWTNCSLDGKSVLN 149
QY 120 GNKTHNAVCPVG-----SPPA---EP 137
Db 150 GTRKRDVCGSPADLSPGASSVTPPAPAREP 181

RESULT 13
PCT-US96-03965-8
; Sequence 8, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; APPLICANT: Kang, Chang-yuil
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03965
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 16-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,269
; FILING DATE: 01-FEB-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/267,577
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KW05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 8:

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Db 140 NKTHNAVCPGSPAP 156  
|||||

## RESULT 4

US-08-911-423-7

; Sequence 7, Application US/08911423

; Patent No. 611090

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED

; TITLE OF INVENTION: REAGENTS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/911,423

; FILING DATE: 14-AUG-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/023,419

; FILING DATE: 16-AUG-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/027,901

; FILING DATE: 07-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0612K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-496-1200

; TELEFAX: 650-496-1200

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 232 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-911-423-7

Query Match 60.5%; Score 509; DB 3; Length 232;

Best Local Similarity 74.6%; Pred No. 2.1e-37;

Matches 88; Conservative 5; Mismatches 17; Indels 8; Gaps 3;

Qy 1 QRTPGCGPGRLLLTGTARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPC 60

|||||

Db 20 QRTPGCGPGRLLLTGTARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPC 79

|||||

Qy 61 CTTCHRHCPGQGVQSGKSFQFCI-----DCASGTFSGGH-EGHCKPWTCTQFG 113

|||||

Db 80 CTTCHRHCPGQGVQSGK-----SWRLWESTQARGSTRARGRHRCPARTCGVWG 134

## RESULT 5

US-08-911-423-2

; Sequence 2, Application US/08911423

; Patent No. 611090

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED

; TITLE OF INVENTION: REAGENTS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/911,423

; FILING DATE: 14-AUG-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/023,419

; FILING DATE: 16-AUG-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/027,901

; FILING DATE: 07-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0612K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9196

; TELEFAX: 650-496-1200

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-911-423-2

Query Match 55.4%; Score 465.5; DB 3; Length 228;

Best Local Similarity 56.9%; Pred. No. 1.2e-33;

Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;

Qy 7 PGCGPGRLLLTGTARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPCCTTCHH 66

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Db 27 PGCGPCKVQNGSNNTRCCSLYA-----PGKEDCKERCICVTPEYHCGDPCKICKH 79

Qy 67 HPCPPGQGVQSGKSFQFCIDCAGTFSGGHGHCKPWTCTQFGFLVFPNGKTHNA 126

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Db 80 YPCQPGQGVQSGDIVFGFRCVACAMGTFSGAGRDGHCLRWLWTCNSQFGFLTFMFGNKTHNA 139

Qy 127 VCVPGSPAP 136

|||||

Db 140 VCIPEPLTE 149

## RESULT 6

US-09-188-930-191

; Sequence 191, Application US/09188930A

; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; TITLE OF INVENTION: and Methods For Their Use

; FILE REFERENCE: 11000.1011c1





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:34 ; Search time 65.86 Seconds  
(without alignments)  
42.831 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162

Perfect score: 841

Sequence: 1 QRPTGGPGCGRLLLTGT.....FPGKTHNAVCPGSPAP 137

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Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	841	100.0	311	3	US-08-911-423-8
4	509	60.5	232	3	US-08-911-423-7
5	465.5	55.4	228	3	US-08-911-423-2
6	219.5	26.1	89	4	US-09-188-930-191
7	166.5	19.8	206	1	US-08-097-827-7
8	166.5	19.8	206	1	US-08-494-574-7
9	166.5	19.8	438	1	US-08-097-827-11
10	166.5	19.8	438	1	US-08-494-574-11
11	160.5	19.1	255	1	US-08-236-918A-8
12	160.5	19.1	255	5	PCT-US96-605-9
13	160.5	19.1	255	5	PCT-US96-03965-8
14	158.5	18.8	219	2	US-08-816-605-2
15	158.5	18.8	277	2	US-08-147-784-2
16	158.5	18.8	277	4	US-08-193-967-2
17	153	18.2	191	3	US-08-974-022-52
18	153	18.2	256	5	PCT-US96-03965-2
19	153	18.2	256	3	US-08-974-022-51
20	151	18.0	205	3	US-08-974-022-51
21	150.5	17.9	300	2	US-08-794-796-2
22	149	17.7	140	4	US-08-477-347-17
23	140	16.6	401	3	US-08-974-022-2
24	139.5	16.6	139	2	US-08-219-237B-8
25	139	16.5	401	3	US-08-974-022-4
26	139	16.5	401	4	US-09-042-785A-13
27	133	15.8	401	3	US-08-974-022-6

28	133	15.8	401	4	US-09-042-785A-12	Sequence 12, Appl
29	131	15.6	451	3	US-08-996-139-4	Sequence 4, Appl
30	131	15.6	451	4	US-08-995-659-4	Sequence 4, Appl
31	131	15.6	591	3	US-08-996-139-2	Sequence 2, Appl
32	131	15.6	591	4	US-08-995-659-2	Sequence 2, Appl
33	131	15.6	616	3	US-08-996-139-6	Sequence 6, Appl
34	131	15.6	616	4	US-08-995-659-6	Sequence 6, Appl
35	129.5	15.4	605	4	US-09-042-785A-4	Sequence 4, Appl
36	129.5	15.4	253	4	US-09-042-785A-23	Sequence 23, Appl
37	129.5	15.4	655	3	US-08-959-382-2	Sequence 2, Appl
38	127.5	15.2	197	3	US-08-974-022-49	Sequence 49, Appl
39	127.5	15.2	289	4	US-09-042-785A-11	Sequence 11, Appl
40	123	14.6	625	3	US-08-996-139-15	Sequence 15, Appl
41	123	14.6	625	4	US-08-995-659-15	Sequence 15, Appl
42	121	14.4	227	3	US-08-974-022-48	Sequence 48, Appl
43	121	14.4	461	4	US-09-042-785A-7	Sequence 7, Appl
44	119	14.1	461	1	US-08-385-229-2	Sequence 2, Appl
45	119	14.1	461	6	5395760-2	Patent No. 5395760

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCE: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

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Query Match 100.0%; Score 841; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.2e-66; Mismatches 0; Indels 0; Gaps 0;
Matches 137; Conservative 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
DB 20 QRTGGPGCGPGRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
QY 61 CTTCTRHHPGCGVQSGKSFQICDASGTFSGGHEGHCCKPWTDTCTQFGFLTVPFG 120
DB 80 CTTCTRHHPGCGVQSGKSFQICDASGTFSGGHEGHCCKPWTDTCTQFGFLTVPFG 139
QY 121 NKTHNAVCPGSPPAEP 137
DB 140 NKTHNAVCPGSPPAEP 156

RESULT 2
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-4

Query Match 100.0%; Score 841; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
DB 26 QRTGGPGCGPGRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 85

Query Match 100.0%; Score 841; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 4.2e-66;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
DB 20 QRTGGPGCGPGRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
QY 61 CTTCTRHHPGCGVQSGKSFQICDASGTFSGGHEGHCCKPWTDTCTQFGFLTVPFG 120
DB 80 CTTCTRHHPGCGVQSGKSFQICDASGTFSGGHEGHCCKPWTDTCTQFGFLTVPFG 139
QY 121 NKTHNAVCPGSPPAEP 137
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;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Barnard, Brown & Michaels  
;; STREET: 306 East State Street, Suite 220  
;; CITY: Ithaca  
;; STATE: NY  
;; COUNTRY: USA  
;; ZIP: 14850  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US96/03965  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/122,796  
;; FILING DATE: 16-SEP-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/012,269  
;; FILING DATE: 01-FEB-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/922,996  
;; FILING DATE: 30-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/267,577  
;; FILING DATE: 07-NOV-1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Michaels, Christopher A  
;; REGISTRATION NUMBER: 34,390  
;; REFERENCE/DOCKET NUMBER: KWO5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 607-273-1711  
;; TELEFAX: 607-273-2609  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 256 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
PCT-US96-03965-2

Query Match 19.7%; Score 140; DB 5; Length 256;  
Best Local Similarity 32.7%; Pred. No. 2.4e-05;  
Matches 36; Conservative 15; Mismatches 41; Indels 18; Gaps 7;  
Qy 9 CGPGLR-LLGTGTDARCCRVHTTCCRDYPGEECCSEW---DCMGVQPFHCGDPCCTTC 64  
Db 47 CPPFTFSIGQPNICNRV----CAGYFRKFKCSSTHNAECEIE-GFHLGLGQCITRC 101  
Qy 65 RHHPCPGGVQSGQKFSFGQICDASGTFSGGH-EGHCKPWTDTCTQFG 113  
Db 102 -EKDCRPGQLTKG-----CKTCSLGTENDQNGTGVCRPWTNCSLDG 143

RESULT 15  
US-08-477-347-17  
Sequence 17, Application US/08477347  
Patent No. 6232446  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BIGDA, Jacek  
APPLICANT: BELETSKY, Igor  
APPLICANT: METT, Igor  
TITLE OF INVENTION: TNF LIGANDS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.

;; COUNTRY: USA  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/477,347  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/115,685  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: IL 106271  
;; FILING DATE: 08-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Townsend, G. Kevin  
;; REGISTRATION NUMBER: 34,033  
;; REFERENCE/DOCKET NUMBER: WALLACH-10  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; TELEX: 248633  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 140 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-477-347-17

Query Match 19.5%; Score 139; DB 4; Length 140;  
Best Local Similarity 30.1%; Pred. No. 1.8e-05;  
Matches 34; Conservative 7; Mismatches 42; Indels 30; Gaps 5;  
Qy 31 RCRD-YPGEECCSEWD-----CMCVQPFHCG-----DPC--CTTCRHH----- 67  
Db 12 KCCRCQPGHGMVSRGCDHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNRHSGSELKQNC 71  
Qy 68 -----PCPPGOGVQSGKFSFGFCIDCASGTFSGHGHCKPWTDTCTQFG 113  
Db 72 PTEDTVCCQCRPGTQPRQDSSHKLGVDVCPGPGHFGSPGNOACKPWTNCTLSG 124

Search completed: September 4, 2001, 15:57:35  
Job time: 377 sec





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;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-974-022-51

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[illegible]

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RESULT 12
US-08-974-022-52
; Sequence 52, Application US/08974022
; Patent No. 6015938
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; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
;
; TITLE OF INVENTION: OSTEOPROTEGER
;
; NUMBER OF SEQUENCES: 53
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
;
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0
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; CURRENT APPLICATION DATA:
; FILING APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995

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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/577,788
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Winter, Robert B.
/ REFERENCE/DOCKET NUMBER: A-378
/ INFORMATION FOR SEQ ID NO: 52:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 191 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-574-022-52

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Query Match      19.7%  Score 140;  DB 3;  Length 191;
Best Local Similarity 32.7%;  Pred. No. 1.9e-05;
Matches 36;  Conservative 15;  Mismatches 41;  Indels 18;  Gaps 7;
QY 9 CGPGL-LLGTGTDARCRVHTTRCCRDYPGEECCSEW---DCMCVQPEHFCGDPCCCTC 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 47 CPSTFSSIGQPNCNICTRV---CAGYFRFKFCSTTHNAECIEI-GFICLGPQCTRC 101

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Qy 65 RHHPCPQGVSQGFSGGH-EGHCKPWTCTQFG 113  
 102 -EKDCRGGELTKQG-----CKTCSLGTFFNDQNGTGVCPRPWTNCSLDG 143

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RESULT 13
US-08-236-918A-6
; Sequence 6, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101

```

```

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,
, COMPUTER READABLE FORM:
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, MEDIUM TYPE: Floppy disk
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, COMPUTER: Apple Power Macintosh
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, OPERATING SYSTEM: Apple 7.5.3
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, SOFTWARE: Microsoft Word, Version #6.0.1
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, CURRENT APPLICATION DATA: US/08/236,918A
,
, APPLICATION NUMBER: US/08/236,918A
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, FILING DATE: 06-May-1994
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, CLASSIFICATION: 435
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, PRIOR APPLICATION DATA:
,
, APPLICATION NUMBER: US 08/060,843
,
, FILING DATE: 07-May-1993
,
, CLASSIFICATION: 435
,
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Anderson, Kathryn A.
,
, REGISTRATION NUMBER: 32,172
,
, REFERENCE/DOCKET NUMBER: 2801-B
,
, TELECOMMUNICATION INFORMATION:
,
, TELEPHONE: (206) 587-0430
,
, TELEFAX: (206) 233-0644
,
, INFORMATION FOR SEQ ID NO: 6:
,
, SEQUENCE CHARACTERISTICS:
,
, LENGTH: 256 amino acids
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, TYPE: amino acid
,
, TOPOLOGY: linear
,
, MOLECULE TYPE: protein
,
, US-08-236-918A-6

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Query Match 19.7%; Score 140; DB 1; Length 256;  
Best Local Similarity 32.7%; Pred. No. 2.4e-05;  
Matches 36: Conservative 15; Mismatches 41; Indels 18; Gaps 7;

QY	9	CGPRL-LLGTGTDACRCRVHTRCCRDYGECECCSEW----	DMCVQPEPHCGDPCCTTC	64
Db	47	CPPTFSSIGGQNCNCRV----	CAGYFRFKCSSTHNAECETC-GEFHCLGPOCTRC	101
QY	65	RHHPCPPGQVQSGKFSFGQICASGTFSGGH-EGHCKPWTDC	TFQ	113
Db	102	EKDCRGOELTKG-----	CKTSLGTFNDONGTGVCPRWTCNSLDG	143

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RESULT 14
PCT-US96-03965-2
; Sequence 2, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: KWON, Byoung Se
; APPLICANT: Kang, Chang-Yuul
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10

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; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-496-1200
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-911-423-7

Query Match 71.6%; Score 509; DB 3; Length 232;
Best Local Similarity 74.6%; Pred. No. 4.8e-37;
Matches 88; Conservative 5; Mismatches 17; Indels 8; Gaps 3;

QY 1 QRTGGGCGGPRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
Db 20 QRTGGGCGGPRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
QY 61 CTTCTRHHPCCPGQVQSGKFSFGQCI----DCASGTFSGGH-BGHCKPWTDCQFG 113
Db 80 CTTCTRHHPCCPGQVQSGK---SWRCLWESTQARGSTRARGRHRCPARTCGVWG 134

RESULT 5
US-08-911-423-2
; Sequence 2, Application US/08911423
; Patent No. 611090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-911-423-2

Query Match 52.5%; Score 373.5; DB 3; Length 228;
Best Local Similarity 53.7%; Pred. No. 2e-25;
Matches 58; Conservative 19; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCH 66
Db 27 PGCGPGRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCH 79
QY 67 HPCPPGQVQSGKFSFGQCIDCASGTFSGGHGEGHCKPWTDCQFGF 114
Db 80 YPCQPGRVESQGDIVFGFRVCACAMGTFSGRDRHCLRLWNTCSQFGF 127

RESULT 6
US-09-188-930-191
; Sequence 191, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 89
; TYPE: PRT
; ORGANISM: mouse
; US-09-188-930-191

Query Match 30.9%; Score 219.5; DB 4; Length 89;
Best Local Similarity 48.6%; Pred. No. 1.5e-12;
Matches 34; Conservative 13; Mismatches 16; Indels 7; Gaps 1;
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QY 7 PGCGPGRLLLTGTDAACRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCH 66
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GenCore version 4.5  
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OM protein - protein search, using sw model

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Searched: 197339 seqs, 20590346 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	228	3	US-08-911-423-6
2	711	100.0	241	3	US-08-911-423-4
3	711	100.0	311	3	US-08-911-423-8
4	509	71.6	232	3	US-08-911-423-7
5	373.5	52.5	228	3	US-08-911-423-2
6	219.5	30.9	89	4	US-08-188-930-191
7	147.5	20.7	206	1	US-08-097-827-7
8	147.5	20.7	206	1	US-08-494-574-7
9	147.5	20.7	438	1	US-08-097-827-11
10	147.5	20.7	438	1	US-08-494-574-11
11	141	19.8	205	3	US-08-974-022-51
12	140	19.7	191	3	US-08-974-022-52
13	140	19.7	256	1	US-08-236-918A-6
14	140	19.7	256	5	PCT-US96-03965-2
15	139	19.5	140	4	US-08-477-347-17
16	135.5	19.1	255	1	US-08-236-918A-8
17	135.5	19.1	255	2	US-08-816-605-9
18	135.5	19.1	255	5	PCT-US96-03965-8
19	129.5	18.2	139	2	US-08-219-237B-8
20	129.5	18.2	219	2	US-08-816-605-2
21	123.5	17.4	277	2	US-08-147-784-2
22	123.5	17.4	277	4	US-08-195-967-2
23	117	16.5	300	2	US-08-794-796-2
24	116.5	16.4	197	3	US-08-974-022-49
25	116.5	16.4	289	4	US-09-042-785A-11
26	108.5	15.3	276	4	US-09-041-886-27
27	108.5	15.3	277	4	US-09-042-785A-10

28	108	15.2	451	3	US-08-996-139-4	Sequence 4, Appli
29	108	15.2	451	4	US-08-995-659-4	Sequence 4, Appli
30	108	15.2	591	3	US-08-996-139-2	Sequence 2, Appli
31	108	15.2	591	4	US-08-995-659-2	Sequence 2, Appli
32	108	15.2	616	3	US-08-996-139-6	Sequence 6, Appli
33	108	15.2	616	4	US-08-995-659-6	Sequence 6, Appli
34	106	14.9	625	3	US-08-996-139-15	Sequence 15, Appl
35	106	14.9	625	4	US-08-995-659-15	Sequence 15, Appl
36	104.5	14.7	253	4	US-09-042-785A-4	Sequence 4, Appli
37	104.5	14.7	605	4	US-09-042-785A-23	Sequence 23, Appl
38	104.5	14.7	655	3	US-08-959-382-2	Sequence 2, Appli
39	102	14.3	401	3	US-08-974-022-2	Sequence 2, Appli
40	101	14.2	401	3	US-08-974-022-4	Sequence 4, Appli
41	101	14.2	401	4	US-09-042-785A-13	Sequence 13, Appl
42	99	13.9	401	3	US-08-974-022-6	Sequence 6, Appli
43	99	13.9	401	4	US-09-042-785A-12	Sequence 12, Appl
44	98.5	13.9	1345	2	US-08-977-767-3	Sequence 3, Appli
45	98	13.8	573	4	US-09-042-785A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-911-423-6

; Sequence 6, Application US/08911423

; Patent No. 6111090

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED

; TITLE OF INVENTION: REAGENTS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/911,423

; FILING DATE: 14-AUG-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/023,419

; FILING DATE: 16-AUG-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/027,901

; FILING DATE: 07-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0612K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9196

; TELEFAX: 650-496-1200

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-911-423-6

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Query Match      100.0%; Score 711; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.2e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 20 QRTGGPGCGPGRLLLTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
    |||

QY 61 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGF 114
    |||
DB 80 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGF 133
    |||

RESULT 2
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-4

Query Match      100.0%; Score 711; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
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DB 26 QRTGGPGCGPGRLLLTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 85
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QY 61 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGF 114
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DB 86 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGF 139
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RESULT 3
US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-8

Query Match      100.0%; Score 711; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.8e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
    |||
DB 20 QRTGGPGCGPGRLLLTGTDAACRVRHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79
    |||

QY 61 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGF 114
    |||
DB 80 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGF 133
    |||

RESULT 4
US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
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145 GNRHNAVCVF-----SPPA---EP 162  
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150 GTKERDVVCGPSADLSPGASSVTPPAPAREP 181

RESULT 15  
PCT-US96-03965-8  
; Sequence 8, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuil  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-1BB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KW05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-03965-8

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	Best Local Similarity	30.9%	Pred. No. 4.8e-07		
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Qy	85	CCTTCRHHPCPPGGVGSQSGFSGFCIDACASTGSGHEGCKPWTDCDTQGFGLTVFP	144		
Db	98	GCSMG-EGDCKQGQGLTKKG-----CKCCCFCTFNDRKGRICRPWTNCSLDGKSVLVN	149		
Qy	145	GNKTHNAVYVCPG-----SPPA---EP	162		
Db	150	GTKRDVYCGPSPADLSFGASSVTPAPARP	181		

Search completed: September 4, 2001, 15:57:37  
Job time: 379 sec

QY 100 VQSOGKFSFGFCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVFPNGKTHNAV 153  
Db 111 PRODSYKLGVDVCPGPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDVAV 164

## RESULT 9

US-08-097-827-11  
; Sequence 11, Application US/08097827  
; Patent No. 5457035  
; GENERAL INFORMATION:  
; APPLICANT: Baum, Peter  
; APPLICANT: Goodwin, Ray  
; APPLICANT: Fanslow, William  
; APPLICANT: Gayle, Richard  
; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for  
; TITLE OF INVENTION: OX40  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/097,827  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2806  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0730  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 438 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-097-827-11

Query Match 17.0%; Score 166.5; DB 1; Length 438;  
Best Local Similarity 28.7%; Pred. No. 2.4e-07;  
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;  
QY 26 QRTGGGCGGGRLLLG--TGTDAR--CCRVHT---TRCCRD--YPG---EECCSEWDC 72  
Db 6 QOQT-----ALLLLGLTGVARRLNCVKHTVPSGKCKKRECQCPGHGMVNRCDHTRDT 58  
QY 73 MCQVPEFHCGDPC-----CTTCRHHP-----CPPGQG 99  
Db 59 LC-----HPCETGYNEAVNYDTCKQCTCNHRSGSELKQNCPTQDVTVCRCRPGTQ 110  
QY 100 VQSOGKFSFGFCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVFPNGKTHNAV 153  
Db 111 PRODSYKLGVDVCPGPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDVAV 164

## RESULT 10

US-08-494-574-11  
; Sequence 11, Application US/08494574  
; Patent No. 5783665  
; GENERAL INFORMATION:  
; APPLICANT: Baum, Peter  
; APPLICANT: Goodwin, Ray  
; APPLICANT: Fanslow, William

; APPLICANT: Gayle, Richard  
; TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for  
; TITLE OF INVENTION: OX40  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/494,574  
; FILING DATE: 22-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/097,827  
; FILING DATE: 23-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2806  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0730  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 438 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-494-574-11

Query Match 17.0%; Score 166.5; DB 1; Length 438;  
Best Local Similarity 28.7%; Pred. No. 2.4e-07;  
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;  
QY 26 QRTGGGCGGGRLLLG--TGTDAR--CCRVHT---TRCCRD--YPG---EECCSEWDC 72  
Db 6 QOQT-----ALLLLGLTGVARRLNCVKHTVPSGKCKKRECQCPGHGMVNRCDHTRDT 58  
QY 73 MCQVPEFHCGDPC-----CTTCRHHP-----CPPGQG 99  
Db 59 LC-----HPCETGYNEAVNYDTCKQCTCNHRSGSELKQNCPTQDVTVCRCRPGTQ 110  
QY 100 VQSOGKFSFGFCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVFPNGKTHNAV 153  
Db 111 PRODSYKLGVDVCPGPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDVAV 164  
RESULT 11  
US-08-147-784-2  
; Sequence 2, Application US/08147784  
; Patent No. 5821332  
; GENERAL INFORMATION:  
; APPLICANT: Godfrey, Wayne  
; APPLICANT: Buck, David  
; APPLICANT: Engleman, Edgar G.  
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED  
; TITLE OF INVENTION: CD4+ T-CELLS: ACT-4  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,784
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-147-784-2

Query Match 16.5%; Score 162; DB 2; Length 277;
Best Local Similarity 29.7%; Pred. No. 3.8e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGLALCALSLG-----QRPTEGGCGPGRLLLGTTGTDARCRVHT 54
Db 4 GARRLGRGPCAALLLGLLGLSTVTGLHCYVDTPNSDRCCHECR--PGNGMVSRCRSQN 61
QY 55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
Db 62 TVCRPCGPGFYNDVSSKPCPKCTWNLRSRGSERKQLCTATQDTCRCRAGTQPLDSYKP 121
QY 109 GFQCIDCASGTFSGGHCGKPKWTCTQFGFLTVPFNKTHNAVCPGSPPA 160
Db 122 GVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPA 173

RESULT 12
US-08-195-967-2
; Sequence 2, Application US/08195967
; Patent No. 6242566
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-195-967-2

Query Match 16.5%; Score 162; DB 4; Length 277;
Best Local Similarity 29.7%; Pred. No. 3.8e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGLALCALSLG-----QRPTEGGCGPGRLLLGTTGTDARCRVHT 54
Db 4 GARRLGRGPCAALLLGLLGLSTVTGLHCYVDTPNSDRCCHECR--PGNGMVSRCRSQN 61
QY 55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
Db 62 TVCRPCGPGFYNDVSSKPCPKCTWNLRSRGSERKQLCTATQDTCRCRAGTQPLDSYKP 121
QY 109 GFQCIDCASGTFSGGHCGKPKWTCTQFGFLTVPFNKTHNAVCPGSPPA 160
Db 122 GVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPA 173

RESULT 13
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-236-918A-8
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Db 121 HCKPMTDCTQGFELTVFPGKTHNAVCPGSPPAEPLG 158

RESULT 4

US-08-911-423-7

; Sequence 7, Application US/08911423

; Patent No. 6111090

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED

; TITLE OF INVENTION: REAGENTS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/911,423

; FILING DATE: 14-AUG-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/023,419

; FILING DATE: 16-AUG-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/027,901

; FILING DATE: 07-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0612K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9196

; TELEFAX: 650-496-1200

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 232 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-911-423-7

Query Match 61.8%; Score 605; DB 3; Length 232;

Best Local Similarity 78.1%; Pred. No. 1.4e-45;

Matches 107; Conservative 5; Mismatches 17; Indels 8; Gaps 3;

QY 7 MGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66

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Db 1 MGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60

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QY 67 CSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQVQSGKFSFGQCI----DCASGTFSG 122

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Db 61 CSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQVQSGKFSFGQCI----SWRCLWESTQARGSTRAR 117

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QY 123 GH-EGHCKPMTDCTQFG 138

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Db 118 GRARGHRCPARTCGVWG 134

RESULT 5

US-08-911-423-2

; Sequence 2, Application US/08911423

; Patent No. 6111090

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED

; TITLE OF INVENTION: REAGENTS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/911,423

; FILING DATE: 14-AUG-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/023,419

; FILING DATE: 16-AUG-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/027,901

; FILING DATE: 07-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0612K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9196

; TELEFAX: 650-496-1200

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-911-423-2

Query Match 52.1%; Score 510; DB 3; Length 228;

Best Local Similarity 54.1%; Pred. No. 2.3e-37;

Matches 86; Conservative 25; Mismatches 40; Indels 8; Gaps 2;

QY 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65

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Db 1 MGAWAMLYGVSMCLVLDLQGPSVVVEEPCGPGKVGSGNNTRCCSLVA-----PKKE 53

|||||

QY 66 CSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQVQSGKFSFGQCI--DCASGTFSGHE 125

|||||

Db 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVRVESQGDIVFGPRVCACAMGTFSGARD 113

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QY 126 GHCKPMTDCTQFGELTVFPGKTHNAVCPGSPPAEPLG 164

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Db 114 GHCLWNTNCSQFGELTVFPGKTHNAVCIPEPLPTEQYG 152

RESULT 6

US-09-188-930-191

; Sequence 191, Application US/09188930A

; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene



```

; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 89
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-191

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Query Match	26.0%;	Score 255;	DB 4;	Length 89;
Best Local Similarity	46.3%;	Pred. No. 1.2e-15;		
Matches 44;	Conservative 17;	Mismatches 26;	Indels 8;	Gaps 2;

Qy	8	GAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLTGTDAKCCRVHTTRCCRDPYGEEC	66
		:::        :::  ::  :   ::  ::   :	
Db	1	GAWAMLYGVSMCLVLDLGQPSSVVVEEPPGCCGPKVGKQGSGNNTRCCSLYA-----PGKD	53
		:  :  ::      ::    :  :  :  :: :	

**Qy** 67 CSEWDCMCVQPEFHC G D P C T T C R H H P C P P G Q G V Q 10D  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Db** 54 CPKERCICVTPEYHCG D P OCKICKHYPCOPGORVE 88

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RESULT 7
US-08-097-827-7
; Sequence 7, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
; TITLE OF INVENTION: Ox40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-097-827-7

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Best Local Similarity	28.7%;	Pred. No. 1.2e-07;		

Matches	50;	Conservative	12;	Mismatches	51;	Indels	61;	Gaps
Qy	26	QRPTGPGCGPRLLLG---	TGTGAR---CCRVHT---	TRCCRD-YPG----	BECCSEWDC	72		
		I::I	IIII	II	II	III:	II	
Db	6	QQPT-----ALLLGLTLGV	TARRLNCVKHTYP	PSGHKCCRCPQHG	MVNRCDHTRDT	58		
Qy	73	MCVQPEFHCGDPC-----	CTTCRRHP-			-CPEGQG	99	
		II	II	II	II	II		
Db	59	LC-----HFCEYTGNEAVNY	DFCKOCTCNHRSSGSEL	KQNCTPTQTVCRCRPGQT	110			
Qy	100	VOSQGFSGFGCIDCASTF	GGHEGHCCKPWTDTQ	FGLVFPGNKTHNAV	C	153		
		II	II	IIIIII	II	IIII	II	
Db	111	PRODGSYKLGVDPVCP	PPCHGFSFGNNOACKPWNT	NCTLSGKTORHPASDS	LIDAVC	164		

RESULT 8  
 US-08-494-574-7  
 ; Sequence 7, Application US/08494574  
 ; Patent No. 5783665  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baum, Peter  
 ; APPLICANT: Goodwin, Ray  
 ; APPLICANT: Fanslow, William  
 ; APPLICANT: Gayle, Richard  
 ; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for  
 ; TITLE OF INVENTION: OX40  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/494,574  
 ; FILING DATE: 22-JUN-1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/097,827  
 ; FILING DATE: 23-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia A.  
 ; REGISTRATION NUMBER: 34,693  
 ; REFERENCE/DOCKET NUMBER: 2806  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-587-0730  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 206 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-494-574-7

Query Match	17.0%	Score 166.5	DB 1	Length 206
Best Local Similarity	28.7%	Pred. No. 1.2e-07		
Matches 50	Conservative 12	Mismatches 51	Indels 61	Gaps
Qy	26	ORPTGPGCGPGRLLLG	---TGTDA--CCRVHT---TRCCD-YPG-----EECCSEWDC	72
Db	6	QOQPT-----ALLLGLTLGVTARRLNCVKHTYPSGHKCCRECPHGHWNRCDHTRD	58	
Qy	73	MCVQPEEFHGDCPC	-----CTTCRHHP-----	99
Db	59	LC-----HCETGTFYNEAVNYDTCQCTOCNHRSGSELKQNCPTQDTCVCRPRGTH	11	

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:36 ; Search time 65.86 Seconds  
(without alignments)  
51.273 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_164  
Perfect score: 979  
Sequence: 1 MAOHGAMGAFRALGCLALLC.....GNKTHNAVCPGSPAEPLG 164

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	979	100.0	241	3 US-08-911-423-4	Sequence 4, Appli
2	947	96.7	228	3 US-08-911-423-6	Sequence 6, Appli
3	947	96.7	311	3 US-08-911-423-8	Sequence 8, Appli
4	605	61.8	232	3 US-08-911-423-7	Sequence 7, Appli
5	510	52.1	228	3 US-08-911-423-2	Sequence 2, Appli
6	255	26.0	89	4 US-09-188-930-191	Sequence 191, App
7	166.5	17.0	206	1 US-08-097-827-7	Sequence 7, Appli
8	166.5	17.0	206	1 US-08-494-574-7	Sequence 7, Appli
9	166.5	17.0	438	1 US-08-097-827-11	Sequence 11, Appl
10	166.5	17.0	438	1 US-08-494-574-11	Sequence 11, Appl
11	162	16.5	277	2 US-08-147-784-2	Sequence 2, Appli
12	162	16.5	277	4 US-08-195-967-2	Sequence 2, Appli
13	160.5	16.4	255	1 US-08-236-918A-8	Sequence 8, Appli
14	160.5	16.4	255	2 US-08-816-605-9	Sequence 9, Appli
15	160.5	16.4	255	5 PCT-US96-03965-8	Sequence 8, Appli
16	158.5	16.2	219	2 US-08-816-605-2	Sequence 2, Appli
17	153	15.6	191	3 US-08-974-022-52	Sequence 52, Appl
18	153	15.6	256	1 US-08-236-918A-6	Sequence 6, Appli
19	153	15.6	256	5 PCT-US96-03965-2	Sequence 2, Appli
20	153	15.6	300	2 US-08-794-796-2	Sequence 2, Appli
21	151	15.4	205	3 US-08-974-022-51	Sequence 51, Appl
22	149	15.2	140	4 US-08-477-347-17	Sequence 17, Appl
23	141.5	14.5	401	3 US-08-974-022-2	Sequence 2, Appli
24	139.5	14.2	139	2 US-08-219-237B-8	Sequence 8, Appli
25	139.5	14.2	401	3 US-08-974-022-4	Sequence 4, Appli
26	139.5	14.2	401	4 US-09-042-785A-13	Sequence 13, Appl
27	138.5	14.1	451	3 US-08-996-139-4	Sequence 4, Appli

Sequence 4, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
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Sequence 12, Appli  
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Sequence 11, Appli  
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Sequence 48, Appli  
Sequence 7, Appli  
Patent No. 5395760-2

28 138.5 14.1 451 4 US-08-995-659-4  
29 138.5 14.1 616 3 US-08-996-139-6  
30 138.5 14.1 616 4 US-08-995-659-6  
31 137 14.0 401 3 US-08-974-022-6  
32 137 14.0 401 4 US-09-042-785A-12  
33 135.5 13.8 197 3 US-08-974-022-49  
34 135.5 13.8 289 4 US-09-042-785A-11  
35 131 13.4 591 3 US-08-996-139-2  
36 131 13.4 591 4 US-08-995-659-2  
37 129.5 13.2 253 4 US-09-042-785A-4  
38 129.5 13.2 605 4 US-09-042-785A-23  
39 129.5 13.2 655 3 US-08-959-382-2  
40 123 12.6 625 3 US-08-996-139-15  
41 123 12.6 625 4 US-08-995-659-15  
42 121 12.4 197 2 US-08-505-606-1  
43 121 12.4 227 3 US-08-974-022-48  
44 121 12.4 461 4 US-09-042-785A-7  
45 119 12.2 461 6 5395760-2

ALIGNMENTS

RESULT 1  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0% Score 979; DB 3; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.7e-78;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGFALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 MAQHGMAGFALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164  
DB 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164

## RESULT 2

US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 611090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

Query Match 96.7%; Score 947; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.2e-75;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFRALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60

QY 67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTFSGGHEG 120  
QY 127 HCKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164  
DB 121 HCKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 158

## RESULT 3

US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 611090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 96.7%; Score 947; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 4.3e-75;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFRALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTFSGGHEG 120  
QY 127 HCKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164

	Query Match	20.4%	Score 150;	DB 2;	Length 277;
	Best Local Similarity	30.88;	Pred. No. 1.7e-06;		
	Matches 41;	Conservative 11;	Mismatches 53;	Indels 28;	Gaps 7;
Qy	11	RCCRD-YPG----	EECCSEWDCMC-	VQPFPH-----	CGDPC--CTTC-----
Db	41	RCCHCPGNGMVSRC	SRSQNTVTC	PCGPGFYNDV	SSKPKCTC
Qy	51	PGQ-----	GVQSCKKFFG	FGFCIDAC	STFGSGHGCKPMTDCTQ
Db	101	ATQDTVCRC	RAGTQPLDSY	KPGVNCAC	PCPCHESPGNGNOACKPMTNTCT

Qy	5	CRVHT-----TRCCRD-YPG-----EECSEWDCMCVQPEFHCGDPC-----40
Db	27	CVKHTPSGHGHCRCRCPGGHGMVNRCDDHTRDTLC-----HPCEGFYNEAVNYDTCK78

RESULT 15  
US-08-147-784-2  
: Sequence 2, Application US/08147784  
: Patent No. 5821332  
: GENERAL INFORMATION:  
: APPLICANT: Goodfrey, Wayne  
: APPLICANT: Buck, David  
: APPLICANT: Engleman, Edgar G.  
: TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED  
: TITLE OF INVENTION: CD4+ T-CELLS: ACT-4  
: NUMBER OF SEQUENCES: 2  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Townsend and Crew

Search completed: September 4, 2001, 15:57:35  
Job time: 377 sec

---

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03965  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,796  
FILING DATE: 16-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,269  
FILING DATE: 01-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,996  
FILING DATE: 30-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/267,577  
FILING DATE: 07-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A  
REGISTRATION NUMBER: 34,390  
REFERENCE/DOCKET NUMBER: KW05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-8

Query Match 21.6%; Score 159.5; DB 5; Length 255;

Best Local Similarity 31.9%; Pred. No. 2.3e-07;  
Matches 44; Conservative 12; Mismatches 43; Indels 39; Gaps 8;

QY 3 RCRVHTTRCCRDYPG-----EBCCS-----EWDCMCVQPEFHGDPCCCTTCRHHPCPPGQ 53  
Db 60 RYCDI-----CRCKGVFTRKCSSTSNAECDC---TPGFHCLGAGCSMC-EQDCKQGG 110  
QY 54 GVQSCKFSGFCIDCASGTGSGGHEGCKPWTCTQFGFLTVFPGNKTHNAVCPG-- 111  
Db 111 ELTKKG-----CKDCCGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPA 163  
QY 112 -----SPPA---EP 117  
Db 164 DLSPGASSVTPPAPAREP 181

RESULT 10  
US-08-816-605-2  
Sequence 2, Application US/08816605  
Patent No. 5874240  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Gentz, Reiner  
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,605  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-605-2

Query Match 21.5%; Score 158.5; DB 2; Length 219;  
Best Local Similarity 33.0%; Pred. No. 2.4e-07;  
Matches 38; Conservative 11; Mismatches 45; Indels 21; Gaps 5;

QY 13 CRDYPG-----EBCCS-----EWDCMCVQPEFHGDPCCCTTCRHHPCPPGQVSGKFS 62  
Db 28 CSNCPAGVFRTRKCSSTSNAECDC---TPGFHCLGAGCSMC-EQDCKQGGELTKKG--- 80  
QY 63 FGQCIDCASGTGSGGHEGCKPWTCTQFGFLTVFPGNKTHNAVCPGSPAP 117  
Db 81 ----CKDCCGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSADLSP 131

RESULT 11

US-08-097-827-7  
Sequence 7, Application US/08097827  
Patent No. 5457035

GENERAL INFORMATION:  
APPLICANT: Baum, Peter  
APPLICANT: Goodwin, Ray  
APPLICANT: Fanslow, William  
APPLICANT: Gayle, Richard  
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for  
TITLE OF INVENTION: OX40  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,827  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2806  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 206 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-097-827-7

Query Match 21.4%; Score 158; DB 1; Length 206;  
Best Local Similarity 27.4%; Pred. No. 2.5e-07;  
Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;

QY 5 CRVHT-----TRCCRD-YPG-----ECCSEWDCMCVQPFHCGDPC----- 40  
DB 27 CVKHTYPSGHKCCRECQPGHGMVNRCDHTRDTLC-----HPCETGYNEAVNYDTCK 78

QY 41 -CTTCRRHP-----CPPGQGVQSGKFSFGFCIDCASGTFSGGHEGH 82  
DB 79 QCTOCNHRSGSELKQNCPTQDVTVCRCRGTQPRQDSGYKLGVDVCPCPPGHFSPGNNOA 138

QY 83 CKPWTDCQTFQGLTVFPGNKTHNAV 108  
DB 139 CKPWTNCTLSGKQTRHPASDSLDAVC 164

## RESULT 12

US-08-494-574-7

; Sequence 7, Application US/08494574

; Patent No. 5783665

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; APPLICANT: Goodwin, Ray

; APPLICANT: Fanslow, William

; APPLICANT: Gayle, Richard

; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/494,574

; FILING DATE: 22-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/097,827

; FILING DATE: 23-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2806

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-0730

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 206 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-494-574-7

Query Match 21.4%; Score 158; DB 1; Length 206;  
Best Local Similarity 27.4%; Pred. No. 2.5e-07;  
Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;

QY 5 CRVHT-----TRCCRD-YPG-----ECCSEWDCMCVQPFHCGDPC----- 40  
DB 27 CVKHTYPSGHKCCRECQPGHGMVNRCDHTRDTLC-----HPCETGYNEAVNYDTCK 78

QY 41 -CTTCRRHP-----CPPGQGVQSGKFSFGFCIDCASGTFSGGHEGH 82  
DB 79 QCTOCNHRSGSELKQNCPTQDVTVCRCRGTQPRQDSGYKLGVDVCPCPPGHFSPGNNOA 138  
QY 83 CKPWTDCQTFQGLTVFPGNKTHNAV 108  
DB 139 CAPWTNCTLSGKQTRHPASDSLDAVC 164

## RESULT 13

US-08-097-827-11

; Sequence 11, Application US/08097827

; Patent No. 5457035

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; APPLICANT: Goodwin, Ray

; APPLICANT: Fanslow, William

; APPLICANT: Gayle, Richard

; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/097,827

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2806

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-0730

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 438 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-097-827-11

Query Match 21.4%; Score 158; DB 1; Length 438;  
Best Local Similarity 27.4%; Pred. No. 5.1e-07;  
Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;

QY 5 CRVHT-----TRCCRD-YPG-----ECCSEWDCMCVQPFHCGDPC----- 40  
DB 27 CVKHTYPSGHKCCRECQPGHGMVNRCDHTRDTLC-----HPCETGYNEAVNYDTCK 78

QY 41 -CTTCRRHP-----CPPGQGVQSGKFSFGFCIDCASGTFSGGHEGH 82  
DB 79 QCTOCNHRSGSELKQNCPTQDVTVCRCRGTQPRQDSGYKLGVDVCPCPPGHFSPGNNOA 138

QY 83 CKPWTDCQTFQGLTVFPGNKTHNAV 108

DB 139 CKPWTNCTLSGKQTRHPASDSLDAVC 164

## RESULT 14

US-08-494-574-11

; Sequence 11, Application US/08494574

```

; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-2

Query Match 57.7%; Score 425.5; DB 3; Length 228;
Best Local Similarity 61.1%; Pred. No. 5.1e-31;
Matches 69; Conservative 16; Mismatches 27; Indels 1; Gaps 1;

QY 8 HTTRCCRDY-PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGCGVQSQGKFEFGQ 66
DB 40 NNTCCSLYAPCKEDGPKERCICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFR 99
QY 67 CIDCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTNAVCVPGSPAPPLG 119
DB 100 CVACAMGTESAGRDGHCRLWTNCSQFGFLTVPFGNKTNAVCIPLEPLTEQYG 152

RESULT 5
US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-7

Query Match 53.6%; Score 395; DB 3; Length 232;
Best Local Similarity 69.4%; Pred. No. 2.6e-28;
Matches 68; Conservative 5; Mismatches 17; Indels 8; Gaps 3;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGK 60
DB 40 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGK 99
QY 61 FSFGFQCI----DCASGTFSGGH-EGHCKPWTCTQFG 93
DB 100 ---SWRCLWESTQARGSTRARGRARGHRCPARTCGVWG 134

RESULT 6
US-09-188-930-191
; Sequence 191, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 89
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-191

Query Match 23.8%; Score 175.5; DB 4; Length 89;
Best Local Similarity 56.0%; Pred. No. 3.3e-09;
Matches 28; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 8 HTTRCCRDY-PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQ 56

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Db 39 NNTRCCSLYAPGKEDCPKERCICVTPEYHCGDPPQCKICKHYPCQPQRVE 88

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RESULT 7
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-LBB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA: US/08/236,918A
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-236-918A-8

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Query Match	21.6%	Score 159.5	DB 1	Length 255
Best Local Similarity	31.9%	Pred. No. 2.3e-07		
Matches	44	Conservative	12	Mismatches 43
			Indels	39
			Gaps	
				8;
Qy	3	RCRRVHTTRCRDYPG-----EECCS----	EWDCMCVQPEFHCGDPCTTCRHHPCP	PGQ 53
Db	60	RTCDI-----CRQCKGVFRTRKCSSTNAECDC--	TPGFHCLGAGCSMC-EQDCKQGQ	110
Qy	54	GVQSGHFSFGFCQIDCASGTFSGGHGHCXKPTWDC	TQFGFLTVPFGNKTINAVCPG	-- 111
Db	111	ELTKKG-----CKDCCFGTFNDQKRGICRPWNC	SLDGKSVLVNGTKERDVVCGPSPA	163
Qy	112	-----SPPA---EP	117	
Db	164	DLSPGASSVTPPPAPAREP	181	

RESULT 8  
US-08-816-605-9  
; Sequence 9, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: NI, Jian

APPLICANT: Yu, Guo-Liang  
 APPLICANT: Gentz, Reiner  
 TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/816,605  
 FILING DATE: 13-MAR-1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36,373  
 REFERENCE/DOCKET NUMBER: PF254  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-309-8504  
 TELEFAX: 301-309-8512  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 255 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-816-605-9

Query Match	21.6%	Score 159.5;	DB 2;	Length 255;
Best Local Similarity	31.9%	Pred. No. 2.3e-07;		
Matches	44;	Conservative 12;	Mismatches 43;	Indels 39;
Gaps	8;			

  

QY	3	RCCRHHTRCCRDYDG----	EECCS----	EWDCMCVQPEFHCGDPCTTCRHHCPPGQ	53
DB	60	RYCDI-----	CRQKGVFTRKECSTNAECDC---	TPGFHCLGAGCSMC--EQDCKGQ	110
QY	54	GVQSGCKFSFGQCIDCASGTFSGGHEGHCCKPWTBCTGFLTVPFGKNTHNACVPG--	111		
DB	111	ELTKG-----	CKDCGFGFNDKRGICRPWTNCSLDGKSVLNGTKERDVVCGPSA	163	
QY	112	-----	SPPA-----	EP	117
DB	164	DLSPGASSVTTPAPAPREP	181		

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RESULT          9
PCT-US96-03965-8
; Sequence 8, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; APPLICANT: Kang, Chang-Yuil
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:35 ; Search time 65.86 Seconds  
(without alignments)  
37.204 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DACCRRVHTTRCCRDYPGEE.....GNKTHNAVCPGSPAPPLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
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- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	737	100.0	228	3	US-08-911-423-6
2	737	100.0	241	3	US-08-911-423-4
3	737	100.0	311	3	US-08-911-423-8
4	425.5	57.7	228	3	US-08-911-423-2
5	395	53.6	232	3	US-08-911-423-7
6	175.5	23.8	89	4	US-09-188-930-191
7	159.5	21.6	255	1	US-08-236-918A-8
8	159.5	21.6	255	2	US-08-816-605-9
9	159.5	21.6	255	5	PCT-US96-03965-8
10	158.5	21.5	219	2	US-08-816-605-2
11	158	21.4	206	1	US-08-097-827-7
12	158	21.4	206	1	US-08-494-574-7
13	158	21.4	438	1	US-08-097-827-11
14	158	21.4	438	1	US-08-494-574-11
15	150	20.4	277	2	US-08-147-784-2
16	150	20.4	277	4	US-08-195-967-2
17	149.5	20.3	191	3	US-08-974-022-52
18	149.5	20.3	256	1	US-08-236-918A-6
19	149.5	20.3	256	5	PCT-US96-03965-2
20	149	20.2	140	4	US-08-477-347-17
21	149	20.2	205	3	US-08-974-022-51
22	145	19.7	300	2	US-08-794-796-2
23	139.5	18.9	139	2	US-08-219-237B-8
24	137	18.6	401	3	US-08-974-022-6
25	137	18.6	401	4	US-09-042-785A-12
26	131	17.8	401	3	US-08-974-022-4
27	131	17.8	401	4	US-09-042-785A-13

28	131	17.8	451	3	US-08-996-139-4	Sequence 4, Appl
29	131	17.8	451	4	US-08-995-659-4	Sequence 4, Appl
30	131	17.8	591	3	US-08-996-139-2	Sequence 2, Appl
31	131	17.8	591	4	US-08-995-659-2	Sequence 2, Appl
32	131	17.8	616	3	US-08-996-139-6	Sequence 6, Appl
33	131	17.8	616	4	US-08-995-659-6	Sequence 6, Appl
34	130.5	17.7	401	3	US-08-974-022-2	Sequence 2, Appl
35	128	17.4	253	4	US-09-042-785A-4	Sequence 4, Appl
36	128	17.4	605	4	US-09-042-785A-23	Sequence 23, Appl
37	128	17.4	655	3	US-08-959-382-2	Sequence 2, Appl
38	123	16.7	197	3	US-08-974-022-49	Sequence 49, Appl
39	123	16.7	289	4	US-09-042-785A-11	Sequence 11, Appl
40	123	16.7	625	3	US-08-996-139-15	Sequence 15, Appl
41	123	16.7	625	4	US-08-995-659-15	Sequence 15, Appl
42	119	16.1	227	3	US-08-974-022-48	Sequence 48, Appl
43	119	16.1	461	4	US-09-042-785A-7	Sequence 7, Appl
44	119	16.1	474	2	US-08-650-000-4	Sequence 4, Appl
45	119	16.1	474	5	5395760-4	Patent No. 5395760

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

11

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:35 ; Search time 65.86 Seconds  
(without alignments)  
38.142 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_154

Perfect score: 753

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	228	3	US-08-911-423-6
2	753	100.0	241	3	US-08-911-423-4
3	753	100.0	311	3	US-08-911-423-8
4	468	62.2	232	3	US-08-911-423-7
5	445.5	59.2	228	3	US-08-911-423-2
6	212.5	28.2	89	4	US-09-188-930-191
7	164	21.8	206	1	US-08-097-827-7
8	164	21.8	206	1	US-08-494-574-7
9	164	21.8	438	1	US-08-097-827-11
10	164	21.8	438	1	US-08-494-574-11
11	152.5	20.3	255	1	US-08-236-918A-8
12	152.5	20.3	255	2	US-08-816-605-9
13	152.5	20.3	255	5	PCT-US96-03965-8
14	149.5	19.9	205	3	US-08-974-022-51
15	149	19.8	140	4	US-08-477-347-17
16	149	19.8	191	3	US-08-974-022-52
17	149	19.8	256	1	US-08-236-918A-6
18	149	19.8	256	5	PCT-US96-03965-2
19	146.5	19.5	219	2	US-08-816-605-2
20	145.5	19.3	277	2	US-08-147-784-2
21	145.5	19.3	277	4	US-08-195-967-2
22	145	19.3	300	2	US-08-794-796-2
23	140	18.6	401	3	US-08-974-022-2
24	139.5	18.5	139	2	US-08-219-237B-8
25	139	18.5	401	3	US-08-974-022-4
26	139	18.5	401	4	US-09-042-785A-13
27	133	17.7	401	3	US-08-974-022-6

28 133 17.7 401 4 US-09-042-785A-12 Sequence 12, Appl  
29 128.5 17.1 253 4 US-09-042-785A-4 Sequence 4, Appl  
30 128.5 17.1 605 4 US-09-042-785A-23 Sequence 23, Appl  
31 128.5 17.1 655 3 US-08-959-382-2 Sequence 2, Appl  
32 127.5 16.9 197 3 US-08-974-022-49 Sequence 49, Appl  
33 127.5 16.9 289 4 US-09-042-785A-11 Sequence 11, Appl  
34 121 16.1 451 3 US-08-996-139-4 Sequence 4, Appl  
35 121 16.1 451 4 US-08-995-659-4 Sequence 4, Appl  
36 121 16.1 591 3 US-08-996-139-2 Sequence 2, Appl  
37 121 16.1 591 4 US-08-995-659-2 Sequence 2, Appl  
38 121 16.1 616 3 US-08-996-139-6 Sequence 6, Appl  
39 121 16.1 616 4 US-08-995-659-6 Sequence 6, Appl  
40 121 16.1 625 3 US-08-996-139-15 Sequence 15, Appl  
41 121 16.1 625 4 US-08-995-659-15 Sequence 15, Appl  
42 117 15.5 573 4 US-09-042-785A-2 Sequence 2, Appl  
43 114.5 15.2 276 4 US-09-041-886-27 Sequence 27, Appl  
44 114.5 15.2 277 4 US-09-042-785A-10 Sequence 10, Appl  
45 113 15.0 227 3 US-08-974-022-48 Sequence 48, Appl

#### ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

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QY 121 CV 122  
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RESULT 2  
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; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

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Best Local Similarity 100.0%; Pred. No. 6.3e-60;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCCKPWTCTQFGFLTVPFGNKTHNAV 120  
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QY 121 CV 122  
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Db 153 CV 154  
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RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

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Best Local Similarity 100.0%; Pred. No. 7.9e-60;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 27 GCGPGRLLLTGTGDARCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRHH 86  
|||||

QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCCKPWTCTQFGFLTVPFGNKTHNAV 120  
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Db 87 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCCKPWTCTQFGFLTVPFGNKTHNAV 146  
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QY 121 CV 122

SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-8

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Best Local Similarity 31.8%; Pred. No. 9.6e-07;  
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QY 53 CTTTCHRHPCPGQVQSGKFSFGQICDASGTSGGHGHCKPWTCTQFGFLTVFP 112  
Db 98 GCSMC-EQDCKQGOELTKG-----CKDCGFTFNDQKRGICRPWTNCSLDGKSVLNV 149  
QY 113 GNKTHNAV 121  
Db 150 GYKRDVVC 158

RESULT 14  
US-08-974-022-51  
Sequence 51, Application US/08974022  
Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Behavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-51

Query Match 19.9%; Score 149.5; DB 3; Length 205;  
Best Local Similarity 28.9%; Pred. No. 1.5e-06;  
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Db 12 LLLGLSLGVTVKLNCVADTYPGSHKCCRCQPGHGMVSRCDHTRDTVCHPCPEPGFYNEAV 71  
QY 51 --DPC--CTTCRHH-----PCPPGQVQSGKFSFGQICDASGTSFS 89  
Db 72 NYDTCKQCTQCNRHSGSELKQNCPTFTEDTVCCQRPQTQPRODSSHKLGVDVCPGPGHFS 131  
QY 90 GGHEGCHKPWTCTQFGFLTVFPGNKTHNAV 121  
Db 132 PGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163  
RESULT 15  
US-08-477-347-17  
Sequence 17, Application US/08477347  
Patent No. 6232446  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BIGDA, Jakek  
APPLICANT: BELETSKY, Igor  
APPLICANT: METT, Igor  
TITLE OF INVENTION: TNF LIGANDS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,347  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/115,685  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106271  
FILING DATE: 08-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, G. Kevin  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: WALLACH-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-347-17

Query Match 19.8%; Score 149; DB 4; Length 140;  
Best Local Similarity 28.9%; Pred. No. 1.1e-06;  
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Db 132 SNSLDTV 139

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RESULT 9
US-08-097-827-11
; Sequence 11, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-097-827-11

Query Match 21.8%; Score 164; DB 1; Length 438;
Best Local Similarity 29.2%; Pred. No. 1.5e-07;
Matches 47; Conservative 11; Mismatches 49; Indels 54; Gaps 8;

Qy 7 LLLG--TGTAR--CCRVHT---TRCCRD--YPG---EECCSEWDCMCVQPEFHCGDPC 53
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Db 12 LLLGLTGVTAARRLNCVKHTYPSGHKCCRCQPGHGMVNRCDHTRDTLC-----HPC 63

Qy 54 -----CTTCRHHP-----CPPGGVQSGKFSFGFC 80
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Db 64 ETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTQDTVCRCPGTQPRQDSGYKLGVC 123

Qy 81 IDCASGTFSGHGHCKPWTCTQFGFLTVFPNGKTHNAV 121
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Db 124 VPCPPGHFSPGNNAQKPNWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 10
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
```

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

Query Match 21.8%; Score 164; DB 1; Length 438;
Best Local Similarity 29.2%; Pred. No. 1.5e-07;
Matches 47; Conservative 11; Mismatches 49; Indels 54; Gaps 8;

Qy 7 LLLG--TGTAR--CCRVHT---TRCCRD--YPG---EECCSEWDCMCVQPEFHCGDPC 53
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 LLLGLTGVTAARRLNCVKHTYPSGHKCCRCQPGHGMVNRCDHTRDTLC-----HPC 63

Qy 54 -----CTTCRHHP-----CPPGGVQSGKFSFGFC 80
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Db 64 ETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTQDTVCRCPGTQPRQDSGYKLGVC 123

Qy 81 IDCASGTFSGHGHCKPWTCTQFGFLTVFPNGKTHNAV 121
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Db 124 VPCPPGHFSPGNNAQKPNWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 11
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/236,918A  
;; FILING DATE: 06-May-1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/060,843  
;; FILING DATE: 07-May-1993  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Anderson, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2801-B  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 587-0430  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 255 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-236-918A-8

Query Match 20.3%; Score 152.5; DB 1; Length 255;  
Best Local Similarity 31.8%; Pred. No. 9.6e-07;  
Matches 41; Conservative 11; Mismatches 50; Indels 27; Gaps 7;

QY 2 CGPGRLLLGTTDARCCRVHTTRCCRDYPG-----EECCS----EWDCCMCVQPEFHCGDP 52  
DB 48 CPNPSFSSAGG--QRTCDI-----CROCKGVTRTRKECSSTNSAECDC---TPGFHCLGA 97  
QY 53 CQTCRHHPPGPGQVQSGKFSFGFCIDCASGTFSGHGHGCKPWTDCQFGFLTVP 112  
DB 98 GCSMC-EQDCKQOGLTKKG-----CKDCCFGTFNDQKRGICRPWTNCSLDGKSLVN 149  
QY 113 GNKTHNAV 121  
DB 150 GTKERDVVC 158

RESULT 12  
US-08-816-605-9  
; Sequence 9.6 Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,605  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504

;; TELEFAX: 301-309-8512  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 255 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-816-605-9  
  
Query Match 20.3%; Score 152.5; DB 2; Length 255;  
Best Local Similarity 31.8%; Pred. No. 9.6e-07;  
Matches 41; Conservative 11; Mismatches 50; Indels 27; Gaps 7;  
  
QY 2 CGPGRLLLGTTDARCCRVHTTRCCRDYPG-----EECCS----EWDCCMCVQPEFHCGDP 52  
DB 48 CPNPSFSSAGG--QRTCDI-----CROCKGVTRTRKECSSTNSAECDC---TPGFHCLGA 97  
QY 53 CQTCRHHPPGPGQVQSGKFSFGFCIDCASGTFSGHGHGCKPWTDCQFGFLTVP 112  
DB 98 GCSMC-EQDCKQOGLTKKG-----CKDCCFGTFNDQKRGICRPWTNCSLDGKSLVN 149  
QY 113 GNKTHNAV 121  
DB 150 GTKERDVVC 158  
  
RESULT 13  
PCT-US96-03965-8  
; Sequence 8, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yul  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-IBB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KWO5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 8:



Query Match 21.8%; Score 164; DB 1; Length 206;  
Best Local Similarity 29.2%; pred. No. 7.6e-08;  
Matches 47; Conservative 11; Mismatches 49; Indels 54; Gaps 8;

QY 7 LLLG--TGTDAAR--CCRVHT-----TRCCRD-YPG-----EECCSESDMCVQPEFHCGDPC 53  
||||| |||| | |||| : |||| || | : |  
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Query Match	21.8%	Score 164;	DB 1;	Length 206;
Best Local Similarity	29.2%	Pred. No. 7.6e-08;		
Matches	47;	Conservative 11;	Mismatches 49;	Indels 54; Gaps 8;
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Qy	54	-----CPTCRHHP-----CPCQGVQSGCKFSGFQC	80	
Db	64	ETGYNEAVNYDTCKQCTQCNRHSGSELKQNCPTQDVTVCRCRPGTQPRQDSGYKLGVD	123	
Qy	81	IDCAGSTFSGHGEGHCKPWTCTQTFGLTVFPGNKTHNAV	121	
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Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGTCRCRVTHTTCRCRDYPGEECCSEWDCM 41
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Db 27 GCGPGRLLLTGTGTCRCRVTHTTCRCRDYPGEECCSEWDCM 67

RESULT 2
US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-496-1200
; TELEFAX: 650-852-9196
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-7

Query Match      100.0%; Score 255; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGTCRCRVTHTTCRCRDYPGEECCSEWDCM 41
      |||||
Db 27 GCGPGRLLLTGTGTCRCRVTHTTCRCRDYPGEECCSEWDCM 67

RESULT 3
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-08-911-423-4

Query Match      100.0%; Score 255; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGTCRCRVTHTTCRCRDYPGEECCSEWDCM 41
      |||||
Db 33 GCGPGRLLLTGTGTCRCRVTHTTCRCRDYPGEECCSEWDCM 73

RESULT 4
US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-08-911-423-8
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:35 ; Search time 65.86 Seconds  
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12.818 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_73

Perfect score: 255

Sequence: 1 GCGFGRLLLTGTGDARCRV.....TTCCRDYVGECCSEDCM 41

Scoring table: BLOSUM62

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Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

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- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	255	100.0	232	3	US-08-911-423-7
3	255	100.0	241	3	US-08-911-423-4
4	255	100.0	311	3	US-08-911-423-8
5	87.5	34.3	89	4	US-09-188-930-191
6	87.5	34.3	228	3	US-08-911-423-2
7	64.5	25.3	788	2	US-08-918-914-4
8	64	25.1	109	2	US-08-527-044-2
9	64	25.1	109	3	US-09-013-780-2
10	64	25.1	443	4	US-08-821-994-65
11	64	25.1	801	1	US-07-906-349A-6
12	61.5	24.1	434	2	US-08-815-718-3
13	61.5	24.1	559	2	US-08-884-072-6
14	58.5	22.9	430	3	US-08-997-897-2
15	58.5	22.9	430	4	US-09-156-836B-2
16	56.5	22.2	263	1	US-07-927-071-2
17	56.5	22.2	1063	1	US-08-093-453B-3
18	56.5	22.2	1063	1	US-08-127-499A-8
19	56.5	22.2	1063	1	US-08-482-847-8
20	55.5	21.8	94	3	US-08-851-843A-215
21	55.5	21.8	94	4	US-08-974-549A-334
22	55.5	21.8	323	4	US-08-878-474-7
23	55.5	21.8	4544	1	US-08-469-486-52
24	55.5	21.8	4544	2	US-08-469-658-52
25	55	21.6	143	4	US-08-990-823-112
26	55	21.6	861	1	US-08-346-455B-67
27	55	21.6	861	3	US-08-977-221-67

28	55	21.6	861	5	PCT-US95-06613-67	Sequence 67, Appl
29	55	21.6	915	1	US-08-346-455B-69	Sequence 69, Appl
30	55	21.6	915	3	US-08-977-221-69	Sequence 69, Appl
31	55	21.6	915	5	PCT-US95-06613-69	Sequence 69, Appl
32	55	21.6	979	1	US-08-346-455B-38	Sequence 38, Appl
33	55	21.6	979	3	US-08-977-221-38	Sequence 38, Appl
34	55	21.6	979	5	PCT-US95-06613-38	Sequence 38, Appl
35	54.5	21.4	1345	2	US-08-977-767-3	Sequence 3, Appl
36	54	21.2	359	3	US-08-586-165-4	Sequence 4, Appl
37	52.5	20.6	87	2	US-08-465-380-44	Sequence 44, Appl
38	52.5	20.6	87	2	US-08-486-397-44	Sequence 44, Appl
39	52.5	20.6	87	2	US-08-486-399-44	Sequence 44, Appl
40	52.5	20.6	87	2	US-08-461-965-44	Sequence 44, Appl
41	52.5	20.6	87	2	US-08-634-641-44	Sequence 44, Appl
42	52.5	20.6	87	3	US-09-249-471-44	Sequence 44, Appl
43	52.5	20.6	87	3	US-09-249-472-44	Sequence 44, Appl
44	52.5	20.6	87	3	US-09-249-451-44	Sequence 44, Appl
45	52.5	20.6	87	3	US-08-809-455-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chang, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6



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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-8
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Query Match 100.0%; Score 255; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 4.7e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GCGPGRLLLTGTDAACCRVHTTCCRDYDGECCSEWDCM 41
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DB 27 GCGPGRLLLTGTDAACCRVHTTCCRDYDGECCSEWDCM 67
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## RESULT 5

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US-09-188-930-191
; Sequence 191, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 89
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-191
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Query Match 34.3%; Score 87.5; DB 4; Length 89;
Best Local Similarity 36.6%; Pred. No. 0.0034;
Matches 15; Conservative 9; Mismatches 10; Indels 7; Gaps 1;
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QY 1 GCGPGRLLLTGTDAACCRVHTTCCRDYDGECCSEWDCM 41
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DB 27 GCGPGKVGQSGNTRCCSLYA-----PGKEDCPKRCI 60
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## RESULT 6

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US-08-911-423-2
; Sequence 2, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlocnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-2
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Query Match 34.3%; Score 87.5; DB 3; Length 228;
Best Local Similarity 36.6%; Pred. No. 0.0078;
Matches 15; Conservative 9; Mismatches 10; Indels 7; Gaps 1;
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QY 1 GCGPGRLLLTGTDAACCRVHTTCCRDYDGECCSEWDCM 41
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DB 28 GCGPGKVGQSGNTRCCSLYA-----PGKEDCPKRCI 61
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## RESULT 7

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US-08-918-914-4
; Sequence 4, Application US/08918914
; Patent No. 5876963
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Peter
; APPLICANT: Hutchinson, Nancy
; APPLICANT: Lawton, Michael
; APPLICANT: Magna, Holly
; APPLICANT: Yocum, Sue
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHORYLASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
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; Sequence 65, Application US/08821994A  
; Patent No. 6228643  
; GENERAL INFORMATION:  
; APPLICANT: Greenland, Andrew J  
; APPLICANT: Thomas, Didier RP  
; APPLICANT: Jepson, Ian  
; TITLE OF INVENTION: Promoters  
; FILE REFERENCE: PPD 50108  
; CURRENT APPLICATION NUMBER: US/08/821,994A  
; CURRENT FILING DATE: 1997-03-22  
; EARLIER APPLICATION NUMBER: PCT/GB97/00729  
; EARLIER FILING DATE: 1997-03-18  
; EARLIER APPLICATION NUMBER: GB 9606062.9  
; EARLIER FILING DATE: 1996-03-22  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 65  
; LENGTH: 443  
; TYPE: PRT  
; ORGANISM: Brassica napus  
US-08-821-994-65

Query Match 25.1%; Score 64; DB 4; Length 443;  
Best Local Similarity 35.3%; Pred. No. 5.2;  
Matches 12; Conservative 4; Mismatches 16; Indels 2; Gaps 1;  
QY 2 CGPGRLLGTGTGTCARCCRVHTTCCRDYPGECC 35  
DB 368 CCCARNLFLCFSWKCCLESASVCKD--GRHCC 399

RESULT 11  
US-07-906-349A-6  
; Sequence 6, Application US/07906349A  
; Patent No. 5434064  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Skolnik, Edward Y.  
; APPLICANT: Margolis, Benjamin L.  
; TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR  
; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AND  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/906,349A  
; FILING DATE: 30-JUN-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/643,237  
; FILING DATE: 18-JAN-1991  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-638-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 801 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-07-906-349A-6

Query Match 25.1%; Score 64; DB 1; Length 801;  
Best Local Similarity 37.1%; Pred. No. 8.8;  
Matches 13; Conservative 1; Mismatches 21; Indels 0; Gaps 0;  
QY 2 CGPGRLLGTGTGTCARCCRVHTTCCRDYPGECCS 36  
DB 326 CACGTCCTGTGTGGCGCGGTACCCCTGTGACCT 360

RESULT 12  
US-08-815-718-3  
; Sequence 3, Application US/08815718  
; Patent No. 5981220  
; GENERAL INFORMATION:  
; APPLICANT: NI, JIAN  
; APPLICANT: FENG, PING  
; APPLICANT: DILLON, PATRICK  
; APPLICANT: GENTZ, REINER  
; TITLE OF INVENTION: EPIDERMAL DIFFERENTIATION FACTOR  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
; ADDRESSEE: STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07069  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,718  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201) 994-1700  
; TELEFAX: (201) 994-1744  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 434 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-815-718-3

Query Match 24.1%; Score 61.5; DB 2; Length 434;  
Best Local Similarity 37.8%; Pred. No. 9.6;  
Matches 14; Conservative 3; Mismatches 19; Indels 1; Gaps 1;  
QY 2 CGPGRLLGTGTGTCARCCRVHTTCCRDYPGECCSE 37  
DB 320 CGSGRVLKHKQIPGLIQNTVRCCLPYPQACCGE 356

RESULT 13  
US-08-884-072-6  
; Sequence 6, Application US/08884072  
; Patent No. 5872234  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.



FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (421)  
US-08-997-897-2

Query Match 22.9%; Score 58.5; DB 3; Length 430;  
Best Local Similarity 40.0%; Pred. No. 20;  
Matches 10; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Qy 17 CCRVHTTRCCRDYPGEECCSEWDCM 41  
||| |||| || | :  
Db 200 CCRWTRTCC-----CCRCWQSL 217

RESULT 15  
US-09-156-836B-2  
Sequence 2, Application US/09156836B  
Patent No. 6242585  
GENERAL INFORMATION:  
APPLICANT: Srivastava, Ranjana  
APPLICANT: Kumar, Deepak  
APPLICANT: Srivastava, Brahm Shanker  
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT  
FILE REFERENCE: U 011876-4  
CURRENT APPLICATION NUMBER: US/09/156,836B  
CURRENT FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 08/997,897  
PRIOR FILING DATE: 1997-12-24  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2

LENGTH: 430  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (4)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (6)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (20)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (29)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (54)  
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NAME/KEY: UNSURE  
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OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
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OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE

LOCATION: (159)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (169)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
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OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
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NAME/KEY: UNSURE  
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NAME/KEY: UNSURE  
LOCATION: (366)  
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NAME/KEY: UNSURE  
LOCATION: (410)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (421)  
OTHER INFORMATION: amino acid has not been identified  
US-09-156-836B-2

Query Match 22.9%; Score 58.5; DB 4; Length 430;  
Best Local Similarity 40.0%; Pred. No. 20;  
Matches 10; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Qy 17 CCRVHTTRCCRDYPGEECCSEWDCM 41  
||| |||| || | :  
Db 200 CCRWTRTCC-----CCRCWQSL 217

Search completed: September 4, 2001, 15:57:36  
Job time: 378 sec

Query Match 100.0%; Score 252; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.4e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 40  
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Db 68 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 107

## RESULT 2

US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0., Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION NUMBER: 50/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 252; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.5e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 40  
|||||  
Db 74 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 113

## RESULT 3

US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION NUMBER: 50/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 252; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 3.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 40  
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Db 68 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 107

## RESULT 4

US-08-911-423-7  
; Sequence 7, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:36 ; Search time 65.86 Seconds  
(without alignments)  
12.506 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_74\_113  
Perfect score: 252  
Sequence: 1 CVQEFHGGDCCTCRHPCPGGVQSGKSFSGFCI 40

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	252	100.0	228	3	US-08-911-423-6
2	252	100.0	241	3	US-08-911-423-4
3	252	100.0	311	3	US-08-911-423-8
4	207.5	82.3	232	3	US-08-911-423-7
5	168	66.7	228	3	US-08-911-423-2
6	125	49.6	89	4	US-09-188-930-191
7	67	26.6	191	3	US-08-974-022-52
8	67	26.6	256	1	US-08-236-918A-6
9	67	26.6	256	5	PCT-US96-03965-2
10	63	25.0	283	5	PCT-US96-12374-2
11	60	23.8	644	1	US-08-336-708A-9
12	60	23.8	1210	2	US-08-484-438-7
13	60	23.8	1210	2	US-08-475-035-4
14	59.5	23.6	1104	2	US-08-327-832-5
15	59.5	23.6	1104	2	US-08-828-584-5
16	58	23.0	140	4	US-08-477-347-17
17	58	23.0	205	3	US-08-974-022-51
18	57.5	22.8	197	3	US-08-974-022-49
19	57.5	22.8	289	4	US-09-042-785A-11
20	57.5	22.8	961	5	PCT-US93-11725-4
21	56.5	22.4	41	1	US-08-050-319B-39
22	56.5	22.4	41	2	US-08-465-982-39
23	56.5	22.4	162	2	US-08-219-237B-7
24	56.5	22.4	162	4	US-08-477-347-16
25	56.5	22.4	276	4	US-09-041-886-27
26	56.5	22.4	277	4	US-09-042-785A-10
27	55.5	22.0	277	2	US-08-147-784-2

28 55.5 22.0 277 4 US-08-195-967-2 Sequence 2, Appli  
29 55.5 22.0 426 4 US-09-082-092-6 Sequence 6, Appli  
30 55 21.8 623 4 US-09-029-348-3 Sequence 3, Appli  
31 55 21.8 626 4 US-09-029-348-2 Sequence 2, Appli  
32 54 21.4 73 2 US-08-972-008-5 Sequence 5, Appli  
33 54 21.4 263 2 US-08-972-008-2 Sequence 2, Appli  
34 54 21.4 300 2 US-08-794-796-2 Sequence 2, Appli  
35 54 21.4 317 4 US-09-383-586-20 Sequence 20, Appli  
36 53.5 21.2 1833 3 US-08-479-722B-2 Sequence 2, Appli  
37 53.5 21.2 1833 5 PCT-US95-02251-18 Sequence 18, Appli  
38 53 21.0 292 3 US-08-403-852D-25 Sequence 26, Appli  
39 53 21.0 292 3 US-08-510-646B-26 Sequence 25, Appli  
40 53 21.0 292 4 US-09-231-818-25 Sequence 103, App  
41 53 21.0 366 4 US-08-857-076-103 Sequence 5, Appli  
42 53 21.0 486 3 US-08-746-559A-5 Sequence 4, Appli  
43 53 21.0 516 3 US-08-746-559A-4 Sequence 2, Appli  
44 53 21.0 1367 2 US-08-249-687C-2 Sequence 2, Appli  
45 53 21.0 1367 2 US-08-625-819-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
APPLICATION NUMBER: US/08/974,022  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-52

Query Match 26.6%; Score 67; DB 3; Length 191;  
Best Local Similarity 45.2%; Pred. No. 1.5;  
Matches 14; Conservative 3; Mismatches 12; Indels 2; Gaps 2;

QY 1 CVQPEFHCGDPCCTTCHRHPCPPGQGVQSQG 31  
DB 87 CIE-GFHLGPQCTRC-EKDCRPGQELTKQG 115

RESULT 8  
US-08-236-918A-6  
Sequence 6, Application US/08236918A  
Patent No. 5674704  
GENERAL INFORMATION:  
APPLICANT: Alderson, Mark R.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple 7.5.3  
SOFTWARE: Microsoft Word, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/236,918A  
FILING DATE: 06-May-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/060,843  
FILING DATE: 07-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2801-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-236-918A-6

Query Match 26.6%; Score 67; DB 1; Length 256;  
Best Local Similarity 45.2%; Pred. No. 1.9;  
Matches 14; Conservative 3; Mismatches 12; Indels 2; Gaps 2;

QY 1 CVQPEFHCGDPCCTTCHRHPCPPGQGVQSQG 31  
DB 87 CIE-GFHLGPQCTRC-EKDCRPGQELTKQG 115

RESULT 9  
PCT-US96-03965-2  
Sequence 2, Application PC/TUS9603965  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung Se  
APPLICANT: Kang, Chang-yull  
TITLE OF INVENTION: Monoclonal antibody against human  
TITLE OF INVENTION: receptor 4-1BB  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Barnard, Brown & Michaels  
STREET: 306 East State Street, Suite 220  
CITY: Ithaca  
STATE: NY  
COUNTRY: USA  
ZIP: 14850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03965  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,796  
FILING DATE: 16-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,269  
FILING DATE: 01-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,996  
FILING DATE: 30-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/267,577  
FILING DATE: 07-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A.  
REGISTRATION NUMBER: 34,390  
REFERENCE/DOCKET NUMBER: KWO5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-2

Query Match 26.6%; Score 67; DB 5; Length 256;  
Best Local Similarity 45.2%; Pred. No. 1.9;

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/911,423
;   FILING DATE: 14-AUG-1997
;   CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/023,419
;   FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/027,901
;   FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ching, Edwin P.
;   REGISTRATION NUMBER: 34,090
;   REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-852-9196
;   TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 232 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;
US-08-911-423-7

Query Match      82.3%; Score 207.5; DB 3; Length 232;
Best Local Similarity 82.5%; Pred. No. 1.4e-15;
Matches 33; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 CVQPEFHCGDPCCCTCRHHPCPPGQGVQSGKFSFGQCI 40
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Db 68 CVQPEFHCGDPCCCTCRHHPCPPGQGVQSGKFSFGQCI 104
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RESULT 5
US-08-911-423-2
; Sequence 2, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
;   APPLICANT: Gorman, Daniel M.
;   APPLICANT: Randall, Troy D.
;   APPLICANT: Zlotnik, Albert
;   TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
;   TITLE OF INVENTION: REAGENTS
;   NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: DNAX Research Institute
;   STREET: 901 California Avenue
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94304-1104
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/911,423
;   FILING DATE: 14-AUG-1997
;   CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/023,419
;   FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/027,901
;   FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
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;
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-852-9196
;   TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 228 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
US-08-911-423-2

Query Match      66.7%; Score 168; DB 3; Length 228;
Best Local Similarity 62.5%; Pred. No. 2.5e-11;
Matches 25; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCCTCRHHPCPPGQGVQSGKFSFGQCI 40
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Db 62 CVTPEYHCGDPQCKICKHYPCQGVQSGDIVGFRVCV 101
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RESULT 6
US-09-188-930-191
; Sequence 191, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;   APPLICANT: Watson, James D.
;   APPLICANT: Strachan, Lorna
;   APPLICANT: Sleeman, Matthew
;   APPLICANT: Onrust, Rene
;   APPLICANT: Murison, James Greg
;   TITLE OF INVENTION: Compositions Isolated From Skin Cells
;   TITLE OF INVENTION: and Methods For Their Use
;   FILE REFERENCE: 11000.1011c1
;   CURRENT APPLICATION NUMBER: US/09/188,930A
;   CURRENT FILING DATE: 1998-11-09
;   NUMBER OF SEQ ID NOS: 348
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 191
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: mouse
;
US-09-188-930-191

Query Match      49.6%; Score 125; DB 4; Length 89;
Best Local Similarity 64.3%; Pred. No. 4.4e-07;
Matches 18; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCCTCRHHPCPPGQGVQ 28
   |||||
Db 61 CVTPEYHCGDPQCKICKHYPCQGVQ 88
   |||||

RESULT 7
US-08-974-022-52
; Sequence 52, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
;   APPLICANT: Boyle, William J.
;   APPLICANT: Lacey, David L.
;   APPLICANT: Calzone, Frank J.
;   APPLICANT: Chang, Ming-Shi
;   TITLE OF INVENTION: OSTEOPROTEGERIN
;   NUMBER OF SEQUENCES: 53
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Amgen Inc.
;   STREET: 1840 Dehavilland Drive
;   CITY: Thousand Oaks
;   STATE: California
```

Query Match 23.8%; Score 60; DB 2; Length 1210;  
Best Local Similarity 33.3%; Pred. No. 45;  
Matches 12; Conservative 5; Mismatches 19; Indels

OY 5 EFHCGDPCTCTCRHHPCPPGQGVQSGKFSFGQCI 40

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Db      257 EATCKDTCPPMLNPTTYQMDVAPGKYSFGATCV 292
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RESULT 14
US-08-327-832-5
; Sequence 5, Application US/08327832
; Patent No. 5840832
; GENERAL INFORMATION:
; APPLICANT: Ono, Santa J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: Transcription Factor Reg
; TITLE OF INVENTION: Expression, cDNA and Gen
; TITLE OF INVENTION: Retroviral Expression Co
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,832
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.46362
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 20-2 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-832-5

Query Match          23.6%; Score 59.5; DB
Best Local Similarity 43.5%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches

QY      1 CVQPEFHCGDPCCCTCR-HHPCP 22
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Db      840 CTTPRADCGHFCMAPCHTSSFCP 862

RESULT 15
US-08-828-584-5
; Sequence 5, Application US/08828584
; Patent No. 5908762
; GENERAL INFORMATION:
; APPLICANT: Ono, Santa J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: Transcription Factor Reg
; TITLE OF INVENTION: Expression, cDNA and Gen
; TITLE OF INVENTION: Retroviral Expression Co
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
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;; ZIP: 20001  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/828,584  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Posorske, Laurence H.  
;; REGISTRATION NUMBER: 34,698  
;; REFERENCE/DOCKET NUMBER: 1107.46362  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 20-2 508-9153  
;; TELEFAX: 202 508-9299  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1104 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-828-584-5

Query Match 23.6%; Score 59.5; DB 2; Length 1104;  
Best Local Similarity 43.5%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 12; Indels 1; Gaps 1;  
QY 1 CVOPEFHCGDPCCTTCR-HHPCP 22  
Db 840 CTTPRADCGHPCMAPCHTSSPCP 862

Search completed: September 4, 2001, 15:57:36  
Job time: 378 sec

Query Match 100.0%; Score 246; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.2e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 41  
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DB 108 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 148

RESULT 2  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 07-OCT-1996  
; NAME: Ching, Edwin P.  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 246; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 41  
|||||  
DB 114 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 154

RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 246; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 41  
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DB 108 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 148

RESULT 4  
US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:36 ; Search time 65.86 Seconds  
(without alignments)  
12.818 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_114\_154  
Perfect score: 246  
Sequence: 1 DCASGTFSGHGCHKPWT.....TQFGFLTFVPGKGNTHAVCV 41

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	246	100.0	241	3	US-08-911-423-4
3	246	100.0	311	3	US-08-911-423-8
4	192	78.0	228	3	US-08-911-423-2
5	96	39.0	277	2	US-08-147-784-2
6	96	39.0	277	4	US-08-195-967-2
7	95	38.6	206	1	US-08-097-827-7
8	95	38.6	206	1	US-08-494-574-7
9	95	38.6	438	1	US-08-097-827-11
10	95	38.6	438	1	US-08-494-574-11
11	93	37.8	219	2	US-08-816-605-2
12	93	37.8	255	1	US-08-236-918A-8
13	93	37.8	255	1	US-08-816-605-9
14	93	37.8	255	5	PCT-US96-03965-8
15	84	34.1	41	1	US-08-050-319B-44
16	84	34.1	41	2	US-08-465-982-44
17	84	34.1	139	2	US-08-219-237B-8
18	84	34.1	140	4	US-08-477-347-17
19	84	34.1	205	3	US-08-974-022-51
20	83	33.7	401	3	US-08-974-022-2
21	83	33.7	401	3	US-08-974-022-4
22	83	33.7	401	4	US-09-042-785A-13
23	78	31.7	300	2	US-08-794-796-2
24	77	31.3	401	3	US-08-974-022-6
25	77	31.3	401	4	US-09-042-785A-12
26	75	30.5	625	3	US-08-996-139-15
27	75	30.5	625	4	US-08-995-659-15

28	74	30.1	253	4	US-09-042-785A-4	Sequence 4, Appli
29	74	30.1	451	3	US-08-996-139-4	Sequence 4, Appli
30	74	30.1	451	4	US-08-995-659-4	Sequence 4, Appli
31	74	30.1	591	3	US-08-996-139-2	Sequence 2, Appli
32	74	30.1	591	4	US-08-995-659-2	Sequence 2, Appli
33	74	30.1	605	4	US-09-042-785A-23	Sequence 23, Appli
34	74	30.1	616	3	US-08-996-139-6	Sequence 6, Appli
35	74	30.1	616	4	US-08-995-659-6	Sequence 6, Appli
36	74	30.1	655	3	US-08-959-382-2	Sequence 2, Appli
37	70.5	28.7	191	3	US-08-974-022-52	Sequence 52, Appli
38	70.5	28.7	256	1	US-08-236-918A-6	Sequence 6, Appli
39	70.5	28.7	256	5	PCT-US96-03965-2	Sequence 2, Appli
40	65	26.4	573	4	US-09-042-785A-2	Sequence 2, Appli
41	63	25.6	227	3	US-08-974-022-48	Sequence 48, Appli
42	63	25.6	461	4	US-09-042-785A-7	Sequence 7, Appli
43	61	24.8	39	1	US-08-050-319B-41	Sequence 41, Appli
44	61	24.8	39	2	US-08-465-982-41	Sequence 41, Appli
45	61	24.8	163	2	US-08-219-237B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chang, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

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;
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-097-827-7

Query Match 38.6%; Score 95; DB 1; Length 206;
Best Local Similarity 46.2%; Pred. No. 7.9e-05;
Matches 18; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 2 CASGTFSGHGHCKPWTDCTQGFGLTFVPGNKTHNAVC 40
| | | | | : | | | | | : | | | | | : | | | | |
Db 126 CPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 8
US-08-494-574-7
; Sequence 7, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574

Query Match 38.6%; Score 95; DB 1; Length 206;
Best Local Similarity 46.2%; Pred. No. 7.9e-05;
Matches 18; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 2 CASGTFSGHGHCKPWTDCTQGFGLTFVPGNKTHNAVC 40
| | | | | : | | | | | : | | | | | : | | | | |
Db 126 CPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 9
US-08-097-827-11
; Sequence 11, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-097-827-11

Query Match 38.6%; Score 95; DB 1; Length 438;
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; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-494-574-7

Query Match 38.6%; Score 95; DB 1; Length 206;
Best Local Similarity 46.2%; Pred. No. 7.9e-05;
Matches 18; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 2 CASGTFSGHGHCKPWTDCTQGFGLTFVPGNKTHNAVC 40
| | | | | : | | | | | : | | | | | : | | | | |
Db 126 CPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 9
US-08-097-827-11
; Sequence 11, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-097-827-11

Query Match 38.6%; Score 95; DB 1; Length 438;
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-911-423-2

Query Match 78.0%; Score 192; DB 3; Length 228;
Best Local Similarity 75.0%; Pred. No. 6.8e-17;
Matches 30; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Oy 2 CASGTFSGHGCHKPTWDTCTQFGFLTVFPGNKTHNAVCV 41
Db 103 CAMGTFSGAGRDGCHRLWNCISGFLTMFPGNKTHNAVCI 142

RESULT 5
US-08-147-784-2
; Sequence 2, Application US/08147784
; Patent No. 5821332
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Buck, David
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,784
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-220
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-147-784-2
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-147-784-2

Query Match 39.0%; Score 96; DB 2; Length 277;
Best Local Similarity 43.6%; Pred. No. 8.1e-05;
Matches 17; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Oy 2 CASGTFSGHGCHKPTWDTCTQFGFLTVFPGNKTHNAVVC 40
Db 128 CPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSDAIC 166

RESULT 6
US-08-195-967-2
; Sequence 2, Application US/08195967
; Patent No. 6242566
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-195-967-2

Query Match 39.0%; Score 96; DB 4; Length 277;
Best Local Similarity 43.6%; Pred. No. 8.1e-05;
Matches 17; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Oy 2 CASGTFSGHGCHKPTWDTCTQFGFLTVFPGNKTHNAVVC 40
Db 128 CPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSDAIC 166

RESULT 7
US-08-097-827-7
; Sequence 7, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
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REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2801-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-236-918A-8

Query Match 37.8%; Score 93; DB 1; Length 255;  
Best Local Similarity 40.0%; Pred. No. 0.00018;  
Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 DCASGTFSGHGHCKPWTDCQTQFGFLTVFPGNKTHNAV 40  
DB 119 DCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVC 158

RESULT 13  
US-08-816-605-9  
Sequence 9, Application US/08816605  
Patent No. 5874240  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Gentz, Reiner  
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816.605  
FILING DATE: 13-MAR-1997

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-605-9

Query Match 37.8%; Score 93; DB 2; Length 255;  
Best Local Similarity 40.0%; Pred. No. 0.00018;  
Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 DCASGTFSGHGHCKPWTDCQTQFGFLTVFPGNKTHNAV 40  
DB 119 DCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVC 158

RESULT 14  
PCT-US96-03965-8  
Sequence 8, Application PC/TUS9603965  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung Se  
APPLICANT: Kang, Chang-Yull  
TITLE OF INVENTION: Monoclonal antibody against human  
TITLE OF INVENTION: receptor 4-1BB  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Barnard, Brown & Michaels  
STREET: 306 East State Street, Suite 220  
CITY: Ithaca  
STATE: NY  
COUNTRY: USA  
ZIP: 14850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03965  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,796  
FILING DATE: 16-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,269  
FILING DATE: 01-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,996  
FILING DATE: 30-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/267,577  
FILING DATE: 07-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A  
REGISTRATION NUMBER: 34,390  
REFERENCE/DOCKET NUMBER: KW05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-8

Query Match 37.8%; Score 93; DB 5; Length 255;  
Best Local Similarity 40.0%; Pred. No. 0.00018;  
Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 DCASGTFSGHGHCKPWTDCQTQFGFLTVFPGNKTHNAV 40  
DB 119 DCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVC 158

RESULT 15  
US-08-050-319B-44  
Sequence 44, Application US/08050319B  
Patent No. 5633145  
GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray  
APPLICANT: M.J.C. Turner, F.M. Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
Necrosis Factor alpha) Receptor

NUMBER OF SEQUENCES: 3

NAME: Anderson, Kathryn A.



Search completed: September 4, 2001, 15:57:36  
Job time: 378 sec

C:Accession: T13954  
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
Genomics 51, 27-34, 1998  
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs  
A:Reference number: Z14126; MUID:98360089  
A:Accession: T13954  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1574 <NAK>  
A:Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294  
A:Experimental source: strain Sprague-Dawley; brain  
C:Genetics:  
A:Gene: MEGF6

Query Match 8.9%; Score 119; DB 2; Length 1574;  
Best Local Similarity 28.3%; Pred No. 0.092;  
Matches 52; Conservative 10; Mismatches 68; Indels 54; Gaps 11;  
Qy 45 TDARCCRVHTTRCCRDY---PGE--CCSEWDCMCVQPEFHCQDPCCCT-----CRHHPCP 95  
Db 99 TEART---VFCCPGWSQKPGQEGCLSDVD-ECASANGCEGPCCNTVGGFYCR---CP 150  
Qy 96 PCQGVQSQGKESFGQCIDCAGTSGGHEGHCKPWTDCTQFGELTVFPGNKTTHNAVCP 155  
Db 151 PGYQLQGDGK-----TCQDVDECRAHNGCQ-----HRCVNTP 183  
Qy 156 GS-----PPAEPLGLMTVVLLAVAAACVLLLTSAQLGLHIWLRKTKQLLEVPSPS---TED 207  
Db 184 GSYLCECKPGFRLHTDGRFTCLAISSTLNGGCQ--HOCVQLTVTQHRCCRCRPQYQLQED 241  
Qy 208 ARSC 211  
Db 242 GRC 245

Search completed: September 4, 2001, 16:12:10  
Job time: 1107 sec

Db 117 TSKRTQCR-OPGMFCAAWALECHTCELLSDCPGTEAEELKDEVGKGNHCVPCAGHF 175  
QY 121 --SGGHEGCHKPWTCTQFGFLTVTPGNKTHNAVCPGSPRAEPGLG-----WLTVVLL 171  
Db 176 QNTSSPSARCQPHTRCENOGLEVAAPGTAQSTTCC---KNLEPLPPMSGTMLMLAVLL 232  
QY 172 AVAACVLLTSAQLGLHIWQ-----LRKTQLLEVPSPSTE 206  
Db 233 PLAFFLLLATVFC---IWKSHPSLCRLKGLSLLKRRPQGE 269

RESULT 10  
NMRTS  
laminin beta-2 chain precursor - rat  
N:Alternate names: laminin chain B3; S-laminin  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C:Accession: S03539  
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro  
A:Reference number: S03539; MUID:89159410  
A:Accession: S03539  
A:Molecule type: mRNA  
A:Residues: 1-1801 <HUN>  
A:Cross-references: EMBL:X16563; NID:Q57250; PIDN:CAA34561.1; PID:G57251  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: Interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F:36-285/Domain: VI <DOM6>  
F:286-535/Domain: V <DOM5>  
F:286-347/Domain: laminin-type EGF-like homology <LE01>  
F:350-410/Domain: laminin-type EGF-like homology <LE02>  
F:413-470/Domain: laminin-type EGF-like homology <LE03>  
F:473-522/Domain: laminin-type EGF-like homology <LE04>  
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:556-784/Domain: IV <DOM4>  
F:785-831/Domain: laminin-type EGF-like homology <LE06>  
F:788-1196/Domain: laminin-type EGF-like homology <LE07>  
F:834-877/Domain: laminin-type EGF-like homology <LE08>  
F:880-927/Domain: laminin-type EGF-like homology <LE09>  
F:930-986/Domain: laminin-type EGF-like homology <LE10>  
F:989-1038/Domain: laminin-type EGF-like homology <LE11>  
F:1041-1095/Domain: laminin-type EGF-like homology <LE12>  
F:1098-1143/Domain: laminin-type EGF-like homology <LE13>  
F:1146-1190/Domain: laminin-type EGF-like homology <LE14>  
F:1197-1412/Domain: II <DOM2>  
F:1197-1412/Region: heptad repeats  
F:1413-1445/Domain: alpha <ALP>  
F:1446-1801/Region: heptad repeats  
F:1446-1801/Domain: I <DOM1>  
F:45-50/Disulfide bonds: #status predicted  
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p  
F:1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 10.0%; Score 134.5; DB 1; Length 1801;  
Best Local Similarity 26.9%; Pred. No. 0.0063;  
Matches 63; Conservative 6; Mismatches 60; Indels 105; Gaps 15;

QY 8 GAFRALC-GLALLCALSLG-----QRPTGG-PCGCP-----GRLLLTGTDCRCRV 52  
Db 840 GALSALCEGTSQCLCRCTGAFGLRCDHCGQGWGFNCRPCVCNGR-----ADECCA 891

QY 53 HTTRC--CRDYPGECCSWDCMCVQPEPHCGDPCT---TCRHHPCCPGQVSGKGS 107  
Db 892 HTGACLGCRDYGGBHCEH-----CT-AGFH-GDPLRYPVGQCRPCPCPEPGG--SORHEA 943

QY 108 -----FGQCIDCASGTF----- 120  
Db 944 TSCHRDGYSOIVCHCRAGVTGLRCEACAPGHGFGPSKPGRCQCLCECSGNDIDTPDCAC 1003  
QY 121 -----SGGHEGCHKPWTCTQFGFLTVTPGNKTHNAVCPGSP 159  
Db 1004 DPHTGQCLRLHHTGPHGCHKP-----GFHQQAARQSHCRCTNLLGTDP 1050

RESULT 11  
A60771  
B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)  
C:Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
EMBO J. 8, 1403-1410, 1989  
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A:Reference number: S04460; MUID:89356608  
A:Accession: S04460  
A:Molecule type: mRNA  
A:Residues: 1-277 <STA>  
A:Cross-references: EMBL:X60592; NID:G29850; PIDN:CAA43045.1; PID:G29851  
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-  
A:Reference number: A60771; MUID:89093941  
A:Accession: A60771  
A:Molecule type: protein  
A:Residues: 21-50 <BRA>  
A:Experimental source: Burkitt lymphoma cell line Raji  
C:Genetics:  
A:Gene: GDB:CD40  
A:Cross-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F:21-193/Domain: extracellular #status predicted <EXT>  
F:194-215/Domain: transmembrane #status predicted <TM>  
F:216-277/Domain: intracellular #status predicted <CYT>  
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 126.5; DB 2; Length 277;  
Best Local Similarity 24.0%; Pred. No. 0.0069;  
Matches 48; Conservative 27; Mismatches 102; Indels 23; Gaps 9;

QY 34 CGPGRLLLTGTDCRCRVHTRCCRDYPG-----EECCSEWDCMCVQPE-PHCGDPCTT 88  
Db 62 CGSEFLDTWNRETHC---HQHRYCDPNLGLRVQOKTSETDITCTCEGWHCTSEACES 118  
QY 89 C-RHHPCCPGQVQSQCKSFQGCIDCASGTFSGGHEG--HCKPWTDCQFGFLTVFP 145  
Db 119 CVLHRSCEPGFGVKQIATGSDICEPCPVGFFSNVSSAFKCHPWTSCETKDLVQOAG 178  
QY 146 NKTHNAVCPGSPAPPLGLWTV--VLLAVAACVLLTSAQLGLHIWOLRKTQLLEVP 203  
Db 179 TNKTDVVC-----GPDRLRALVVIPIIFGLFALLVL-----VFIRKVK-KPTNKAPH 228  
QY 204 STEDARSCQFPEERGERSA 223  
Db 229 PKQEPQEIFPDPLPGSNTA 248

RESULT 12  
I48854  
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
C:Accession: I48854



Db 182 PPARITVQPTAEWPTSGPSTRPEVPGGRAVAAILGLVLGLGGLPLAILLALYLLR 241  
Qy 194 KQQLLEVP 203  
Db 242 RDQRL---PP 248  
RESULT 5  
S12783  
Ox40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: S12783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC Ox40 antigen of activated CD4 positive T lymphocyte  
A:Reference number: S12783; MUID:90214614  
A:Accession: S12783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:CROSS-references: EMBL:X17037; NID:G57830; PIDN:CAA34897.1; PID:G57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homolog  
C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: Ox40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 12.0%; Score 160.5; DB 2; Length 271;  
Best Local Similarity 26.0%; Pred. No. 1.6e-05;  
Matches 59; Conservative 18; Mismatches 79; Indels 71; Gaps 11;  
Qy 26 ORPTGGPGCGPRLILG--TGFDAKCCRVHTT-----RCRD-YPEECCSEWD----- 71  
Db 6 QQPT-----AFLILGLSLGVTVVNLNVKDYTPSGHKCCRCQGHGMVSRCDTRDTV 58  
Qy 72 CMCVQPEFHCG---DPC--CTTCRHH-----PCPPQGVQSQGKFSF 108  
Db 59 CHPCEPGFVNEAVNYDTCKQTCQNRSGSELKQNTPTEDTVQCRCPTQPRQDSSHL 118  
Qy 109 GFQCTDCASGTFSGHGHECKPWTCTQGFVTPGNKTHNAVPGSPPAEPGLWLTV 168  
Db 119 GVDCVPCPPGHFSPGNOACKPWTCTLSGKQIRHPASNSLDTVCEDRS----- 167  
Qy 169 VLLAVACVLLLTLSAQLGLHIWLKTKQLL-LEVPPSTEDARSCQFP 214  
Db 168 -LLATPL-----LMETQRTFRPTVPSTVWPRTSOLP 199  
RESULT 6  
A3356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A3356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.  
Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
A:Reference number: A3356; MUID:90260639  
A:Accession: A3356  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:CROSS-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,  
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A>Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:CROSS-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,  
Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <DEM>  
A:CROSS-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649  
A:Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A:CROSS-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus,  
J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden  
A:Reference number: A35010; MUID:90110215  
A:Accession: B35010  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kuhnert, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region  
A:Reference number: I38094; MUID:95121934  
A:Accession: I38094  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:CROSS-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:CROSS-references: GDB:125914; OMIM:191191  
A:Map position: 1p36.2-1p36.2  
A:Introns: 26/3  
A:Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homolog  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
F:40-76/Domain: NGF receptor repeat homolog <NG1>  
F:78-119/Domain: NGF receptor repeat homolog <NG2>  
F:120-162/Domain: NGF receptor repeat homolog <NG3>  
F:164-201/Domain: NGF receptor repeat homolog <NG4>  
F:262-279/Domain: transmembrane #status predicted <TM>  
F:280-461/Domain: intracellular #status predicted <INT>  
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 139.5; DB 1; Length 461;  
Best Local Similarity 23.0%; Pred. No. 0.00097;  
Matches 64; Conservative 26; Mismatches 77; Indels 111; Gaps 15;  
Qy 34 CGPG---RLLLGTGTDCAR-----CRVHTTCCRDYPCGCCSEWD-- 71  
Db 57 CSPGQHAKEVCTKTSDFVCDSEDTSTYQLWNWPECLSCGSRCSDDOVTQACTREQNR 116

QY 72 -CMVQPEFHC-----GDFCTTCRHHPGPGVQSGKFSFGFCIDCASGTFSG-- 122  
Db 117 ICTC-RPGWYCALSKQBCRLCAPLR--KCRPGFGVARPGTETSDVYVCKPCAPGTFSNTT 173  
QY 123 GHEGCHKPWTDCQTQFGFLTVFPNGKTHNVC-----VPG----- 156  
Db 174 SSTDICRPHQICN-----VVAIPGNASMDVACTSTSPTRSMAPGAVHLPQPVSTRSQHTQP 229  
QY 157 -----SPPAE-----PLGW-----LTVLLAAVAAACVLLLTSAQ 184  
Db 230 TPEPSTAPSTSLFLPMGPPSPAEAGSTGDFALPVGLIIVGTALGILLIIGVNCVIMT----- 285  
QY 185 LGHIHQLRKTQLLLE-----VPSTED-ARSCQFPPEE 217  
Db 286 -----QVRKKPLCLQREAKVPHLPADKARGTQGPQQ 317

RESULT 7  
JC5559  
lectin-B - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: JC5559  
R:Yamauchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)  
A:Reference number: JC5559; MUID:97290889  
A:Accession: JC5559  
A:Molecule type: protein  
A:Residues: 1-295 <YAM>  
A:Experimental source: root  
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharides  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant lectins  
C:Keywords: glycoprotein  
F:96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 139; DB 2; Length 295;  
Best Local Similarity 28.8%; Pred. No. 0.00077;  
Matches 36; Conservative 18; Mismatches 41; Indels 30; Gaps 8;

QY 20 CALSLGQRTGGP-----GCGPRLILGTGTDAACRCRVHTTRCCRDYGP-----EECC 67  
Db 133 CGVDFGNRTCPNDLCCSEWGWCIGTEGYCGEGCQSQC---NHQRCKGKDFAGRTCLNDLCC 189  
QY 68 SEWDCMCVQPEFHCQDPCCCTTCRHHPGPGVQSGKFSFGFCIDCASGTFSGG 123  
Db 190 SEWG-WCGSSEAHCGGCGGCSNCRNC-----GR-NFGFTCPNELCCSSGGWCGS 238  
QY 124 HEGHC 128  
Db 239 NDAHC 243

RESULT 8  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C:Accession: A46476; A46515  
R:Torres, R.M.; Clark, E.A.  
J. Immunol. 148, 620-626, 1992.  
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40  
A:Reference number: A46476; MUID:92105763  
A:Accession: A46476  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-305 <TOR>  
A:Cross-references: GB:M83312; NID:g1553058  
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)  
A:Note: this translation is not annotated in Genbank entry MUSCD40A, release 113.0  
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Howard, M.; Cockayne, J.

J. Immunol. 149, 3921-3926, 1992  
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A:Reference number: A46515; MUID:93094586  
A:Accession: A46515  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-287, 'LV' <GRI>  
A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126  
A:Experimental source: BALB/c, liver  
A:Note: sequence extracted from NCBI backbone (NCBIP:120357)  
C:Comment: For an alternative splice form, see PIR:A46515  
C:Comment: For an alternative splice form, see PIR:A46476  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: alternative splicing; transmembrane protein  
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 10.4%; Score 139; DB 2; Length 305;  
Best Local Similarity 23.3%; Pred. No. 0.00079;  
Matches 65; Conservative 23; Mismatches 107; Indels 84; Gaps 11;

QY 13 LCGL--ALLCALSLGQRTGGPGGPGRLLLTGTGTDAACRCRVHTTRCCRDYGP-----EECC 50  
Db 7 LCALWGCLLTAVHLGQCVT-----CSDKQYL-----HDGQCCDLCPGSLTSHCTALEKTQ 58  
QY 51 -----RVHTTRCCRDYGP-----EECCSEWDCMCVQPE-FHCQDPCCCTT 88  
Db 59 CHPCDSGEFSAQWNREIRCHQHRCPEPQGLRVKKEGTAESDTVCTCKEGHCTSKDCEA 118  
QY 89 C-RHHPGPGVQSGKFSFGFCIDCASGTFSGGHE--GHCKPWTDCQTQFGFLTVFPV 145  
Db 119 CAQHTPCIPGFGVMEMATETDTTVCHPCPVGFFNQSSSLFEKCYPMWTSCEKDNLEVLQK 178  
QY 146 NKTNAVCVCPSPAPPLGLVTVLLAAVAAACVLLLTSAQLGHIWOLRK----- 194  
Db 179 TSQTNVTCGLKSR-----WRALLVTPVMGILITFGVFLYIKVVKPKDNEMLP 231

QY 195 -----TQLLLEVP-----PSTEDARSCQFPPEERERS 222  
Db 232 ARRDQPEMEDYPCGHNTAAAPVQETLHGCPVTVQEDGKES 270

RESULT 9  
I54182  
tumor necrosis factor receptor 2-related protein - human  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
C:Accession: I54182  
R:Baens, M.; Chafanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
Genomics 16, 214-218, 1993  
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq  
A:Reference number: I54182; MUID:93252381  
A:Accession: I54182  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-435 <RES>  
A:Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762  
C:Genetics:  
A:Gene: GDB:LTBR  
A:Cross-references: GDB:1230195; OMIM:600979  
A:Map position: 12p13.3-12p13.1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 10.0%; Score 134.5; DB 2; Length 435;  
Best Local Similarity 26.4%; Pred. No. 0.0023;  
Matches 58; Conservative 17; Mismatches 86; Indels 59; Gaps 13;

QY 34 CGPGRLLLTGTDAACRCRVHTTRC-----CRDYPGEE---C 66  
Db 62 CPP-----GYVSAKSRIRDTVCATCAENSYNHNWYLTICQLCRPCDPVWGLEEIA 116  
QY 67 CS--EWDCCMCVQPEFHCQDPCC--CTTCR-HHPCPPGGVQSGKFSFG-FOCIDCASGTF 120

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:53:43 ; Search time 80.15 Seconds  
(without alignments)  
222.394 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 1340  
Sequence: 1 MAQHGMGAFRALGGLALC.....EEERGSABEKRGLGLWV 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201.5	15.0	256	2 B32393	T-cell antigen 4-1
2	197	14.7	255	2 I38426	lymphocyte activat
3	168.5	12.6	272	2 I48700	gene ox40 protein
4	165	12.3	277	2 I37552	OX40 homolog - hum
5	160.5	12.0	271	2 S12783	OX40 antigen precu
6	139.5	10.4	461	1 A35356	tumor necrosis fac
7	139	10.4	295	2 J05559	lectin-B - Virgini
8	139	10.4	305	2 A46476	B cell-associated
9	134.5	10.0	435	2 I34182	tumor necrosis fac
10	134.5	10.0	1801	1 NMRTS	laminin beta-2 cha
11	126.5	9.4	277	2 A60771	B-cell activation
12	120.5	9.0	459	2 I48854	gene murine tumour
13	119.5	8.9	1798	2 S53869	laminin beta-2 cha
14	119	8.9	474	2 B38634	tumor necrosis fac
15	119	8.9	1574	2 T13934	MEGF6 protein - ra
16	115.5	8.6	1371	2 A33837	insulin-like transme
17	115	8.6	1687	2 T30176	EGF repeat transme
18	114.5	8.5	329	2 A48805	insulin-like growt
19	112.5	8.4	1797	2 A55677	laminin beta-2 cha
20	112	8.4	152	2 T18975	hypothetical prote
21	112	8.4	2318	2 S45306	notch 3 protein -
22	111	8.3	1111	2 T26972	hypothetical prote
23	110.5	8.2	2907	2 A57278	fibrillin-2 precu
24	109.5	8.2	164	2 T24272	hypothetical prote
25	109.5	8.2	2531	2 A46019	Notch-1 protein -
26	109	8.1	3635	2 T10053	laminin alpha 5 ch
27	108.5	8.1	3566	1 A40701	tenascin-X precurs
28	106.5	7.9	2918	2 A54105	fibrillin-2 precu
29	105	7.8	188	2 T15651	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

B32393 T-cell antigen 4-1BB precursor - mouse

C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000

C:Accession: B32393; I48879

R:Kwon, B.S.; Weissman, S.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989

A:Title: cDNA sequence of two inducible T-cell genes.

A:Reference number: A32393; MUID:89184547

A:Accession: B32393

A:Molecule type: mRNA

A:Residues: 1-256 <KWO>

A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.

J. Immunol. 152, 2256-2262, 1994

A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B

A:Reference number: I48879; MUID:94179805

A:Accession: I48879

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-256 <RES>

A:Cross-references: EMBL:U02567; NID:g117783; PIDN:AAA93113.1; PID:g409178

C:Genetics:

A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: transmembrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 15.0%; Score 201.5; DB 2; Length 256;  
Best Local Similarity 28.7%; Pred. No. 9.8e-09;  
Matches 62; Conservative 26; Mismatches 85; Indels 43; Gaps 10;

QY 34 CGPGRLL-LGTGTDARCCRVHTRCCRDYFGEECCSEW---DCMCVQPEFHCGDPCCTTC 89

DB 47 CPPSTFSSGGQGNICRV-----CAGYFRKFKCSSTHNAECEIE-GFHCLGPGQCTRC 101

QY 90 RHHPCCPGGVQSGQKSFSGFQICDCASTGTFSGGH-EGHCKPWTDCQFGFLTVFPCNKT 148

DB 102 -EKDRPGQELTKQG-----CKTCSLGTFFNDQNGTGVCRPWTNCSLDGRSVLTKGTTE 153

QY 149 HNACVCP-----GSPPAEPLGLWTVVLLAVAAACVLLLTSAQLGLHI--W 190

DB 154 KDVCCGPPVVSFSPSTISVTPEGGPGHSLQVLTFLTAULTSALLALITITLLFSVLKW 213

QY 191 QLRKTKQLLEVP-----PSTEDARSCQFPPEERG 219

DB 214 IRKKFPHFKQPKTKTGAQAQEDACSCRCQPEEG 249

thrombospondin 2 p  
MEGF2 protein - hu  
Doc4 protein, stre  
MEGF8 protein - hu  
thrombospondin 3 -  
fibrillin I - bovi  
agglutinin isolect  
integrin beta-3 ch  
insulin-like growt  
latent transformin  
hypothetical prote  
alpha-2-macroglobu  
integrin beta-5 ch  
notch protein homo  
fibrillin 1 precu  
agglutinin isolect

```
RESULT 2
I38426
lymphocyte activation-induced receptor ILA precursor - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38426; J07052
R:Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; H
Eur. J. Immunol. 24, 2219-2227, 1994
A:Title: Molecular and biological characterization of human 4-1BB and its ligand.
A:Reference number: I38426; MUID:94374434
A:Accession: I38426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-255 <RES>
A:Cross-references: EMBL:003397; NID:g571320; PIDN:AAA53133.1; PID:g571321
R:Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A:Reference number: J07052; MUID:94085794
A:Accession: J07052
A:Molecule type: mRNA
A:Residues: 1-106,'R',108-255 <SCH>
C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:18-255/Product: lymphocyte activation-induced receptor <SIG>
F:187-213/Domain: transmembrane #status predicted <MAT>
F:138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict
F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 14.7%; Score 197; DB 2; Length 255;
Best Local Similarity 30.2%; Pred. No. 2.2e-08;
Matches 67; Conservative 20; Mismatches 81; Indels 54; Gaps 12;

QY 34 CGPGRLLGTGDARCRVHTTCCRDYPG-----ECCS-----EWDGCVQPFHCGDP 84
DB 48 CPNPSFSSAGG--QRTCDI-----CRQGVFTRKECSSTSNACDC---TPGFHCLGA 97

QY 85 CCTCRHHPCCPGQVQSQKFGFCIDCASGTSFGGHEGCKPWTCTQGFGLTVFP 144
DB 98 GCSMC-EQDCQGOELTKG-----CKDCFGTFNDQKRGICRPWTNGLDGKSLVN 149

QY 145 GNKTHNAVCPG-----SPPA---EPLGWLTV--LLAVACVLLLTSAQLGLH 188
DB 150 GTERDVVCGPSADLSPGASSVTPPAPAREGHSPOIISFFLALTSTALLFLFLTLR 209

QY 189 ---IWQLRKTQLLEVP-----STEDARSCQPFEEERG 219
DB 210 FSVVGRKKLLYIFQKPMRPVQTTQEEEGCSCRPEEEG 251

RESULT 3
I48700
gene ox40 protein - mouse
N:Alternate names: Ox40 antigen
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A:Reference number: I48700; MUID:94044750
A:Accession: I48700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
```

```
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
A:Reference number: I48334; MUID:95255413
A:Accession: I48334
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14,'G',16-272 <RE2>
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C:Genetics:
A:Gene: Ox40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 12.6%; Score 168.5; DB 2; Length 272;
Best Local Similarity 24.9%; Pred. No. 3.7e-06;
Matches 60; Conservative 18; Mismatches 70; Indels 93; Gaps 11;

QY 39 LLLGTGTGDAR--CCRVHT---TRCCRD-YPG-----ECCSEWDCMCVQPFHCGDPC-- 85
DB 14 LALTLGVTARLNCVKHTYPSGHKCCRCQPGHGMVSRCDHTRDTLC-----HPCET 65

QY 86 -----CTTCRRHP-----CPPGQGVQSQKFSFGFCID 114
DB 66 GFYNEAVNYDFCKQCTQCNHRSSELKONCTPTQDVTVCRCRPGTQPRODSGYKLGVDVCP 125

QY 115 CASGTFSGGHEGCKPWTCTQGFGLTVFPGNKTHNAV----- 153
DB 126 CPPGHFSPGNNAQCKPWTNCTLSGKQTRHPASDSLDVACEDRSLLATLLWETQRTFRPT 185

QY 154 -----VPGSPP--AEPGLGWLTVLLAVACVLLLTSAQLGLHI----WOLRK 194
DB 186 TVQSTTVMPRTSELP--SPPTLVTPGPAFVLLGLGLLAPLTVLLALYLLRKAMRLPN 244

QY 195 T 195
DB 245 T 245

RESULT 4
OX40 homologue - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
R:Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human OX40 homologue: cDNA structure, expression and chromosomal assignmen
A:Reference number: I37552; MUID:94170844
A:Accession: I37552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 12.3%; Score 165; DB 2; Length 277;
Best Local Similarity 25.2%; Pred. No. 7e-06;
Matches 63; Conservative 18; Mismatches 113; Indels 56; Gaps 7;

QY 5 GAGAFRALCGALALLCALSLG-----ORPTGGPGCGPGRLLLTGTGDARCCRVHT 54
DB 4 GARRLGRPCAALLLLGLGLSTVTLGHCVGDTYPSNDRCCHECR--PGNGMVSRCSRQSN 61

QY 55 TRCCRDYPG--EECCSEWDCM-CVQPFHCGD---PCTTCRHHPCPPGQGVQSQKFSF 108
DB 62 TVCRPCGPGFYNDVYSSKPKCTWNCNLSRGSERKQJCTATQDVTVCRCRAGTQPLDSYKP 121

QY 109 GFQCIDCASGTFSGGHEGCKPWTCTQGFGLTVFPGNKTHNAVCPGSPPA----- 161
DB 122 GVDCAFCPPGHFSGPDNQACKPWTNCTLAGKHTLQPASNSDAICEDDRDPATQPTQEQ 181

QY 162 -----PLGWLTVVLLAVAAACVLLLTSAQLGLHIWOLR 193
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QY 34 CGPGRLLLTGCTDARCCRVHTTCRRDYPG-----BECSEWDCMCVQBE-FHCGBPCCCTT 88  
 DB 62 CGSEFELDTWNRTHC-----HOKYKCDPLNLGRVQKGTSETDTICTCEBWHCTSEACES 118  
 QY 89 C-RHHPGPPGOGVOSQKSFQICDASCSTFSGHGG--HCKPWTCTQFGFLTVPFG 145  
 DB 119 CVLHRSCPGPGVQIATGVSDTICEPCPVGFFSNVSAFEKCHPWTSCETKDLVVQOAG 178  
 QY 146 NKTNSVPCVSPPAEPGLGWLTV--VLAVAACVLLLTSAQLGLHIWOLRKTQLLVEYPP 203  
 DB 179 TNKTDDVC-----GQDRLRALVPIPIRGIILFAILLVL-----VFIRKVKAK-KPINKAPH 228  
 QY 204 STEDARSCQFPEERGERSA 223  
 DB 229 PKQBPQEIINFDDLPGSNTA 248

RESULT 13  
 TNR2\_MOUSE STANDARD; PRT; 415 AA.  
 AC P50284;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.  
 GN LTRB OR TNFCR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CVB; TISSUE=Lung;  
 RX MEDLINE=96072804; PubMed=7594541;  
 RA force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
 RA Browning J.L., Ware C.F.;  
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
 RT and expression.";  
 RL J. Immunol. 155:5280-5288(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96163885; PubMed=8586432;  
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,  
 RA Honjo T.;  
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
 RT sequence trap and chromosomal mapping.";  
 RL Genomics 30:312-319(1995).  
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC IMMUNE DEVELOPMENT.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC EMBL: U29173; AAA68964.1; -;  
 DR EMBL: L38423; AAB00846.1; -;  
 DR EMBL: U30798; AAA81334.1; -;  
 DR HSSP: P25942; ICDF.  
 DR MGD: MGI:104875; Ltrb.  
 DR InterPro: IPR001368; -;  
 DR Pfam: PF00020; TNFR\_C6; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30 POTENTIAL.  
 FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.  
 FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 224 244 POTENTIAL.  
 FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 42 213 4 X TNFR-CYS.  
 FT REPEAT 42 81 TNFR-CYS 1.  
 FT REPEAT 82 124 TNFR-CYS 2.  
 FT REPEAT 125 170 TNFR-CYS 3.  
 FT REPEAT 171 213 TNFR-CYS 4.  
 FT DISULFID 43 58 BY SIMILARITY.  
 FT DISULFID 59 72 BY SIMILARITY.  
 FT DISULFID 62 80 BY SIMILARITY.  
 FT DISULFID 83 98 BY SIMILARITY.  
 FT DISULFID 101 116 BY SIMILARITY.  
 FT DISULFID 104 124 BY SIMILARITY.  
 FT DISULFID 126 132 BY SIMILARITY.  
 FT DISULFID 139 150 BY SIMILARITY.  
 FT DISULFID 142 169 BY SIMILARITY.  
 FT DISULFID 172 187 BY SIMILARITY.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 415 AA; 44956 MW; 298326A566AEF661 CRC64;

Query Match 9.2%; Score 123; DB 1; Length 415;  
 Best Local Similarity 25.3%; Pred. No. 0.0019;  
 Matches 48; Conservative 19; Mismatches 103; Indels 20; Gaps 8;

QY 34 CGPGRLLLTGCTDARCCRVHTTCRRDYPGEECCSEWDCMCVQBEFHCGBPCCCTTCRHHP 93  
 DB 101 CRPCDIVLGFEEVAPCTSDRKAB-CRCQPGMSCV-YLDNECV---HCEERLVLCQ--- 151  
 QY 94 CPGGQGVQSGK-FSGFOCIDCAGTF--SGGHEGHCKPWTCTQFGFLTVPFGNKTN 150  
 DB 152 --PGTEAVTDEIMTDVNCVCKPCHQFQNTSPRARCQPHTRCEIQGLVEAARGTSYSD 209  
 QY 151 AVCVPGSPPAEPGLGWLTVVLLAVAACVLLLTSAQLGL---HIWLARKTQLLLEVPSTED 207  
 DB 210 TIC---KNPPEPGAMLLAILLSLVFLFTTVTLACAMMRHPSLCRKLGTLKRHPGEE 266  
 QY 208 ARSCQFPPEE 217  
 DB 267 SPPCPAPRAD 276

RESULT 14  
 TNR2\_MOUSE STANDARD; PRT; 474 AA.  
 AC P25119; P97893;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).  
 GN TNFRSF1B OR TNFR2 OR TNFR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91187885; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wong G.H., Chen E.Y., Goeddel D.V.;  
 RT "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.";  
 RL Mol. Cell. Biol. 11:3020-3026(1991).

```

[3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Kissenerghis M., Fellows R., Feldmann M., Chernaiovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL; M50469; AAA39752.1; -
DR DR EMBL; M59378; AAA40463.1; -
DR DR EMBL; U39488; AAA85021.1; -
DR DR EMBL; X87128; CAA60618.1; -
DR DR PIR; B38634; B38634.
DR DR HSSP; P19438; INCF.
DR DR MGI; 1314883; Tnfrsf1b.
DR DR InterPro: IPR001368; -
DR DR Pfam; PF00020; TNFR_c6; 4.
DR DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462AE398C4D6563 CRC64;

Query Match 8.9%; Score 119; DB 1; Length 474;
Best Local Similarity 31.0%; Pred. No. 0.0047;
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;

QY 46 DARCCRVHTTRCRRDYPGECSCWDCMCVQPEFHCGDCPCTTC-RHHPCPPGGVGSQ 104
DB 107 EIRACTKQNRVCACAGRYCAL-----KTHSGS--CROCMRLSKCGPFGVASSR 155
QY 105 KFSFGQCIDCAGTSG--GHEGCHKPWTCTQGFGLTVFPKGNKTHNAVCPESP 158
DB 156 APNGNVLRCACAPCTESDTSSTSDVCRPHRICS----ILAIPGNASTDAVCAPESP 207

RESULT 15

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IGIR_RAT
ID IGIR_RAT STANDARD; PRT; 1370 AA.
AC P24062;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
GN IGFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95277910; PubMed=7758167;
RA Du J., Delafontaine P.;
RT "Inhibition of vascular smooth muscle cell growth through antisense
transcription of a rat insulin-like growth factor I receptor cDNA.";
RL Circ. Res. 76:963-972(1995).
[2]
RP SEQUENCE OF 1-364 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=90017496; PubMed=2477843;
RA Warner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
RA Leroith D.;
RT "Developmental regulation of the rat insulin-like growth factor I
receptor gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).
[3]
RP SEQUENCE OF 913-1017 FROM N.A.
RX MEDLINE=92412145; PubMed=1530648;
RA Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
RT "A new member of the insulin receptor family, insulin
receptor-related receptor, is expressed preferentially in the
kidney.";
RL Biochem. Biophys. Res. Commun. 187:934-939(1992).
CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
TYROSINE-PROTEIN KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE
BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
CC EMBL; L29232; AAA41392.1; -
DR EMBL; M27293; AAA41384.1; -
DR PIR; A33837; A33837.
DR HSSP; P06213; IIRK.
DR InterPro: IPR000494; -
DR InterPro: IPR000719; -
DR InterPro: IPR001245; -
DR InterPro: IPR001777; -
DR InterPro: IPR002011; -
DR InterPro: IPR002174; -
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.

```

Db 892 HTGACLCGRDYGGEHCER-----CI-AGEH-GDPRLPYGGQCRPCPCBPGG--SORHFA 943  
Qy 108 -----FGQCIDCASGTF----- 120  
Db 944 TSCHRDGYSQIVCHCRAGYTGRCACAPGHGDPSPKPGRCQLCECSGNDPTDPGAC 1003  
Qy 121 -----SGGHEGCHKPWTDCQTFGLVFPNGKTHNAV--VPGSPP 159  
Db 1004 DPHTGQCLRLHHTGPHGCHKP-----GFHGQAARQSRCHRCTNLLGTD 1050

RESULT 11  
LMB2\_MOUSE  
ID LMB2\_MOUSE STANDARD; PRT: 1799 AA.  
AC Q61292; Q62182;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE LAMININ BETA-2 CHAIN PRECURSOR.  
GN LAMB2 OR S-LAM OR LAMS.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN SEQUENCE FROM N.A.  
RP STRAIN=129/J;  
RC MEDLINE=962701; PubMed=8662701;  
RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,  
RA Albrechtsen R., Wewer U.M.;  
RT "Structural organization of the human and mouse laminin beta2 chain  
genes, and alternative splicing at the 5' end of the human  
transcript.";  
RL J. Biol. Chem. 271:13407-13416(1996).  
RN [2]  
RP SEQUENCE OF 348-428 FROM N.A.  
RC TISSUE=Lung;  
RA MEDLINE=94319092; PubMed=8043959;  
RA Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;  
RT "S-laminin gene (Lams) maps to F1 band of mouse chromosome 9.";  
RL Mamm. Genome 5:393-394(1994).  
RN [3]  
RP FUNCTION.  
RC STRAIN=129/J;  
RX MEDLINE=95191650; PubMed=7885444;  
RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;  
RT "Aberrant differentiation of neuromuscular junctions in mice lacking  
s-laminin/laminin beta 2.";  
RL Nature 374:258-262(1995).  
CC -|- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC -|- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR  
NERVE TERMINALS.  
CC -|- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT  
MEMBRANES (MAJOR COMPONENT).  
CC -|- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.  
CC -|- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC -|- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
CC -|- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC -|- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
CC -|- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: U43541; AAC53535.1; -;  
CC EMBL: U42624; AAC53535.1; JOINED.  
CC EMBL: X75928; CAA53532.1; -;  
CC HSSP: P02468; IKLO.  
CC MGD: MGI:99916; Lamb2.  
CC InterPro: IPR000561; -;  
CC InterPro: IPR001886; -;  
CC InterPro: IPR002049; -;  
CC Pfam: PF00053; laminin\_EGF; 13.  
CC PRINTS: PR00011; EGF\_LAMININ.  
CC PROSITE: PS00022; EGF\_1; 10.  
CC PROSITE: PS01186; EGF\_2; 2.  
CC PROSITE: PS01248; LAMININ\_TYPE\_EGF; 12.  
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 35  
FT CHAIN 36 1799 LAMININ BETA-2 CHAIN.  
FT DOMAIN 283 283 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 284 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN  
V).  
FT DOMAIN 286 349 LAMININ EGF-LIKE 1.  
FT DOMAIN 350 412 LAMININ EGF-LIKE 2.  
FT DOMAIN 413 472 LAMININ EGF-LIKE 3.  
FT DOMAIN 473 524 LAMININ EGF-LIKE 4.  
FT DOMAIN 525 555 LAMININ EGF-LIKE 5 (INCOMPLETE).  
FT DOMAIN 556 782 LAMININ DOMAIN IV.  
FT DOMAIN 783 1191 8 X LAMININ EGF-LIKE REPEATS (DOMAIN  
III).  
FT DOMAIN 784 831 LAMININ EGF-LIKE 6.  
FT DOMAIN 832 877 LAMININ EGF-LIKE 7.  
FT DOMAIN 878 927 LAMININ EGF-LIKE 8.  
FT DOMAIN 928 986 LAMININ EGF-LIKE 9.  
FT DOMAIN 987 1038 LAMININ EGF-LIKE 10.  
FT DOMAIN 1039 1095 LAMININ EGF-LIKE 11.  
FT DOMAIN 1096 1143 LAMININ EGF-LIKE 12.  
FT DOMAIN 1144 1190 LAMININ EGF-LIKE 13.  
FT DOMAIN 1191 1410 DOMAIN II.  
FT DOMAIN 1411 1443 DOMAIN ALPHA.  
FT DOMAIN 1444 1799 DOMAIN I.  
FT DOMAIN 1257 1304 COILED COIL (POTENTIAL).  
FT DOMAIN 1473 1527 COILED COIL (POTENTIAL).  
FT DOMAIN 1577 1791 COILED COIL (POTENTIAL).  
FT DISULFID 286 295 BY SIMILARITY.  
FT DISULFID 288 313 BY SIMILARITY.  
FT DISULFID 315 324 BY SIMILARITY.  
FT DISULFID 327 347 BY SIMILARITY.  
FT DISULFID 350 359 BY SIMILARITY.  
FT DISULFID 352 377 BY SIMILARITY.  
FT DISULFID 380 389 BY SIMILARITY.  
FT DISULFID 392 410 BY SIMILARITY.  
FT DISULFID 413 426 BY SIMILARITY.  
FT DISULFID 415 441 BY SIMILARITY.  
FT DISULFID 443 452 BY SIMILARITY.  
FT DISULFID 455 470 BY SIMILARITY.  
FT DISULFID 473 487 BY SIMILARITY.  
FT DISULFID 475 494 BY SIMILARITY.  
FT DISULFID 496 505 BY SIMILARITY.  
FT DISULFID 508 522 BY SIMILARITY.  
FT DISULFID 784 796 BY SIMILARITY.  
FT DISULFID 786 803 BY SIMILARITY.  
FT DISULFID 805 814 BY SIMILARITY.  
FT DISULFID 817 829 BY SIMILARITY.  
FT DISULFID 832 844 BY SIMILARITY.  
FT DISULFID 834 851 BY SIMILARITY.  
FT DISULFID 853 862 BY SIMILARITY.  
FT DISULFID 865 875 BY SIMILARITY.

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FT DISULFID 878 887 BY SIMILARITY.
FT DISULFID 880 894 BY SIMILARITY.
FT DISULFID 887 906 BY SIMILARITY.
FT DISULFID 909 925 BY SIMILARITY.
FT DISULFID 928 944 BY SIMILARITY.
FT DISULFID 930 955 BY SIMILARITY.
FT DISULFID 957 966 BY SIMILARITY.
FT DISULFID 969 984 BY SIMILARITY.
FT DISULFID 987 1001 BY SIMILARITY.
FT DISULFID 989 1008 BY SIMILARITY.
FT DISULFID 1011 1020 BY SIMILARITY.
FT DISULFID 1023 1036 BY SIMILARITY.
FT DISULFID 1096 1108 BY SIMILARITY.
FT DISULFID 1098 1115 BY SIMILARITY.
FT DISULFID 1117 1126 BY SIMILARITY.
FT DISULFID 1129 1141 BY SIMILARITY.
FT DISULFID 1144 1156 BY SIMILARITY.
FT DISULFID 1146 1163 BY SIMILARITY.
FT DISULFID 1165 1174 BY SIMILARITY.
FT DISULFID 1177 1188 BY SIMILARITY.
FT DISULFID 1191 1191 INTERCHAIN (PROBABLE).
FT DISULFID 1194 1194 INTERCHAIN (PROBABLE).
FT DISULFID 1198 1798 INTERCHAIN (PROBABLE).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1086 1086 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1250 1250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1309 1309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1349 1349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1500 1500 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1799 AA; 196352 MW; 1F28967A67AEDE33 CRC64;

Query Match 9.5%; Score 127.5; DB 1; Length 1799;
Best Local Similarity 24.7%; Pred. No. 0.0026;
Matches 61; Conservative 8; Mismatches 63; Indels 115; Gaps 14;

QY 5 GAMGAFRALC-----GLALLCALSLGQRPT-----GGPGCGP-----GRL 39
Db 825 GPAGCQACQSPDGLSALCEGTSALCGTSGQCPGPRGAFGLRCHQRCQGWGFPNCRPCVCNGR- 883
QY 40 LLGTGTDCRCRVHTTRC--CRDYPGECCSEWDCMCVQPEFHCGDPCCT---TCRHPC 94
Db 884 -----ADECDTHTGACLGCDYTGGEHCE-----CI-AGFH-GDRLPYGGQCRCPC 930
QY 95 PPGQGVQSGKFS-----PGFCIDCASGTF----- 120
Db 931 PEGPG--SQRFATSCHRDGYSGQIVCHCRAGYTGRLCEACAPGFGDPSPKPGRCQICE 988
QY 121 -----SGGHEGHCCKPWTCTQFGFLTVPFGNTHNAV 153
Db 989 CSGNIDPMDPADPHTGQCLRLCHNTEGPHCGYCKP-----GFHQAAARQSCHRCTC 1041
QY 154 -VGSPP 159
Db 1042 NLLGTD 1048

RESULT 12
CD40_HUMAN STANDARD; PRT; 277 AA.
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
```

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RP SEQUENCE FROM N.A.
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RL factor receptor and induced by cytokines in carcinomas.";
RN EMO J. 8:1403-1410(1989).
RP [2]
RX 3D-STRUCTURE MODELING OF 24-144.
RA MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RL the ligand binding domain of the human B cell receptor CD40.";
RN Proteins 27:59-70(1997).
RP [3]
RX 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RA MEDLINE=98266353; PubMed=9605317;
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RT Zheng Z., Naismith J.H., Thomas D.;
RL "The role of polar interactions in the molecular recognition of CD40L
RN with its receptor CD40.";
RX Protein Sci. 7:1124-1135(1998).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
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CC -----
DR EMBL; X60592; CAA43045.1;
DR PIR; S04460; S04460.
DR PDB; 1CDF; 01-APR-97.
DR MIM; 109535;
DR InterPro; IPR001368;
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 277 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 36 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;
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Query Match 9.4%; Score 126.5; DB 1; Length 277;  
Best Local Similarity 24.0%; Pred. No. 0.00071;  
Matches 48; Conservative 27; Mismatches 102; Indels 23; Gaps 9;

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FT CHAIN 20 289 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

Query Match 10.4%; Score 139; DB 1; Length 289;
Best Local Similarity 23.3%; Pred. No. 6.6e-05;
Matches 65; Conservative 23; Mismatches 107; Indels 84; Gaps 11;

Qy 13 LCGL--ALLCALSIGRTGGCGGRLLTGTGDARC-----50
Db 7 LCALWGCLLTAVHLGCQVT---CSDKQVL---HDGQCCLCQPGSRLTSHCTALEKTQ 58
Qy 51 -----RVHTRCCRDYPG-----BECCSEWDCMCVQPE-FHCGDPCCTT 88
Db 59 CHPCDSGFSAQWNRIRCHQHRHCEPNQGLRVKKEGTAESTDVCTCKEGQCHTSKDCEA 118
Qy 89 C-RHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHE--GHCKPWTDCQFGFLTVFPG 145
Db 119 CAQHTPCIPGFGVEMATETDTVCHPCVPVGFSSQSSLFKCYPWTSCEADKNLEVLQKG 178
Qy 146 NKTHNAVCPGSPAPGLWLTAVLLAVAACVLLTSAQLGLHIWLQRK-----194
Db 179 TSQTNVIGLKS-----MRALLVPMVIGILITFGVLYIKKVKPKDNEMLPRA 231
Qy 195 -----TQLLEVP-----PSTEDARSCQFPPEERGRS 222
Db 232 ARRDQPEMEDYPGHATAAPVQETLHGCPVTDGDKES 270

RESULT 9
TNRC_HUMAN
ID TNRC_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTBR OR TNFR OR TNFRSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
RT transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; L04270; AAA36757.1; -.
DR HSSP; P25942; 1CDF.
DR MIM; 600979; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_G6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 248 POTENTIAL.
FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 211 4 X TNFR-CYS.
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 10.0%; Score 134.5; DB 1; Length 435;
Best Local Similarity 26.4%; Pred. No. 0.00022;
Matches 58; Conservative 17; Mismatches 86; Indels 59; Gaps 13;

Qy 34 CGGRLLLGTGTARCCRVHTTRC-----CRDYPGE---C 66
Db 62 CPP-----GTVSAKCSIRDTVCATCAENSYNEHWNLYTICQLCRPCDPVNGLEETAP 116
Qy 67 CS--EWDCCMCVQPEFHCQDPC--CTTCR-HHPCPPGGVQSGKFSFG-FOCIDCASGTF 120
Db 117 TSKRKTCRC-QFGMFCANALECTHCELLSDCPGTEAEKLDKGVGNHCVCKAGHF 175
Qy 121 --SGHEGHCCKPWTDCQFGFLTVFPGNKTHNAVCPGSPAPPEPLG-----WLTVVLL 171
Db 176 QNTSSPSARCOPHTRCENOGLEAVEAPTAQSDTTC---KNPLEPLPPMSECTMLMLAVLL 232
Qy 172 AVAACVLLTSAQLGLHIWQ-----LRKTQLLLEVPESTE 206
Db 233 PLAFFLLLATVFSQ---IKWSHPSLCRKLGLSLKRRPQGE 269

RESULT 10
LMB2_RAT
ID LMB2_RAT STANDARD; PRT; 1801 AA.
AC P15800;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).
GN LAMB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
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QY 157 -----SPAE-----PLGW-----LTWLLAVAAACVLLLTSAQ 184
Db 230 TPESTAPSTSFLLPMGSPAPAGSTGDFALPVLGVGTALGLLIIGVNCVIMT----- 285
QY 185 LGLHIWLRKTQLLE-----VPPSTED-ARSCQFPPEE 217
Db 286 -----QVKKKPLCLQREAKVPHLPADKARGTQGPQQ 317

RESULT 7
CD40_BOVIN
ID CD40_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle.";
RL Immunology 90:294-300(1997).
CC -|- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U57745; AAC48710.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT DOMAIN.
FT CHAIN 20 >269 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269 269
SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

Query Match
Best Local Similarity 10.4%; Score 139; DB 1; Length 269;
Matches 52; Conservative 17; Mismatches 82; Indels 36; Gaps 9;

QY 34 CGPGRLLTGTDARCCRVHTTRCCRDYDPEECSEWD-----CMQVQPEFHCGDPCCT 87
Db 62 CGKGEFLSTWNRKYC---HEHYRCVNPNLRLRQSEGLTNTDITICVCEQV-HCTSHTCE 117

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QY 88 TCRHHP-CPPCQGVQSGKFSFGQIDCASGTSGGHEG--HCKPWTDCQFGFLTFVP 144
Db 118 SCTPHSLCLPGFGVKQIATGLLDTVCEPCPLGFGFSNVSSAFKCHRWFTSCERKGLVEQHV 177
QY 145 GNKTHNAV-----VPGSPPAEPLGWLTVVLLAVAAACVLLLTSAOGLGLHWLR 193
Db 178 GTNKTDVVCGFQSRMRLVIVPVT-----MGVLFAVLL-VSACIRNITKKR-----QLR 225
QY 194 KTQLLE 200
Db 226 PCTLWLK 232

RESULT 8
CD40_MOUSE
ID CD40_MOUSE STANDARD; PRT; 289 AA.
AC P27512;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
RT species of murine CD40 upon B lymphocyte activation.";
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN=BALB/C;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Gimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RL J. Immunol. 149:3921-3926(1992).
CC -|- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC -----
DR EMBL; M83312; AAB08705.1; -
DR EMBL; M94126; AAA37404.1; -
DR EMBL; M94129; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94127; AAA37404.1; JOINED.
DR PIR; A46476; A46476.
DR HSSP; P25942; ICDF.
DR MGD; MGI:88336; Tnfrsf5.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
DR Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT DOMAIN.
FT CHAIN 1 19 POTENTIAL.
FT DOMAIN 20 >269 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269 269
SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

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RESULT 3
OX40_MOUSE
ID OX40_MOUSE STANDARD; PRT; 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
GN TNFRSF4 OR TXGP1 OR OX40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94044750; PubMed=8228223;
RA Calderhead D.M., Buhmann J.E., van den Eertwegh A.J.,
RA Claassen E., Noelle R.J., Fell H.;
RT "Cloning of mouse OX40: a T cell activation marker that may mediate
RT T-B cell interactions.";
RL J. Immunol. 151:5261-5271(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255413; PubMed=7737295;
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
RT of rat OX40 protein.";
RL Eur. J. Immunol. 25:926-930(1995).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC
CC EMBL; Z21674; CAA79772.1; -
CC DR EMBL; X85214; CAA59476.1; -
CC DR HSP; P25942; ICDF.
CC DR MGD; MGI:104512; Tnfrsf4.
CC DR InterPro; IPR001368; -
CC DR PROSITE; PS00652; TNFR_NGFR_1; 3.
CC DR PROSITE; PS50050; TNFR_NGFR_2; 2.
CC KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
CC Signal.
FT SIGNAL 1 19
FT CHAIN 20 272
FT DOMAIN 20 211
FT TRANSMEM 212 236
FT DOMAIN 237 272
FT DOMAIN 26 165
FT REPEAT 26 61
FT REPEAT 62 103
FT REPEAT 104 124
FT REPEAT 125 165
FT CARBOHYD 144 144
FT CONFLICT 15 15
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

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Query Match 12.6%; Score 168.5; DB 1; Length 272;  
 Best Local Similarity 24.9%; Pred. No. 2.le-07;  
 Matches 60; Conservative 18; Mismatches 70; Indels 93; Gaps 11;

QY 39 LLLGTGTADAR--CCRVHT-----TRCCRD-YPG-----EBCCSWDCMCVQPEFHCGDPC-- 85

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Db 14 LALTGLVTARRLNCVKHTYPSGHKKCCRECPGHGMVSRCDHTRTDLC-----HPCET 65
QY 86 -----CTTCRHP-----CPPGGVOSQCKFSFGFOCID 114
Db 66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTPTQDTVCRRCRPGTQPRQDSGYKLGVDVCP 125
QY 115 CASGTFSGGHEGCHKPWTCTQFGFLTVPFGNKTTHNAV----- 153
Db 126 CPPGHESPGNQACKPWTNCTLSGKQTRHPASDSLDVAVCEDRSLLATLLWETQRTFRPT 185
QY 154 -----VPGSP--AEPLGLWLTVVLLAVACVLLLTSAQLGLHI-----WOLRK 194
Db 186 TVQSTTWPTPTSELP-SPPTLVTPGPAFAVLGLGLLAPLTVLLVLLYLLRKAWRLPN 244
QY 195 T 195
Db 245 T 245

RESULT 4
OX40_HUMAN
ID OX40_HUMAN STANDARD; PRT; 277 AA.
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
GN TNFRSF4 OR TXGP1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94170844; PubMed=7510240;
RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
RA Hummel M., Fonatsch C., Stein H.;
RT "The human OX40 homolog: cDNA structure, expression and chromosomal
RT assignment of the ACT35 antigen.";
RL Eur. J. Immunol. 24:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95219871; PubMed=7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Scrinivasan S., Sorensen R.A.,
RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of
RT its activities on OX40 receptor.";
RL Circ. Shock 44:30-34(1994).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
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CC EMBL; X75962; CAA53576.1; -
CC DR EMBL; S76792; AAB33944.1; ALT_INIT.
CC DR HSP; P25942; ICDF.
CC DR MIM; 600315; -
CC DR InterPro; IPR001368; -
CC DR Pfam; PF00020; TNFR_c6; 3.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 3.
CC DR PROSITE; PS50050; TNFR_NGFR_2; 2.
CC KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

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KW SIGNAL.
FT CHAIN 1 28 POTENTIAL.
FT CHAIN 29 277 OX40L RECEPTOR.
FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 235 POTENTIAL.
FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 30 169 4 X TNFR-CYS.
FT REPEAT 30 65 TNFR-CYS 1.
FT REPEAT 66 107 TNFR-CYS 2.
FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 127 167 TNFR-CYS 4.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 12.3%; Score 165; DB 1; Length 277;
Best Local Similarity 25.2%; Pred. No. 4.2e-07;
Matches 63; Conservative 18; Mismatches 113; Indels 56; Gaps 7;

QY 5 GAGAFRALCGLALLCALSLG-----QRTGPGGCGRLLLTGTGTARCCRVHT 54
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 GARRLGRGCAALLLLGLSTVGLHCVDGTPSNDRCHECR--PGNGMVSRCRSQN 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 55 TRCRDYPG--ECCSBDWM--CQVPEHGD---PCITTCRHHPCPPGQVQSGKFSF 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 TVCRPCPGFYNDVYVSKPKCKPTWCLNLSGSRKQLCTATQDTCRCRAGTQPLDSYKP 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 109 GFQCIDCASGTFSGHGCHKCPWTDCQFGFLTVFPGNKNHNAVCPGSPPAE----- 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 GVDCAPCPPGHFSGDNQACKPWTNCTLAKGHTLPASNSDAICEBDRDPATQETQ 181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 162 -----PLGWLTVLLAAVACVLLTSLAQGLHIWQLR 193
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 PPARPTVQTEAMPRTSQGSTPRVPEVPGGRAVAILGLGLVLGLLPLAILLALLR 241
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 194 KTQLLEVP 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 RDQRL-----PP 248

RESULT 5
OX40_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";
RL EMBO J. 9:1063-1068(1990).
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC EMBL; X17037; CAA34897.1; -.
DR PIR; S08036; S08036.
DR PIR; S12783; S12783.
DR HSP; P25942; ICDP.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
FT SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT DOMAIN 20 271 OX40L RECEPTOR.
FT TRANSMEM 20 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 235 POTENTIAL.
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 164 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 102 TNFR-CYS 2.
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 124 164 TNFR-CYS 4.
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 271 AA; 29895 MW; C06465136816821 CRC64;

Query Match 12.0%; Score 160.5; DB 1; Length 271;
Best Local Similarity 26.0%; Pred. No. 9.9e-07;
Matches 59; Conservative 18; Mismatches 79; Indels 71; Gaps 11;

QY 26 QRPVGGGCGGRLLG--TGTARCCRVHT-----RCCRD-YPGECCSBDW----- 71
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 QQPT-----AFLLLGLSLGTVKLNCKVDTPSGHKRCRCQPGHGMVSRCDHTRDTV 58
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 72 CMVQPPFHCG---DPC--CTTCRHH-----PCPPGQGVQSGKFSF 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59 CHPCEPGFYNEAVNYDCKQCTQCNHRSGSELKQNTCTEDTVCCRCGTQPRQDSSHL 118
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 109 GFQCIDCASGTFSGHGCHKCPWTDCQFGFLTVFPGNKNHNAVCPGSPPAELGLWLT 168
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 GVDCAVPCPPGHFSPGNSQACKPWTNCTLSGKQIRHPASNSLDTVCEDRS----- 167
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 169 VLLAVACVLLTSLAQGLHIWQLRKTLQ--LEVPPTEDARSQFP 214
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 168 -LLATL-----LWETQRTTFRPTTVPSTTVPRTSQLP 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
TNR2_HUMAN STANDARD; PRT; 461 AA.
ID TNR2_HUMAN
AC P20333;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TNFRII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
GN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
```

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OM protein - protein search; using sw model

Run on: September 4, 2001, 15:56:28 ; Search time 43.78 Seconds  
(without alignments)  
183.092 Million cell updates/sec

Title: US-09-512-363-2

Perfect score: 1340

Sequence: 1 MAOHGAMGAPRALGGLALLC.....EEERGSABEKGRLGLWV 234

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201.5	15.0	256	1 41BB_MOUSE	P20334 mus musculus
2	197	14.7	255	1 41BB_HUMAN	Q07011 homo sapien
3	168.5	12.6	272	1 41BB_MOUSE	P47741 mus musculus
4	165	12.3	277	1 41BB_HUMAN	P43489 homo sapien
5	160.5	12.0	271	1 41BB_MOUSE	P15725 rattus norv
6	141.5	10.6	461	1 41BB_HUMAN	P20333 homo sapien
7	139	10.4	269	1 41BB_MOUSE	Q28203 bos taurus
8	139	10.4	289	1 41BB_HUMAN	P27512 mus musculus
9	134.5	10.0	435	1 41BB_MOUSE	P36941 homo sapien
10	134.5	10.0	1801	1 41BB_HUMAN	P15800 rattus norv
11	127.5	9.5	1799	1 41BB_MOUSE	Q61292 mus musculus
12	126.5	9.4	277	1 41BB_HUMAN	P25942 homo sapien
13	123	9.2	415	1 41BB_MOUSE	P50284 mus musculus
14	119	8.9	474	1 41BB_HUMAN	P25119 mus musculus
15	115.5	8.6	1370	1 41BB_MOUSE	P24062 rattus norv
16	112	8.4	2318	1 41BB_HUMAN	Q61982 mus musculus
17	111.5	8.3	1798	1 41BB_MOUSE	P55268 homo sapien
18	110.5	8.2	2907	1 41BB_HUMAN	Q61555 mus musculus
19	109.5	8.2	2531	1 41BB_MOUSE	Q01705 mus musculus
20	109	8.1	3635	1 41BB_HUMAN	Q61001 mus musculus
21	108.5	8.1	1373	1 41BB_MOUSE	Q60751 mus musculus
22	106.5	7.9	2911	1 41BB_HUMAN	P35556 homo sapien
23	105	7.8	1172	1 41BB_MOUSE	P35442 homo sapien
24	104.5	7.8	684	1 41BB_HUMAN	O73775 gallus gall
25	103.5	7.7	417	1 41BB_MOUSE	Q93038 h wsl-1 pro
26	102.5	7.6	956	1 41BB_HUMAN	Q05895 mus musculus
27	102.5	7.6	2871	1 41BB_MOUSE	P98133 bos taurus
28	102	7.6	186	1 41BB_HUMAN	P10969 triticum ae
29	102	7.6	787	1 41BB_MOUSE	O54890 mus musculus
30	101.5	7.6	1367	1 41BB_HUMAN	P08069 homo sapien
31	101	7.5	4543	1 41BB_MOUSE	P98157 gallus gall
32	100.5	7.5	655	1 41BB_HUMAN	Q07441 papio cynoc
33	100.5	7.5	2531	1 41BB_MOUSE	Q07008 rattus norv

RESULT 1

ID	41BB_MOUSE	STANDARD;	PRT;	256 AA.
AC	P20334;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).			
GN	TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89184547; PubMed=2784565;			
RA	Kwon B.S., Weissman S.M.			
RT	"CDNA sequences of two inducible T-cell genes."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RX	MEDLINE=94179805; PubMed=8133039;			
RA	Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;			
RT	"Genomic organization and chromosomal localization of the T-cell antigen 4-1BB."			
RL	J. Immunol. 152:2256-2262(1994).			
RN	[3]			
RP	CHARACTERIZATION, AND SEQUENCE OF 25-29.			
RX	MEDLINE=93139510; PubMed=7678621;			
RA	Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,			
RT	Kwon B.S.;			
RT	"Inducible T cell antigen 4-1BB. Analysis of expression and function."			
RL	J. Immunol. 150:771-781(1993).			
CC	-I- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BB. POSSIBLY			
CC	ACTIVE DURING T CELL ACTIVATION.			
CC	-I- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.			
CC	ASSOCIATES WITH P56-LCK.			
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.			
CC	-I- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.			
CC	-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
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CC	or send an email to license@ebi.ac.uk).			
CC	-----			
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ACCESSION AR108737
VERSION AR108737.1 GI:12824224
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Gorman,D.M., Randall,T.D. and Zlotnik,A.
TITLE Mammalian cell surface antigens; related reagents
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DEFINITION Sequence 1 from Patent WO9824895.

ACCESSION A91704

VERSION A91704.1 GI:6740652

PAT

22-JAN-2000



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KEYWORDS      unidentified.
SOURCE        unidentified
ORGANISM      unclassified.
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AUTHORS       Riccardi, C.
TITLE         RECEPTOR BELONGING TO THE TNF/NGF RECEPTOR FAMILY
JOURNAL       Patent: WO 9824895-A 1 11-JUN-1998;
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KEYWORDS  precursor, mRNA, complete cds.
SOURCE    house mouse.
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           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 1020)
AUTHORS   Nocentini,G., Giunchi,L., Ronchetti,S., Krausz,L.T., Bartoli,A.,
           Morace,R., Migliorati,G. and Riccardi,C.
TITLE     A new member of the tumor necrosis factor/nerve growth factor
           receptor family inhibits T cell receptor-induced apoptosis
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6216-6221 (1997)
MEDLINE   97322352
REFERENCE  2 (bases 1 to 1020)
AUTHORS   Nocentini,G., Ronchetti,S., Bartoli,A., Spinicelli,S., Delfino,D.,
           Migliorati,G. and Riccardi,C.
TITLE     Identification of three novel mRNA splice variants of Gitr
JOURNAL   Cell Death Differ. (2000) In press
REFERENCE  3 (bases 1 to 1020)
AUTHORS   Nocentini,G., Bartoli,A., Ronchetti,S., Giunchi,L., Cupelli,A.,
           Delfino,D., Migliorati,G. and Riccardi,C.
TITLE     Gene structure and chromosomal assignment of mouse GITR, a member
           of the tumor necrosis factor/nerve growth factor receptor family
JOURNAL   DNA Cell Biol. (2000) In press
REFERENCE  4 (bases 1 to 1020)
AUTHORS   Riccardi,C.
TITLE     Direct Submission
JOURNAL   Submitted (18-DEC-1996) Dept. of Clinical and Experimental
           Medicine, Perugia University, V. del Giochetto, Perugia, PG 06100,
           Italy
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             1 (bases 1 to 184184)
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             Direct Submission
             Submitted (21-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
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             requests: clonerequests@sanger.ac.uk
             On Mar 24, 2001 this sequence version replaced gi:13396610.
             ----- Genome Center
             Center: Sanger Centre
             Center code: SC
             Web site: http://www.sanger.ac.uk
             Contact: humquery@sanger.ac.uk
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             Center project name: bm465B22
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             Assembly program: XGAP4; version 4.5
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             Consensus quality: 178512 bases at least Q20
             Insert size: 180984; sum-of-contigs
             Insert size: 227650; 6.6% error; agarose-fp
             Quality coverage: 4.53x in Q20 bases; sum-of-contigs Quality
             coverage: 4.07x in Q20 bases; agarose-fp
             -----
             * NOTE: This is a 'working draft' sequence. It currently
             * consists of 33 contigs. The true order of the pieces
             * is not known and their order in this sequence record is
             * arbitrary. Gaps between the contigs are represented as
             * runs of N, but the exact sizes of the gaps are unknown.
             * This record will be updated with the finished sequence
             * as soon as it is available and the accession number will
             * be preserved.
             *
             * 1 5627: contig of 5627 bp in length
             * 5628 5727: gap of 100 bp
             * 5728 8009: contig of 2282 bp in length
             * 8010 8109: gap of 100 bp
             * 8110 11014: contig of 2905 bp in length
             * 11015 11114: gap of 100 bp
             * 11115 23404: contig of 12290 bp in length
             * 23405 23504: gap of 100 bp
             * 23505 26139: contig of 2635 bp in length
             * 26140 26239: gap of 100 bp
             * 26240 29766: contig of 3527 bp in length
             * 29767 29866: gap of 100 bp
             * 29867 33003: contig of 3136 bp in length
             * 33003 33102: gap of 100 bp
             * 33103 48262: contig of 15160 bp in length
             * 48263 48362: gap of 100 bp
             * 48363 52129: contig of 3767 bp in length
             * 52130 52229: gap of 100 bp
             * 52230 61454: contig of 9225 bp in length
             * 61455 61554: gap of 100 bp
             * 61555 63812: contig of 2258 bp in length
             * 63813 63912: gap of 100 bp
             * 63913 68103: contig of 4191 bp in length
             * 68104 68203: gap of 100 bp
             * 68204 73002: contig of 4799 bp in length
             * 73003 73102: gap of 100 bp
             * 73103 79538: contig of 6436 bp in length
             * 79539 79638: gap of 100 bp
             *
             * 79639 83620: contig of 3982 bp in length
             * 83621 83720: gap of 100 bp
             * 83721 97596: contig of 13876 bp in length
             * 97597 97696: gap of 100 bp
             * 97697 104680: contig of 6984 bp in length
             * 104681 104780: gap of 100 bp
             * 104781 107164: contig of 2384 bp in length
             * 107165 107264: gap of 100 bp
             * 107265 113440: contig of 6176 bp in length
             * 113441 113540: gap of 100 bp
             * 113541 121563: contig of 8023 bp in length
             * 121564 121663: gap of 100 bp
             * 121664 124320: contig of 2657 bp in length
             * 124321 124420: gap of 100 bp
             * 124421 128583: contig of 4163 bp in length
             * 128584 128683: gap of 100 bp
             * 128684 131527: contig of 2844 bp in length
             * 131528 131627: gap of 100 bp
             * 131628 134673: contig of 3046 bp in length
             * 134674 134773: gap of 100 bp
             * 134774 139103: contig of 4330 bp in length
             * 139104 139203: gap of 100 bp
             * 139204 145549: contig of 6346 bp in length
             * 145550 145649: gap of 100 bp
             * 145650 148007: contig of 2358 bp in length
             * 148008 148107: gap of 100 bp
             * 148108 151671: contig of 3564 bp in length
             * 151672 151771: gap of 100 bp
             * 151772 157223: contig of 5452 bp in length
             * 157224 157323: gap of 100 bp
             * 157324 161601: contig of 4278 bp in length
             * 161602 161701: gap of 100 bp
             * 161702 170342: contig of 8641 bp in length
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* 68117 68216: gap of 100 bp
* 68217 87865: contig of 19649 bp in length
* 87866 87965: gap of 100 bp
* 87966 95832: contig of 7867 bp in length
* 95833 95932: gap of 100 bp
* 95933 98546: contig of 2614 bp in length
* 98547 98646: gap of 100 bp
* 98647 104772: contig of 6126 bp in length
* 104773 104872: gap of 100 bp
* 104873 110195: contig of 5323 bp in length.

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## FEATURES

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ORIGIN

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  Ratio: 3.870         Gaps: 7
  Percent Similarity: 25.714  Percent Identity: 25.385

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## alignment\_block:

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1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17
|||||
16852 ATGGCACACACACGGCGATGGCGGCTTCCGGCCCTGTGCGGCTGCGC 16803

```

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17 aLeuLeuCysAlaLeuSerLeuGlnArgProThrGlyGlyProGlyC 34
|||||
16802 GCTGCTGTGGCGGCTCAGCCTGGGTGAGCGCCACCGGGGTCCCGGGT 16753

34 yGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50
|||||
16752 CGGGCCCTGGCGGCTCCTGCTTGGGACGGGACGACGCGCGTGTGTC 16703

51 ArgValHisThrThrArgCysCysArgAspTyr ..
|||||
16702 CGGTTTACACACAGACGCGCTGCTGCCGGGATTACCCGGGTAAGTAACCGC 16653

61 ..
16652 GTTTACTTAACGGGACCGGCCAAGCGGTCCCGCGGAAGCGGATGGGT 16603

61 ..
16602 GGGCGCCCCCTTCCCGTGTCTCAGACCGCGCTTCTGAGGTCTAAGGAGG 16553

61 ..
16552 GTGGGCACAGACCGCCCGCAGCAGCGGGAGCCCTTCCGGAGGGAGGAGGATC 16503

61 ..
16502 CCAGAGGGAGCGGAGGTGTGCCAGCTCCAGCCAGTGGCCCCCGCGGA 16453

61 ..
16452 GCAGGGGTGAGCCAGGTGGGAGCGCCCTCAAGAGGGGTCTGGGTCCTGGA 16403

61 ..
16402 GGTGGAGGACGGCTGTTCAGAGTCTCTGCGGCGGGTCTGAGCCCTTGG 16353

61 ..
16352 CCATCGCCACAGCCCCCTTCTGCCAGTTGAGGGCCCCCCTGCACCACCGT 16303

61 ..
16302 CTGCGCTGCTGCTGCTGCTGACCTGCACCTGGGGATGAGGGTTTCAGCTG 16253

61 ..
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61 ..
16202 TTCTCCAGGGCCTGTGGGTTGGGAAGGAGGCTCTGTCCGGAGGCCAG 16153

61 ..
16152 TGTGGTGGTGGTGGGACAGCAGCGCCCGACACACAGGAGCGGCGCTC 16103

61 ..
16102 TGAGGTGTCAGCGGGCTCCAGGGGACTGTGCACTGTGGGGGCCACCC 16053

61 ..
16052 TGGGTCTGCAGGGGACAGCTCCTGGTTGCATATGAGTTAGCACCTGGGC 16003

61 ..
16002 AGGGCAGCTGTGGGGCGCAAGGGGAGTAGCCAGGCCACATGCCCCA 15953

61 ..
15952 GGAGAAAGACAGACAGCTGGATAAACCCAGGGTCCAGACTCCACGACGAG 15903

61 ..

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15902 CCCTCTGCTCCCTGGAGCCAACTGTGGGTGGAGAACGGACAACCTCACTC 15853  
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62 .....Pro.GlyGluGluCysCysSerGluT 70  
15802 GCTGGGGGGCTGGGCTGTCTCTGCCCCAGGGAGGAGTGTCTTCCGAGT 15753  
70 rPAspCysMetCysValGlnProGluPheHisCysGlyAspProCysCys 86  
15752 GGGACTGCATGTGTCTCAGGCTGAATTCCTACTGGGAGACCTTGTCTGC 15703  
87 ThrThrCysArgHisHisProCysProGlyGlnGlyValGlnSer.G 103  
15702 ACGACCTGCCGGCACCACCTTGTCCCCAGGCCAGGGGGTACAGTCCCA 15653  
103 ln..... 103  
15652 GGGTAAGTTCCTGGAGTGCCTCTGGGAGTCCACACAGGCCAGGGGTTCCA 15603  
103 ..... 103  
15602 CTAGGGCCCCGAGGAGAGCTCGTGGGCACAGGTGTCCGGCAGGACATGT 15553  
103 ..... 103  
15552 GGTGTGGGGTCCGGAGTCTCTGTGAGCCCGGGCAGGCCAGCCATGCTC 15503  
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15502 AGGCACCACAGGCCATGAAGCTCTGGGGGTGTCTGTGCCCTGCTTTCTCA 15453  
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103 ..... 103  
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103 ..... 103  
14852 CCCCTGCACCTGGCCTGACGCCCTCTCTCATCCATCCAGCAACTCCACCAG 14803  
104 .....GlyLysPheSerPheG 109  
14802 CCTCCCTCCCTCCCTCCCCACACCCACACAGGGAATTCAGTTTTG 14753  
109 lypheGlnCysIleAspCysAlaSerGlyThrPheSerGlyGlyHisGlu 125  
14752 GCTTCCAGTGTATCGACTGTGCTCGGGAGCCTTCTCCGGGGGCCACGAA 14703  
126 GlyHisCysLysProTrpThrAsp  
14702 GGCACCTGCAAACTTGGACAGAGTGAAGTCTGGTGGGCCCTGCCGGTG 14653  
133 ..... 133  
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133 ..... 133  
14602 CCCACAGCACGAGGAGGAGCAGCGGGGGGTGATCGGAGGCCGTGTCC 14553  
134 .....CysThrGlnPheG 138  
14552 GGGGCTGATAGGAGCGCGCTCCATGTATCCAGCTGCACCCAGTTCCG 14503  
138 yPheLeuThrValPheProGlyAsnLysThrHisAsnAlaValCysValP 155  
14502 GTTCTCACTGTGTTCCTTGGGAACAAGACCCACAACGCTGTGTGGTCC 14453  
155 roGlySerProProAlaGluProLeuGlyTrpLeuThrValValLeuLeu 171  
14452 CAGGCTCCCGCGCGCAGAGCGCTTGGGTGGCTGACCGTCTCTCTCTG 14403  
172 AlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnLeuGlyLeuHi 188  
14402 GCCGTGGCGCGCTGCTCTCTCTGACCTCGGCCACGCTTGGAGTGA 14353  
188 sIleTrpGlnLeuArg..... 193  
14352 CATCTGGCAGCTGAGGAGTCAAGTGTGTGGCCCCGAGGTCTGTACAGC 14303  
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210 SerCysGlnPheProGluGluArgGlyGluArgSerAlaGluGlu 226  
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185 LeuGlyLeuHisIlePrpGlnLeuArg..lys..... 194  
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195 .....ThrGlnLeuLeuGluValProProSerThrG 206  
651 TGGCCCCCTGCATACACGCTGCTGCTGGAGGTGGCGGCTGACCG 700  
206 luAspAlaArgSerCysGlnPheProGluGluArgGlyGluArgSer 222  
701 AAGAGCCAGAGCTGCCAGTTCCTCCGAGAGAGCGGGGCGGAGCATCG 750  
223 AlaGluGluGlyArgLeuGlyAspLeuTrpVal 234  
751 GCAGAGGAGAGGGCGCTGGGAGACCTGTGGGTG 786

seq\_name: gb\_pat1:AR108739

seq\_documentation\_block:  
LOCUS AR108739 723 bp DNA PAT 14-FEB-2001  
DEFINITION Sequence 5 from patent US 6111090.  
ACCESSION AR108739  
VERSION AR108739.1 GI:12824226

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE  
1 (bases 1 to 723)  
AUTHORS Gorman,D.M., Randall,T.D. and Zlotnik,A.  
TITLE Mammalian cell surface antigens; related reagents  
JOURNAL Patent: US 6111090-A 5 29-AUG-2000;  
FEATURES  
Location/Qualifiers  
1..723  
/organism="unknown"

BASE COUNT 80 a 92 c 163 g 94 t 294 others  
ORIGIN

alignment\_scores:  
Quality: 1075.50 Length: 241  
Ratio: 5.487 Gaps: 1  
Percent Similarity: 81.328 Percent Identity: 76.349

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US-09-512-363-2 x AR108739 ..

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17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyProGlyC 34  
51 NVTNTNTGYGCNYTNWSYNTNGGNCARMGNCNACNGGNGCCNGNT 100  
34 yGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
101 GYGNGCCNGGNGNTNTNTNTNGGNCAGGNCACNGAYGCMGNTGYTG 150  
51 ArgValHisThrArgCysArgAspTyrPrpGlyGluGluCysC 67  
151 MNGNTNCAYACACNACNMGNTGTGYMGNGAYTAYCCNGGNGARGARTGTG 200  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
201 YWSNGARTGGAYGTATGTGTGTCNARCNGARTTYCAYTGYGGNGAYC 250

84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
251 CNTGYTGYACNACNTGYMGNCAYCAYCCNTGYCCNCCNGGNCARGNGTN 300  
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
301 CARWSNCARGNAARTTWSNTTYGGNTTYCARTGYATHGAYTGYGCNWS 350  
117 rGlyThrPheSerGlyGlyGluGlyHisCysLysProTrpThrAspC 134  
351 NGGNACNTTWSNGGNGNCAYGARGNCAYTGYAARCCNTGGACNGAYT 400  
134 yThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
401 GYACNCARTTYGGNTTYTNACNTNTTYCCNGGNAAYAAACNCAVAY 450  
151 AlavalCysValProGlySerProAlaGluProLeuGlyTrpLeuTh 167  
451 GCNGTNTGYGTNCCNGGWSNCCNCCNGCARGCNTVTNGTGGYTTCAC 500  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
501 NGTNGTNTNTNGCNGTNGCNGCNTGYGTNTYNTYNTNACNWSNGCNC 550  
184 InLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
551 ARYTNGGNTNCAYATHGGCARTTNMGNWSCARTGYATGTGCCNMGN 600  
194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
601 GARACNCARTYNTNTYNTGARGTNCNCCNWSNACNGARGAYGCMGWS 650  
210 rCysGlnPheProGluGluArgGlyGluArgSerAlaGluGluLysG 227  
651 NTGYCARTTYCCNGARGARGMGNGGNGARMGNWSNCGNARGARGAARG 700  
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seq\_name: gb\_pr5:AF241229

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DEFINITION Homo sapiens GTR-D mRNA, complete cds.  
ACCESSION AF241229

VERSION AF241229.1 GI:7542578

KEYWORDS

SOURCE human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 865)

AUTHORS

Riccardi,C.

TITLE

JOURNAL

REFERENCE

2 (bases 1 to 865)

AUTHORS

Riccardi,C.

TITLE

JOURNAL

Submitted (02-MAR-2000) Clinical and Experimental Medicine,  
University of Perugia, Via del Giochetto 06100, Italy

FEATURES

Location/Qualifiers

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BASE COUNT 141 a 272 c 312 g 140 t  
ORIGIN

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Quality: 948.50 Length: 234  
Ratio: 5.579 Gaps: 1  
Percent Similarity: 72.650 Percent Identity: 72.650

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|||||  
51 GCTGCTGTGGCGCTACGCTGGGTCAGCGGCCACCGCGGGGTCCTCGG 100  
34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
|||||  
101 CGGCGCTTGGCGGCTCTCTGCTGGGCGGGAAGCAGCGCGCTGCTGC 150  
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy 67  
|||||  
151 CGGTTTCACAGCAGCGCTGCTGCGCGCATTACCGCGCGGAGAGTGCTG 200  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP 84  
|||||  
201 TTCGAGTGGGACATGCTGTGTCACGCCCTGAATCCACATCCGCGGAGAC 250  
84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
|||||  
251 CTGTGCTGACGACCTGCGCGGACCACTTGTCCCGCCAGCGCGGGGTA 300  
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
|||||  
301 CAGTCCCAAGGGAAATTCAGTTTGGCTTCCAGTGTATCGACTGTGCTC 350  
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrAspC 134  
|||||  
351 GGGACCTTCCTCCGGGGCCACGAAGGCCACTGCAAACTTGGACAGACT 400  
134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
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401 GCTG..... 404  
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
404 ..... 404  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
404 ..... 404  
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seq\_name: gb\_htg20:AL162741

seq\_documentation\_block:

LOCUS AL162741 110195 bp DNA HTG 06-MAR-2001  
DEFINITION Homo sapiens chromosome 1 clone RP5-902P8, \*\*\* SEQUENCING IN  
PROGRESS \*\*\*, 13 unordered pieces.

ACCESSION AL162741

VERSION AL162741.11 GI:13273625

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 110195)

REFERENCE McIay, K.

TITLE Direct Submission

JOURNAL

Submitted (04-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone  
requests: clonerequest@sanger.ac.uk

On Mar 11, 2001 this sequence version replaced gi:13234857.

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: dj902P8

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator ET-amersham; 23% of reads Chemistry:

Dye-terminator Big Dye; 76% of reads

Consensus quality: 106361 bases at least Q40

Consensus quality: 107393 bases at least Q30

Consensus quality: 108133 bases at least Q20

Insert size: 108995; sum-of-contigs

Insert size: 160089; 6.7% error; agarose-fp

Quality coverage: 6.79x in Q20 bases; sum-of-contigs Quality

coverage: 4.76x in Q20 bases; agarose-fp

-----

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 13 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 3573 3672: contig of 3572 bp in length

\* 3673 7177: contig of 3505 bp in length

\* 7178 7277: gap of 100 bp

\* 7278 11454: contig of 4177 bp in length

\* 11455 11554: gap of 100 bp

\* 11555 22201: contig of 10647 bp in length

\* 22202 22301: gap of 100 bp

\* 22302 35252: contig of 12951 bp in length

\* 35253 35352: gap of 100 bp

\* 35353 42069: contig of 6717 bp in length

\* 42070 42169: gap of 100 bp

\* 42170 62318: contig of 20149 bp in length

\* 62319 62418: gap of 100 bp

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 DEFINITION Sequence 1 from Patent WO0103720.  
 ACCESSION AX074381  
 VERSION AX074381.1 GI:12710522  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1008)  
 AUTHORS Williams, P.M. and Gerritsen, M.E.  
 TITLE Promotion or inhibition of angiogenesis and cardiovascularization  
 by tumor necrosis factor ligand/receptor homologs  
 JOURNAL Patent: WO 0103720-A 1 18-JAN-2001;  
 Genentech, Inc. (US)  
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 DEFINITION Sequence 15 from Patent WO0105972.  
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 REFERENCE 1 (bases 1 to 1008)  
 AUTHORS Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,  
 Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
 Tumas, D., Watanabe, C.K. and Wood, W.I.  
 TITLE Compositions and methods for the treatment of immune related  
 diseases  
 JOURNAL Patent: WO 0105972-A 15 25-JAN-2001;  
 Genentech, Inc. (US)  
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DEFINITION Sequence 4 from Patent WO0103720. PAT 06-FEB-2001

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ORGANISM Homo sapiens  
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AUTHORS Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 951)  
JOURNAL Williams,P.M. and Gerritsen,M.E.  
by tumor necrosis factor ligand/receptor homologs  
Patent: WO 0103720-A 4 18-JAN-2001;  
Genentech, Inc. (US)  
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LOCUS AF125304 726 bp mRNA PRI 02-APR-1999
DEFINITION Homo sapiens glucocorticoid-induced TNFR-related protein (TNFRSF18)
mRNA, complete cds.
ACCESSION AF125304
VERSION AF125304.1 GI:4558502
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 726)
AUTHORS Gurney,A.L., Masters,S.A., Huang,A., Pitti,R.M., Mark,M.,
Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.
TITLE Identification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR
JOURNAL Curr. Biol. (1999) In press
REFERENCE 2 (bases 1 to 726)
AUTHORS Gurney,A.L., Masters,S.A., Huang,A., Pitti,R.M., Mark,M.,
Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-1999) Molecular Oncology, Genentech, 1 DNA Way,
South San Francisco, CA 94080, USA
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VERSION AR108738.1 GI:12824225
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1006)
AUTHORS Gorman,D.M., Randall,T.D. and Zlotnik,A.
TITLE Mammalian cell surface antigens; related reagents
JOURNAL Patent: US 6111090-A 3 29-AUG-2000;
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 DEFINITION Sequence 38 from Patent WO0073452.

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 REFERENCE 1 (bases 1 to 1008)  
 AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,  
 Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,  
 Tumas,D., Watanabe,C.K. and Wood,W.I.  
 TITLE Compositions and methods for the treatment of immune related  
 diseases  
 JOURNAL Patent: WO 0073452-A 38 07-DEC-2000;  
 Genentech, Inc. (US)  
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151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
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234 al 234
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701 TG 702

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seq\_name: gb\_pat2:AX074382

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seq_documentation_block: 723 bp DNA PAT 06-FEB-2001
LOCUS AX074382
DEFINITION Sequence 2 from Patent WO0103720.
ACCESSION AX074382
VERSION AX074382.1 GI:12710523
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 723)
AUTHORS Williams,P.M. and Gerritsen,M.E.
TITLE Promotion or inhibition of angiogenesis and cardiovascularization
by tumor necrosis factor ligand/receptor homologs
JOURNAL Patent: WO 0103720-A 2 18-JAN-2001;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
source
1..723
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 106 a 236 c 254 g 127 t
ORIGIN

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alignment_scores:
Quality: 1322.50 Length: 241
Ratio: 5.652 Gaps: 1
Percent Similarity: 97.095 Percent Identity: 96.680
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34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50
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251 CTTCGTCACACACTGCGCGCACCACTTGTCCCCAGCGAGGGGTA 300
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701 TG 702

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seq\_name: gb\_pr5:AF125304



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seq\_documentation\_block:

ID AAA58588 standard; DNA; 813 BP.

XX AC AAA58588;

XX DT 20-OCT-2000 (first entry)

XX DE DNA encoding tumour necrosis factor receptor ztnfr10.

XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;  
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;  
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;  
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;  
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;  
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;  
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;  
 KW immune response; immunosuppression; graft rejection; joint pain;  
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;  
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;  
 KW renal artery stenosis; occlusion; cholesterol; renal emboli; ztnfr10;  
 KW PCR primer; ss.

XX KW Homo sapiens.

OS WO2000040716-A2.

XX PN 13-JUL-2000.

XX PD 07-JAN-2000; 2000WO-US00396.

XX PF 07-JAN-1999; 99US-0226533.

XX PR (ZYMO ) ZYMOGENETICS INC.

XX PT Gross JA, Xu W, Madden K, Yee DP;

XX DR WPI; 2000-452538/39.

XX PT Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,  
 PT renal disease, graft versus host disease, and inflammation, comprises  
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -  
 XX Example 10; Page 169; 175pp; English.

XX CC The present sequence encodes tumour necrosis factor receptor  
 CC ztnfr10. The specification describes extracellular domains of  
 CC BR43x2 (an isoform of the transmembrane activator and CAML-interactor  
 CC (TACI) receptor), TACI or BCMA (a related B cell protein). These contain  
 CC a cysteine rich domain, and are used for inhibiting ztnf4 activity. They  
 CC may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand  
 CC engagement associated with activated or resting B lymphocytes, effector  
 CC T-cells, or with antibody production. The antibody production is  
 CC associated with an autoimmune disease selected from systemic lupus  
 CC erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid

CC arthritis. The ztnf4 activity and BR43x2, TACI or BCMA receptor-ligand  
 CC engagement is associated with asthma, bronchitis, emphysema, and stage  
 CC renal failure, glomerulonephritis, vasculitis, nephritis, pyelonephritis,  
 CC renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy,  
 CC amyloidosis, moderating immune response, immunosuppression, graft  
 CC rejection, graft versus host disease, inflammation, insulin dependent  
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or  
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,  
 CC agonists or antagonists can be used to treat hypertension, renal artery  
 CC stenosis, or occlusion, and cholesterol or renal emboli.  
 XX  
 SQ Sequence 813 BP; 114 A; 276 C; 283 G; 140 T; 0 other;

alignment\_scores:

Quality: 1317.50 Length: 240  
 Ratio: 5.655 Gaps: 1  
 Percent Similarity: 97.083 Percent Identity: 96.667

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US-09-512-363-2 x AAA58588

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seq\_name: /SDS8/gcdata/geneseq/geneseq/NA2000.DAT:AAZ49948

seq\_documentation\_block:

ID AAZ49948 standard; cDNA; 763 BP.

XX AC AAZ49948;

DT 18-MAY-2000 (first entry)

DE Human molecule associated with cell proliferation, MACP-5 cDNA.

XX Human: molecule associated with cell proliferation: MACP-5;

KW Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;  
 KW anti-inflammatory; antipruritic; anti-HIV; antiasthmatic; anaemia;  
 KW dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic;  
 KW immunosuppressive; osteopathic; antiarthritic; uropathic; antileuker;  
 KW ophthalmological; diagnosis; treatment; prevention; immune disorder;  
 KW cell proliferative disorder; actinic keratosis; arteriosclerosis;  
 KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 17..724

XX /tag= a

XX /product= "MACP-5"

XX misc\_feature 1..763

XX /tag= b

XX /label= MACP-5\_cDNA

XX /note= "This sequence is described as 764 bases long

in the Sequence Listing but a sequence of only 763 bases

is shown"

XX W0200005374-A2.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-US16637.

XX 22-JUL-1998; 98US-0093827.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;

XX WPI; 2000-182699/16.

XX P-PSDB; AAY44825.

XX Polypeptides and polynucleotides useful for treating and detecting cell

proliferation disorders e.g. actinic keratosis, and immune disorders

e.g. Crohn's disease

XX Claim 7; Page 67; 67pp; English.

PS The present sequence is a cDNA encoding molecule associated with cell

proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMN0706

cDNA library. This sequence is expressed in cardiovascular and

haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,

CC hepatotropic, antiinflammatory, antipruritic, cytostatic, antiasthmatic,

CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,

CC immunosuppressive, osteopathic, antiarthritic, uropathic, antileuker,

CC and ophthalmological activities. The present sequence is useful in the

CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.

XX Sequence 763 BP; 114 A; 252 C; 264 G; 133 T; 0 other;

alignment\_scores:

Quality: 1310.50

Ratio: 5.649

Percent Similarity: 96.667

Percent Identity: 96.250

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US-09-512-363-2 x AAZ49948

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 211 sGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysGlyA 228  
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XX WO200073452-A2.  
 XX 07-DEC-2000.  
 XX 02-JUN-2000; 2000WO-US15264.  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WI;

XX WPI: 2001-025253/03.  
 DR P-PSDB; AAB50910.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -

XX Claim 48; Fig 17; 218pp; English.

XX The present sequence is one of thirty three nucleic acids encoding PRO  
 CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.

XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

# alignment\_scores:

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 Ratio: 5.652 Gaps: 1  
 Percent Similarity: 97.095 Percent Identity: 96.680

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AC AAC97479;
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XX 28-FEB-2001 (first entry)
XX
XX Human angiogenesis-associated protein PRO364 cDNA, SEQ ID NO:141.
XX
XX Human; angiogenesis-associated protein; PRO: endothelial cell growth;
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
KW gene therapy; transgenic animal; ss.
XX
XX Homo sapiens.
OS
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XX WO200053753-A2.
XX
XX 14-SEP-2000.
XX
XX 05-JAN-2000; 2000WO-US00219.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 14-MAY-1999; 99US-0134287.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 26-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2001-090793/10.
DR P-PSDB; AAB53090.
XX
XX
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -
XX
XX Claim 58; Fig 53; 293pp; English.
XX
XX The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial

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CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof.
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
CC gene therapy. PRO nucleic acids can also be used to produce transgenic
CC animals useful for the development and screening of potential
CC therapeutic agents. The present sequence represents a cDNA encoding a PRO
CC protein of the invention.
XX
XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;
SQ

```

```

alignment_scores:
Quality: 1322.50      Length: 241
Ratio: 5.652          Gaps: 1
Percent Similarity: 97.095 Percent Identity: 96.680

alignment_block:
US-09-512-363-2 x AAC97479 ..

Align seg 1/1 to: AAC97479 from: 1 to: 1008

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17 aleuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34
171 GCTGCTGTGGCGGCTCAGCTGGGTACGGCCCCACCGGGGGTCCGGGT 220
34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAlaAlaArgCysCys 50
221 GCGGCCCTGGGCGCTCTCTGCTTGGACGGGAACGACGCGCGCTGCTGC 270
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy 67
271 CGGGTTCACACAGCAGCGCTGCTGCGCGGATTACCGGGCGGAGAGTGTG 320
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84
321 TTCGAGTGGGACTGCATGTGTCTCCAGCCTGAATTCACACTGCGGAGACC 370
84 roCysCysThrThrCysArgHisHisProCysProGlyGlnGlyVal 100
371 CTTGTGTCAGCAGCTTCGGCGGACACACCTTGTCCCCAGCCAGGGGTA 420
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
421 CAGTCCCAGGGGAAATTTCAGTTTGGCTTCCAGTGTATCGACTGTGCCCTC 470
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC 134
471 GGGGACCTTCCTCCGGGGGCCACGAAGGCCACTGCAAACTTGGACAGACT 520
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521 GCACCCAGTTCGGGTTCCTCACTGTGTTCCCTGGGAACAAGACCCACAAC 570
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
571 GCTGTGTGCTGCCAGGTTCCCGCGGCGAGACCGCTTGGGTGGCTGAC 620
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621 CGTCGTCTCTCTGGCGGTGGCGGCTGCGTCTCTCTCTGACCTCGGCC 670

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PR 20-JUL-1999; 99US-0144758.  
 PA (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 XX Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
 XX Wood WI;  
 XX WPI; 2001-103149/11.  
 DR P-PSDB; AAB20115.  
 XX  
 XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes -  
 XX  
 XX Claim 21; Fig 15; 127pp; English.  
 PS  
 CC The present sequence is that of cDNA clone DNA47365-1206 (ATCC 209436)  
 CC encoding novel human immunomodulator protein PRO364 (UNQ319) (see  
 CC AAB20115). The clone was isolated from a small intestine library.  
 CC The predicted protein (26 kDa, pI 6.34) shows homology to mouse  
 CC GTR protein and may be its human counterpart. The invention  
 CC provides polynucleotides (see AAF30050-62) encoding novel human PRO  
 CC proteins (see AAB20108-20) including PRO364. Claimed compositions  
 CC comprising these proteins or their agonists are useful for increasing  
 CC infiltration of inflammatory cells into a tissue of a mammal,  
 CC stimulating or enhancing an immune response in a mammal, or  
 CC increasing the proliferation of T-lymphocytes in a mammal in response  
 CC to an antigen. Claimed compositions comprising the PRO polypeptide  
 CC or its antagonist have the opposite effect. A claimed method for  
 CC treating an immune related disorder, such as a T cell disorder,  
 CC involves administering the PRO polypeptide, an agonist antibody or  
 CC an antagonist antibody. The disorder is selected from systemic  
 CC lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, spondyloarthritis, systemic  
 CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
 CC systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,  
 CC autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinated diseases (such as  
 CC multiple sclerosis), autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
 CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
 CC skin diseases (such as bullous skin disease, erythema multiforme and  
 CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
 CC atopic dermatitis, food hypersensitivity and urticaria), immunologic  
 CC diseases of the lung and transplantation associated diseases (such  
 CC as graft rejection and graft-versus-host disease) (all claimed).  
 CC Claimed methods of diagnosing these disorders comprise detecting  
 CC the level of expression of the PRO gene. Also claimed are a method  
 CC of identifying a compound capable of inhibiting the expression or  
 CC activity of the PRO polypeptide, vectors, host cells, antibodies  
 CC and a method of stimulating the proliferation of T-lymphocytes  
 CC using PRO364.  
 XX  
 SQ Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:  
 Quality: 1322.50 Length: 241  
 Ratio: 5.652 Gaps: 1  
 Percent Similarity: 97.095 Percent Identity: 96.680

alignment\_block:  
 US-09-512-363-2 x AAF30057 ..

Align seg 1/1 to: AAF30057 from: 1 to: 1008

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 17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34

||||||||||||||||||||||||||||||||||||||||||||||||  
 171 GCTGCTGTGCGCGCTCAGCTGGGTGAGCGCCACCAGCGGGGTCCCCGGT 220  
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seq\_documentation\_block:

ID AAC90566 standard; cDNA; 1008 BP.

XX AAC90566;

XX AAC90566;

XX 21-MAR-2001 (first entry)

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX Human PRO364 cDNA.

XX WO200073445-A2.  
 XX 07-DEC-2000.  
 XX 17-MAY-2000; 2000WO-US13705.  
 XX 02-JUN-1999; 99WO-US12252.  
 XX 23-JUN-1999; 99US-0141037.  
 XX 20-JUL-1999; 99US-0144758.  
 XX 26-JUL-1999; 99US-0145698.  
 XX 28-JUL-1999; 99US-0146222.  
 XX 01-SEP-1999; 99WO-US20111.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 30-NOV-1999; 99WO-US28409.  
 XX 16-DEC-1999; 99WO-US28565.  
 XX 16-DEC-1999; 99WO-US30095.  
 XX 11-FEB-2000; 2000WO-US03565.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 18-FEB-2000; 2000WO-US04342.  
 XX 24-FEB-2000; 2000WO-US05004.  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX 10-MAR-2000; 2000WO-US06319.  
 XX 15-MAR-2000; 2000WO-US06884.  
 XX 21-MAR-2000; 2000WO-US07532.  
 XX 30-MAR-2000; 2000WO-US08439.  
 XX (GETH ) GENENTECH INC.  
 XX PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 XX PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
 XX PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX DR WPI: 2001-025251/03.  
 XX DR P-PSDB; AAB50954.  
 XX PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 XX PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 XX PT disorders in a mammal -  
 XX PS Claim 60; Fig 7; 182pp; English.  
 XX CC The present sequence is one of seventeen nucleic acids encoding PRO  
 XX CC polypeptides. The PRO nucleic acids, polypeptides, agonists and  
 XX CC antagonists are useful for treating cardiovascular, endothelial or  
 XX CC angiogenic disorders in a mammal. Examples of these disorders include  
 XX CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 XX CC atherosclerosis, hypertension, arterial restenosis, Reynaud's disease,  
 XX CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis  
 XX CC and lymphangitis. The PRO polypeptides and antagonists are also used to  
 XX CC prevent tumour angiogenesis and for treating periodontal diseases. They  
 XX CC are also used to stimulate wound healing and tissue regeneration.  
 XX CC The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful  
 XX CC for diagnosing a cardiovascular, endothelial or angiogenic disorder.  
 XX SQ Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

## alignment\_scores:

Quality: 1322.50 Length: 241  
 Ratio: 5.652 Gaps: 1  
 Percent Similarity: 97.095 Percent Identity: 96.680

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US-09-512-363-2 x AAC90566 ..

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## seq\_documentation\_block:

ID AAC91469 standard; cDNA; 1008 BP.

XX AAC91469;

XX 21-MAR-2001 (first entry)

XX Human PRO364 cDNA.

XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KW antirheumatic; cardiac; antianaemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
 KW antiallergic; antiasthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy; ss.  
 XX Homo sapiens.

PA (GETH ) GENENTECH INC.  
 XX  
 PI Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
 XX  
 DR WPI; 2000-412325/35.  
 XX P-PSDB; AAY71467.  
 DR  
 XX New composition useful for inhibiting neoplastic cell growth and for  
 PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
 PT their antagonists -  
 XX  
 XX Claim 20; Fig 3; 108pp; English.  
 PS  
 XX The present sequence is the cDNA clone, designated as DNA47365-1206,  
 CC encoding the human PRO364 polypeptide. It is isolated from human small  
 CC intestine tissue cDNA library, identified using probes based on the  
 CC consensus sequence DNA44825, relative to the Incyte expressed sequence  
 CC tag (EST) 3003460. This EST has homology to tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows  
 CC homology to members of the TNFR family and mouse GITR protein.  
 CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as  
 CC a neoplastic cell growth inhibitor and is used for treating tumours,  
 CC using an effective amount of PRO655, PRO364 and PRO344. This composition  
 CC is especially useful for treatment of human cancers such as breast,  
 CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.  
 XX  
 SQ Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:  
 Quality: 1322.50 Length: 241  
 Ratio: 5.652 Gaps: 1  
 Percent Similarity: 97.095 Percent Identity: 96.680

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US-09-512-363-2 x AAD01240 ..

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 seq\_documentation\_block:  
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 XX  
 AC AAC85433;  
 XX  
 DT 08-MAY-2001 (first entry)  
 XX  
 DE Clone DNA47365-1206 containing native PRO364 cDNA.  
 XX  
 KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
 KW hGTR; ligand; hGTR; PRO175; tumour necrosis factor receptor; TNFR;  
 KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
 KW myocardial infarction; PGF\_2alpha; trauma; cancer; angiogenesis;  
 KW age-related macular degeneration; antibody; periodontal disease;  
 KW vascular-related drug targeting; atherosclerosis; hypertension;  
 KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
 KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
 KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis; ss.  
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 OS Chimeric - Homo sapiens.  
 OS Chimeric - Synthetic.  
 XX  
 FH Key Location/Qualifiers  
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 FT /product= "PRO364"  
 FT /note= "Human cDNA fragment nucleotides 121..843"  
 FT primer\_bind 498..518  
 FT /\*tag= b  
 FT /bound\_moiety= "47365.tm.f"  
 FT primer\_bind 524..550  
 FT /\*tag= c  
 FT /bound\_moiety= "47365.tm.p"  
 FT /note= "probe binding site"  
 FT primer\_bind complement (555..575)  
 FT /\*tag= d  
 FT /bound\_moiety= "47365.tm.r"  
 XX  
 WO200103720-A2.  
 PN  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 11-JUL-2000; 2000WO-US18867.  
 XX  
 PR 12-JUL-1999; 99US-0143304.



PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.

DR P-PSDB; AAB33431.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

XX Claim 23; Fig 35; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, autoimmune vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

# alignment\_scores:

Quality: 1322.50 Length: 241  
 Ratio: 5.652 Gaps: 1  
 Percent Similarity: 97.095 Percent Identity: 96.680

# alignment\_block:

US-09-512-363-2 x AAC58596 ..

Align seg 1/1 to: AAC58596 from: 1 to: 1008

1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17  
 121 ATGGCACACACGGGCGGATGGCGGCTTTCGGGCGCTGTGGCGGCTGCTGC 170  
 17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
 171 GCTGCTGTGGCGCTCAGCTGGGTGAGCGCCACCGGGGGTCCCGGGT 220  
 34 yGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
 221 GCGGCGCTGGGCGCTCTCTGCTTGGGACGGGAACGGACGCGCTGCTGC 270  
 51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGlyCysC 67  
 271 CGGGTTTCACACGACGCGCTGCTGCGCGATTACCGGGGAGAGAGTGTG 320  
 67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
 321 TTCCGAGTGGGACTGATGTGTCTCAGCGCTGAATTCACCTGGGAGACC 370  
 84 rOCysCysThrThrCysArgHisHisProCysProGlyGlnGlyVal 100  
 371 CTGTGTCACGACCTGCCGACACACCTTGTCCCGACGAGCGGGGTA 420  
 101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlase 117  
 421 CAGTCCCGAGGGAAATTCAGTTTGTGGCTTCCAGTGTATCGACTGTGCTC 470  
 117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysCysLysProTrpThrAspC 134

471 GGGGACCTTCTCCGGGGCCACGAAGCCACTGCAAACTTTGGACAGACT 520  
 134 yThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
 521 GCACCCAGTTCGGGTTTCTCACTGTGTTCCCTGGGAACAAGACCCACCAAC 570  
 151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
 571 GCTGTGCTGCCAGGTCCTCCCGCGGCGAGCGCTTGGGTGGCTGAC 620  
 167 rValValLeuLeuAlaValAlaCysValLeuLeuLeuLeuThrSerAlaG 184  
 621 CGTCTCTCTCTGCGCGGCGCTGCTGCTCTCTCTGACCTCGGCC 670  
 184 InLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
 671 AGCTTGAGCTCACATCTGGCAGCTGAGAGTCAGTGCATGTGGCCCGCA 720  
 194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
 721 GAGACCCAGCTGCTGTGGAGGTGCGCGCTGACCGAGAGCGCCAGAG 770  
 210 rCysGlnPheProGluGluArgGlyGluArgSerAlaGluGlyLysG 227  
 771 CTGCCAGTTCCTCCGAGGAAGAGCGGGGCGAGCGATCGCAGAGGAGAAG 820  
 227 LyArgLeuGlyAspLeuTrpVal 234  
 821 GCGGCTGGGAGACTGTGGGTG 843

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA77604

# seq\_documentation\_block:

ID AAA77604 standard; cDNA; 1008 BP.

XX AAA77604;

XX 07-NOV-2000 (first entry)

XX Human PRO364 cDNA sequence SEQ ID NO:116.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytotstatic; gene therapy; vaccine; ss.

OS Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1998; 98WO-US25108.

XX 16-DEC-1998; 98US-0112850.

XX 12-JAN-1999; 99US-0115554.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 26-JUL-1999; 99US-0144758.

XX 01-SEP-1999; 99WO-US20111.

XX 13-SEP-1999; 99WO-US20594.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-OCT-1999; 99US-0162506.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;

XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;

XX Watanabe CK, Williams PM, Wood WT;

DR WPI; 2000-412154/35.

DR P-PSDB; AAB24409.

XX Nucleic acids encoding PRO polypeptides useful for preventing,

PT diagnosing and treating disorders in mammals

PT angiogenic disorders in mammals

XX Claim 61; Fig 43; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides

CC useful for preventing, diagnosing and treating disorders in mammals

CC cardiovascular, endothelial or angiogenic disorder in mammals by

CC modulating cell proliferation, angiogenesis and cardiovascularisation,

CC and for identifying agonists and antagonists of these processes. The

CC nucleic acids and the proteins they encode may be used in the

CC prevention, treatment and diagnosis of diseases associated with

CC inappropriate PRO expression such as cardiovascular, endothelial or

CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and

CC cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors

CC containing them and the PRO polypeptide may be used to treat disorders

CC associated with decreased PRO expression. AAA77510 to AAA77721 and

CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in

CC the exemplification of the present invention.

XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

## alignment\_scores:

Quality: 1322.50 Length: 241

Ratio: 5.632 Gaps: 1

Percent Similarity: 97.095 Percent Identity: 96.680

## alignment\_block:

US-09-512-363-2 x AAA77604 ..

Align seg 1/1 to: AAA77604 from: 1 to: 1008

1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17

121 ATGCGACAGCAGCGGCGATGGCGCGTTTCGGCCCTGTGGCGCTGGC 170

17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyProGlyC 34

171 GCTGCTGTGGCGGCTCAGCCYGGGTCAAGCCGCCACCGGGGGTCCCGGGT 220

34 ysGlyProGlyArgLeuLeuGlyThrGlyThrArgAlaArgCysCys 50

221 CGCGCCCTGGCGGCTCTGCTTGGAGGGAACGACGCGCGCTGCTGCG 270

51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy 67

271 CGGGTTCACAGCAGCGCGTGTGCGCGGATTAACCGGCGAGGAGTGCTG 320

67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84

321 TTCGGAGTGGGACTGCATGTGTCCAGCCTGAATTCACCTCGCGAGACC 370

84 roCysCysThrThrCysArgHisHisProCysProGlyGlnGlyVal 100

371 CTGCTGCACACCTGCGGCGACCACTTGTCCCGCCAGCGGCGGTA 420

101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaase 117

421 CAGTCCCGAGGGAATTCAGTTTGGCTTCCAGTATCGACTGCGCTC 470

117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrThrAspC 134

471 GGGGACCTTCTCCGGGGCCACGAGGCGCACTGCAACCTTGGACAGACT 520

134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150

521 GCACCCAGTTCGGGTTCCTCACTGTGTTCCTCGGGAACAAGACCCACAC 570

151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167

571 GCTGTGTGTCGTCCTCCAGGGTCCCGCGGAGAGCGCTTGGGTGGCTGAC 620

167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184

621 CGTGTCTCTCTGCGCGTGGCGCTGCTCTCTCTCTCTCTCTCTCTCTG 670

184 InLeuGlyLeuHisIleTrpGlnLeu.....Arg 193

671 AGCTTGGAGCTGCACATCTGGCAGCTGAGGAGTCACTGTCATGTGGCCCGA 720

194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210

721 GAGACCCAGCTGCTGCTGGAGGTGCGCGCTGACCCGAGACCCAGAG 770

210 rCysGlnPheProGluGluArgGlyGluArgSerAlaGluGluLysG 227

771 CTGCGAGTTCCTCCGAGGAGAGCGGGGCGGCGATCGGCGAGAGAGAGG 820

227 lyArgLeuGlyAspLeuTrpVal 234

821 GCGCGCTGGAGACCTGTGGGTG 843

seq\_name: /SDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAD01240

seq\_documentation\_block:

ID AAD01240 standard; cDNA; 1008 BP.

AC AAD01240;

XX 08-NOV-2000 (first entry)

XX Human PRO364 protein encoding cDNA clone, DNA47365-1206.

XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;

KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;

KW breast; prostate; colon; lung; renal; ovarian; central nervous system;

KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;

KW tumour necrosis factor receptor; GTR protein homologue; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 121..846

FT /\*tag= a

FT /product= "Human PRO364 protein"

FT /note= "Derived from clone DNA47365-1206"

FT sig\_peptide 121..195

FT /\*tag= b

FT mat\_peptide 196..843

FT /\*tag= c

FT /product= "Mature human PRO364 protein"

XX WO200032778-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28409.

XX 01-DEC-1998; 98WO-US25108.

XX 16-DEC-1998; 98US-0112850.

XX 22-DEC-1998; 98US-0113296.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.



CC responses in mammalian cells (claimed).

XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:  
Quality: 1322.50 Length: 241  
Ratio: 5.652 Gaps: 1  
Percent Similarity: 97.095 Percent Identity: 96.680

alignment\_block:  
US-09-512-363-2 x AAX87670 ..

Align seg 1/1 to: AAX87670 from: 1 to: 1008

1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17  
121 ATGGACACACAGGGCGATGGCGGTTTCGGGCCCTGTGGGGCTGGC 170

17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
171 GCTGCTGTGGCGCTCAGCTGGGTGAGCCGCCACCGGGGTCCGGGT 220

34 ysGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
221 GCGGCCCTGGGGCCCTCCTGCTTGGACGGGAACGACGCGCGCTGCTG 270

51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysC 67  
271 CGGGTTACACACAGCGCTGCTGCCCGGATTACCCGGGCGAGGAGTGTG 320

67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
321 TTCGAGTGGGACTGATGTGTCCAGCCTGAATTCACCTGGGAGACC 370

84 rCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
371 CTTGTGTGACAGACCTCCCGGACACACCTTGTCCCGCAGCGCGGTA 420

101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAla 117  
421 CAGTCCCGAGGAAATCAGTTTTTGTGCTTCCAGTGTATCGACTGTCCTC 470

117 rGlyThrPheSerGlyHisGlyHisCysLysLysProTrpThrAspC 134  
471 GGGGACCTTCTCGGGGGCCAGAGCCACTGCAAACTTGGACAGACT 520

134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
521 GCACCCAGTTCGGGTTCTCACTGTGTTCCCTGGGAACAAGACCCACAC 570

151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
571 GGTGTGTGCTCCCGAGGTCCTCCCGCGGAGAGCCGCTTGGGTGGTGC 620

167 rValValLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
621 CGTGTCTCTCTGGCGCTGGCGGCTGCTGCTCTCTCTCTGACCTCGGCC 670

184 lInLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
671 AGCTTGACTGCACATCTGGCAGCTGAGGAGTCAAGTGTGTCGCGCCGA 720

194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgse 210  
721 GAGACCCAGCTGTGTGGAGTGGCGCGTTCGACCGAAGACCGCAGAG 770

210 rCysGlnPheProGluGluAlaArgGlyGluArgSerAlaGluLysG 227  
771 CTGCCAGTTCCCGAGAGAGAGCGGGGCGAGCGATCGGCAGAGGAAGG 820

227 lYArgLeuGlyAspLeuTrpVal 234  
|||||

821 GCGGGCTGGGAGACCTGTGGTG 843

seq\_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA99903

seq\_documentation\_block:  
ID AAA99903 standard; cDNA; 1008 BP.  
XX  
AC AAA99903;  
XX  
DT 26-JAN-2001 (first entry)  
XX  
DE cDNA encoding human protein PRO364.  
XX  
KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
XX gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 121..844  
FT a /\*tag= a  
XX  
PN WO200053757-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 24-FEB-2000; 2000WO-US05004.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
(GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pittl RM;  
PI Watanabe CK, Williams PM, Wood WJ;  
XX  
WPI: 2000-611444/58.  
DR P-PSDB; AAB27651.  
XX  
XX Novel PRO polypeptides and agonists and antagonists of them, used to  
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
PT  
XX  
PS Claim 60; Fig 5; 181pp; English.  
XX  
CC The present invention relates to methods for stimulating or inhibiting  
CC angiogenesis and cardiovascularization. The methods involve the use of  
CC pharmaceutical compositions based on the following proteins, PRO179,  
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,  
CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
CC proteins were identified by isolating cDNA clones encoding secreted  
CC proteins. The proteins of the invention may be used to diagnose and  
CC treat cardiovascular, endothelial or angiogenic disorders. The present  
CC sequence is a cDNA clone encoding one of the proteins of the invention.  
XX  
SQ Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:  
Quality: 1322.50 Length: 241

Ratio: 5.652 Gaps: 1  
Percent Similarity: 97.095 Percent Identity: 96.680  
alignment\_block:  
US-09-512-363-2 x AAA99903 ..  
Align seg 1/1 to: AAA99903 from: 1 to: 1008  
1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17  
121 ATGGACACAGCAGCGGCGATGGCGGTTTCGGGCCCTGTGGCGCTGCG 170  
17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
171 GCTGCTGTGCGCGCTCAGCTGGGTTCAGCGGCCACCGGGGGTCCGGGT 220  
34 ysGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
221 CGGGCCCTGGGCGCTCTGCTTGGACGGGAACGACGCGCGCTGCTGC 270  
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysC 67  
271 CGGTTTCACACGACGCGCTGTGCGCGGATTCACCGGCGAGGAGTGCTG 320  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
321 TTCGGAGTGGGACTGCATGTGTGTCAGCTGAATTCACCTCGGAGACC 370  
84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
371 CTGTCGTCACACCTCGCGGCGGACCACTTGTCCCGCAGGCGAGGGGTA 420  
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
421 CAGTCCACAGGGGAATTCAGTTTGGCTTCAGTGTATCGACTGCGCTC 470  
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC 134  
471 GGGGACCTTCTCCGGGGGCCAAGAGGCGACTGCAAACTTTGGACAGACT 520  
134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
521 GCACCCAGTTCGGGTTCCTACTGTGTTCCTGGGAACAAGACCCCAAC 570  
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
571 GCTGTGTGCGTCCCGAGGTCCCGCGCGCAGCGCGCTTGGGTGCTGAC 620  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
621 CGTGTCTCTCTGCGCGGCGGCGCTGCTGCTCTCTCTGACCTCGGCCC 670  
184 InLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
671 AGCTTGGACTCAGTTCGAGCTGAGGAGTCACTGATGTCGCCCCCGA 720  
194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
721 GAGACCCAGCTGCTGTGAGGTCGCGCGCTGACCGAAGACGCGAGAG 770  
210 rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGlyLysG 227  
771 CTGCCAGTTCCCGGAGGAAGAGCGGGGCGGATCGCGCAGAGGAGAAG 820  
227 lyArgLeuGlyAspLeuTrpVal 234  
821 GCGGCTGGGAGACCTGTGGTG 843

seq\_name: /SIDS8/gcdata/geneseq/geneseq/NA2000.DAT: AAC58596  
seq\_documentation\_block:  
ID AAC58596 standard; cdna; 1008 BP.  
XX

AC AAC58596;  
XX 29-JAN-2001 (first entry)  
XX Human PRO364 protein UNQ319 encoding cDNA SEQ ID NO:91.  
XX  
XX Human; immune related disease; diagnosis; antinflammatory; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200053758-A2.  
XX 14-SEP-2000.  
XX  
XX 02-MAR-2000; 2000WO-US05841.  
XX  
XX 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99US-0123618.  
PR 12-MAR-1999; 99US-0123957.  
PR 23-MAR-1999; 99US-0125775.  
PR 12-APR-1999; 99US-0128849.  
PR 20-APR-1999; 99WO-US08615.  
PR 28-APR-1999; 99US-0131445.  
PR 04-MAY-1999; 99US-0132371.  
PR 14-MAY-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 28-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99WO-US20111.  
PR 01-SEP-1999; 99WO-US20594.  
PR 08-SEP-1999; 99WO-US20944.  
PR 13-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;



CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC DiGeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.

XX  
 SQ Sequence 983 BP; 144 A; 326 C; 346 G; 167 T; 0 other;

# alignment\_scores:

Quality: 1340.00 Length: 234  
 Ratio: 5.726 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

US-09-512-363-2 x AA237762 ..

Align seg 1/1 to: AA237762 from: 1 to: 983

1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17  
 118 ATGGACACACAGGGCGGATGGCGGCTTTCGGGCGCTGTGGCGCTGGC 167  
 17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
 168 GCTGCTGTGGCGCTCAGCTGGGTGAGCCGCCACCGGGGTCCCGGT 217  
 34 yGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
 218 GCGGCCCTGGGCGCTCTCTGTGGACGGGAACGGACGCGCGCTGCTG 267  
 51 ArgValHisThrArgCysCysArgAspTyrProGlyGlyGluCysCys 67  
 268 CGGGTTTCACACGACGCGCTGTCGCGGATACCCGGGGAGAGTGCTG 317  
 67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
 318 TTCGAGTGGGACTGATGTGTCTCAGCCTGAATTCACCTCGGAGACC 367  
 84 rCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
 368 CTGTGTCACGACCTCGCGCACCACTTGTCCGCCAGCGCCAGGGGTA 417  
 101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlase 117  
 418 CAGTCCAGGGGAAATCAATTTTGGCTTCCAGTGATCGACTGTGCTC 467  
 117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrAspC 134  
 468 GGGGACCTTCTCGGGGGCCACGAAGCCCACTGCAACCTTGGACAGACT 517  
 134 yThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
 518 GCACCCAGTTCGGGTTCTCACTGTGTTCCCTGGGAACAAGACCCCAAC 567

151 AlavaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
 568 GCTGTGTGCTGCCAGGTCCCGCCGACAGCCGCTTGGTGGCTGAC 617  
 167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
 618 CGTGTGCTCTCTGGCGCTGGCGGCTGCTGCTCTCTGACCTCGGCC 667  
 184 InLeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuGlu 200  
 668 AGCTTGGACTGCACATCTGCAGCTGAGGAAGACCCAGCTGCTGCTG 717  
 201 ValProProSerThrGluAspAlaArgSerCysGlnPheProGluGlu 217  
 718 GTGCGCGCTCGACCGAAGACGCCAGAAAGCTGCCAGTTCCCGGAGA 767  
 217 uArgGlyGluArgSerAlaGluGlyLysGlyArgLeuGlyAspLeuTrp 234  
 768 GCGGGCGCGCATCGGACAGGAGAGAGGGCGGCTGGGACCTGTGGG 817  
 234 al 234  
 818 TG 819

seq\_name: /SID8/gcgdata/geneseq/geneseq/NA1998.DAT:AAV19153

# seq\_documentation\_block:

ID: AAV19153 standard; DNA; 1006 BP.

XX AC AAV19153;

XX DT 28-JUL-1998 (first entry)

XX DE Nucleotide sequence of the human 312C2 T cell gene.

KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell; ss;  
 KW autoimmune disorders.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..726

FT FT /\*tag= a

FT FT /product= "human 312C2 protein"

XX PN WO9806842-A1.

XX PD 19-FEB-1998.

XX PF 14-AUG-1997; 97WO-US13931.

XX PR 07-OCT-1996; 96US-0027901.

XX PR 16-AUG-1996; 96US-0689943.

XX PA (SCHE ) SCHERING CORP.

XX PI Gorman DM, Randall TD, Zlotnik A;

XX DR WPI: 1998-159534/14.

XX DR P-PSDB; AA37839.

XX PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders

XX PS Claim 10; Pages 58-59; 71pp; English.

XX CC This is the nucleotide sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific



CC X-linked agammaglobulinemia, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
CC and/or diagnose an autoimmune disease, especially rheumatoid  
CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
CC antibodies can be administered to cells in vitro, ex vivo or in  
CC vivo or to a multicellular organism. Soluble forms of the  
CC polypeptides may also be used. Methods for screening for  
CC agonist/antagonist compounds are also provided.  
XX  
SQ Sequence 983 BP; 144 A; 326 C; 346 G; 167 T; 0 other;

alignment\_scores:  
Quality: 1340.00 Length: 234  
Ratio: 5.726 Gaps: 0  
Percent Similarity: 100.000 Percent identity: 100.000

alignment\_block:

US-09-512-363-2 x AAA50304 ..

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118 ATGGCACAGCAGCGGCGCATGGCGCGTTTCGGCGCTGTGGCGCTGGC 167  
  
17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
|||||  
168 GCTGTGTGGCGCTCAGCCTGGGTCAGCGCCCGCCACCGGGGTCCCGGT 217  
  
34 yGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
|||||  
218 CGGCGCTGGCGGCTCTCTGTGGACGGAACGACGCGCGCTGCTGC 267  
  
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysC 67  
|||||  
268 CGGTTTCACAGCAGCGCTGTGTGGCGGATACCGGGCGAGGAGTGCTG 317  
  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP 84  
|||||  
318 TTCGAGTGGGACTGCATGTGTGTCCAGCCCTCAATTCCACTCGCGAGAC 367  
  
84 roCysCysThrThrCysArgHisProCysProGlyGlnGlyVal 100  
|||||  
368 CTGTGTCACAGCTCGCGGACACACCTTGTCCCGGAGCGGGGTA 417  
  
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
|||||  
418 CAGTCCCAGGGGAAATTTCAGTTTGGCTTCAGTGTATCGACTGTGCTC 467  
  
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrPheAspC 134  
|||||  
468 GGGGACCTTCTCCGGGGCCACGAGGCGACTGCAAACTTGGACAGACT 517  
  
134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
|||||  
518 GCACCCAGTTCGGGTTCCTACTGTGTTCCTGGGAACAGACCCCAAC 567  
  
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
|||||  
568 GCTGTGTGGTCCCGAGGTTCCTCCCGCGCAGAGCGCTTGGGTGGCTCAC 617  
  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
|||||  
618 CGTGTCTCTCTGGCGCGGCGCGCTGCTCTCTCTGACTGACTCGGCC 667  
  
184 lnLeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuGlu 200  
|||||  
668 AGCTTGGACTGCATCTGGCAGCTGGAGGAGACCCAGCTGCTGCTGGAG 717

201 ValProProSerThrGluAspAlaArgSerCysGlnPheProGluGluG 217  
|||||  
718 GTGCGCGCGTCCAGCGAGACGCCAGAGCTGCCAGTTCCTCCCGAGGA 767  
  
217 uArgGlyGluArgSerAlaGluGluLysGlyArgLeuGlyAspLeuTrpV 234  
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768 GCGGGCGGAGCATCGCAGAGGAGGAGGCGGCTGGGAGACCTGTGGG 817  
  
234 al 234  
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818 TG 819

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAZ37762

seq\_documentation\_block:

ID AAZ37762 standard; cDNA; 983 BP.

AC AAZ37762;

XX DT 01-FEB-2000 (first entry)

DE XX Tumour necrosis factor receptor-like protein (TR11), nucleotide sequence.  
XX  
KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;  
KW GTR; growth; differentiation; cell death; immune deficiency disorder;  
KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; ss;  
KW inflammatory condition.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX CDS 118..822

FT /\*tag= a

/product= TR11\_receptor

/note= "Tumour necrosis factor receptor-like protein"

FT sig\_peptide

FT /\*tag= b

/note= "Putative signal sequence"

FT mat\_peptide

FT /\*tag= c

/note= "TR11"

FT WO9920758-A1.

XX PN 29-APR-1999.

XX PD 21-OCT-1998; 98WO-US22085.

XX PF 21-OCT-1997; 97US-0063212.

XX PR (HUMA-) HUMAN GENOME SCI INC.

XX PA NI J, Ruben SM;

XX PI WPI; 2000-061922/05.

XX DR P-PSDB; AAY52158.

XX DR New tumour necrosis factor receptor-like polypeptides used to, e.g.

XX PT treat Digeorge syndrome -

XX PS Claim 8; Fig 1; 167pp; English.

XX CC This is the nucleotide sequence of the human tumour necrosis factor

CC receptor-like protein (TR11 receptor). The invention relates to TR11 and

CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were

CC determined by sequencing cloned cDNAs AAZ37765-237766. The TR11 receptor

CC and its splice variants show homology to the murine glucocorticoid

CC induced tumour necrosis factor receptor family-related gene (GTR).

CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation

CC of cell-type specific receptor-mediated cell growth, differentiation,

CC and ultimately, cell death. They can be used for screening for



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/db_xref="taxon:9606"
/clone="IMAGE:1840417"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI_CCAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      57 a      86 c      87 g      44 t
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  Quality: 319.50      Length: 90
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  Percent Similarity: 82.222      Percent Identity: 74.444

alignment_block:
US-09-512-363-2 x AI214481/rev ..

Align seg 1/1 to reverse of: AI214481 from: 1 to: 274

131 TrpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLy 147
||||| ||||||| |||||||:||||||| :|||
274 TGGACAGTCTGCACCCAGTCGGGGTTCTCTCAGTGTCCCTGTGACGAA 225
||||| ||||||| ||| |||||||:|||||||
147 sThrHisAsnAlaValCysValProGlySerProAlaGluProLeuG 164
||||| ||||||| ||| |||||||:|||||||
224 GACCCACATCGCTGTGAGTCCGAGGTCGCCGCCGACAGCGCGTTG 175
|| |||||||:|||||||:|||||
164 lyTrpLeuThrValValLeuLeuAlaValAlaCysValLeuLeu 180
|| |||||||:|||||||:||||| |||||||:
174 GGTGACTGACCGTCGTCATGTGCGCGTGTCCGCGTGAGTCCTCCTCATG 125
||||| ||||||| ||||||| ||||||| |||||||
181 ThrSerAlaGlnLeuGlyLeuHisIleTrpGlnLeu..... 192
||||| ||||||| ||||||| ||||||| |||||||
124 ACCTCGGCCAGCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCAT 75
||||| |||:||||| ||||||| ||||||| |||||||
193 .....ArgLysThrGlnLeuLeuGluValProProSerThrGluA 207
||||| |||:||||| ||||||| ||||||| |||||||
74 GTGGCCCCGAGAGACCCAGCTGCTGCTGGAGGTGCCCGCGTCGACCGAAG 25

207 spAlaArgSerCysGlnPhe 213
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24 ACGCCAGAATGTGCCAGTTC 5
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Ratio: 4.721 Gaps: 2  
Percent Similarity: 80.435 Percent Identity: 63.768

alignment\_block:

US-09-512-363-2 x AW483085 ..

Align seg 1/1 to: AW483085 from: 1 to: 393

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1 GGCCAGCAGCCCTCAGCATCTGAGCTGAGCTGAGCCCTGGCCAACTTGTGCA 50
41 uGlyThrGlyThrAspAlaArgCysCysArgValHisThrArgCysC 58
|||||
51 TGGGACGGGGACAGACGACGCTGCTGC.....CGCTGGC 85
58 ysArgAspTyrProGlyGluGluCysSerGluTirpAspCysMetCys 74
:: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
86 CC.....CCAGATGAGGGGACCTGTCTGAGCGGACTGCCAGTGT 126
75 ValGlnProGluPheHisCysGlyAspProCysCysThrThrCysArgH 91
|||||
127 ATCCAGCCCGAGTTCACCTGTGGAGACCCACACAGCTGAAGAGCTGCAAGTA 176
91 sHisProCysProProGlyGlnGlyValGlnSerGlnGlyLysPheSerP 108
|||||
177 CTACTCTCTCCACCTGGCGGAGTGCAGCTGAGGCAACTTCAAAAT 226
108 heGlyPheGlnCysIleAspCysAlaSerGlyThrPheSerGlyGlyHis 124
|||||
227 TGGGCTTTGAGTGTGTGACTGTGCCGTGGGACCTTCTCTAGGGGCCAT 276
125 GluGlyHisCysLysProTrpThrAspCysThrGlnPheGlyPheLeuTh 141
|||||
277 GAGGCGCGCTGCAAACTTGGCAGACTGGTCCAGCTTGGGTTCCTCCAC 326
141 rValPheProGlyAsnLysThrHisAsnAlaValCysValProGlySerP 158
327 CCGTGTTCGGGAAACAGACGACAACTGCTGTGCAGCGCTGGGGCTGC 376
158 roProAlaGluPro 162
377 CGCCCCACTGAACCA 390
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seq\_name: gb\_est50:AW659186

seq\_documentation\_block: 552 bp mRNA EST 14-JUL-2000  
LOCUS AW659186  
DEFINITION 96144 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION AW659186  
VERSION AW659186.1 GI:7425013  
KEYWORDS EST.  
SOURCE cow.

ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 552)  
AUTHORS Smith,R.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,  
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid,  
W.W. and Keale,J.W.

TITLE Design and use of four pooled tissue normalized cDNA libraries for  
EST discovery in cattle

JOURNAL Unpublished (2000)  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390

Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.

PCR Primers  
FORWARD: AGGAACACCTATGACCAT  
BACKWARD: GTTTCCAGTCAGCAGC  
Plate: 83 row: A column: 19  
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Library made from pooled tissue from lymph node, ovary,  
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BASE COUNT 95 a 179 c 175 g 103 t  
ORIGIN

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US-09-512-363-2 x AW659186 ..

Align seg 1/1 to: AW659186 from: 1 to: 552

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|||||
63 TGGCGTGGGGACCTTCTCTAGGGGCCATGAGGGCCCTGCAACACCTTGGG 112
132 hrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThr 148
|||||
113 CAGACTCGGTCCAGCTTGGGTTCCTCCACCTGTTCCCGGAAACACAGACG 162
149 HisAsnAlaValCysValProGlySerProAlaGluProLeuGlyTr 165
163 CACAATGCTGTGTGCAGCTGGGGCTGCCGCCACTGAACACCCAGCC 212
165 pLeuThrValValLeuLeuAlaValAlaAlaCysValLeuLeuThrs 182
|||||
213 AGTGACCATCGTCACTCTCTCTGGCTGCTGCTGCTGCTGCTGCTGACCG 262
182 erAlaGlnLeuGlyHisIleTrpGlnLeuArgLys..... 194
263 TGACCCAGCTAAGCTGCACATCTGGCAGCTGAGGAGCAAGAATGTGG 312
194 ..... 194
313 CCCCCAGGTGAGTGTGCTCTTAGGAGGGGGGGTCCCTGCTGCTGCC 362
195 .....ThrGlnLeuLeuLeuGluValProp 203
363 TGCTGATTGCAGCCCTCTCTGCAGAGACCCAGCTCTCTGGAGCCCGCC 412
203 roSerThrGluAspAlaArgSerCysGlnPheProGluGluGluArgGly 219
413 CCCACCTGAGGATGCTGTCAGTTGCCAGTTCCCTGAGGAGGAGGGGGT 462
220 GluArgSerAlaGluGluLysGlyArgLeuGlyAspLeuTrpVal 234
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seq\_documentation\_block:

LOCUS AW335806 442 bp mRNA EST 10-JUL-2000

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ACCESSION AW335806
VERSION AW335806.1 GI:6832445
KEYWORDS EST.
SOURCE cOW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 442)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.960904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
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            fat, hypothalamus, and pituitary."
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13 GGAGTGAGCGCTAGGCGCACTTCAAAATTCGGCTTGAGTGTGTGACTG 62
115 sAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpT 132
63 TGGCGTGGGACCTTCTCTAGGGCCATGAGGGCCGCTGCAACACCTTGGG 112
132 hrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThr 148
: : : : : : : : : : : : : : : : : : : : : : : : : :
113 CAGACTGGTCCACCTGGGTTCCTCCACCCGTTCCTCCGGAAACAAGACG 162
149 HisAsnAlaValCysValProGlySerProProAlaGluProLeuGlyTr 165
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163 CACAATGCTGTGTGACGCTGGGGCTGCGGCCACTGAACACCCAGGCC 212
165 pLeuThrValLeuLeuAlaAlaAlaCysValLeuLeuLeuThrS 182
: : : : : : : : : : : : : : : : : : : : : : : : : :
213 AGTGACCATGTCATCTCTCTCTGGCTGCTGCATCTCTGGCCCTGACCG 262

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: : : : : : : : : : : : : : : : : : : : : : : : : :
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194 ..... 194
313 CCCCCAGGTGACGTTGTGCTTAGGGAGGGGGTCCCTGCCTGCCTGCC 362
195 .....
363 TGCTGATTGCCAGCCCTCTGCAGAGACCAGCTCTCTGGAGGCCGCCAC 412
203 roSerThrGluAspAlaArgSerCysGln 212
|| .....
413 CCCACCTGAGGATGCTGCAGTTCGACG 441
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DEFINITION 60125221F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3583589 5',
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VERSION BE373185.1 GI:9318548
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 620)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-femail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 580.
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182 CTGTGGAGACCTCAGTGAAGATCTGCAAGCACTACCCCTGCCAACCCAG 231
97 lyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysIle 113
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232 GCCAGAGGGTGGAGTCTCAAGGGGATATTGTGTTGGCTTCGGGTGT 281
114 AspCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysPr 130
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282 GCCTGTGCCATGGCAGCCCTTCCCGCAGGTCGTGACGGTCACTGCAGACT 331
130 chrPthrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnL 147
||||| 111 111 111 111 111 111 111 111 111 111
332 TTGGACCAACTGTCTCAGTTTGGATTTCTCACCATTGTTCCCTGGGAACA 381
147 ysThrHisAsnAlaValCysValProGlySerProProAlaGluProLeu 163
||||| 111 111 111 111 111 111 111 111 111 111
382 AGACCCACAACTGCTGTGTCATCCCGGAGCCACTGCCCACTGAGCAATAC 431
164 GlyTrpLeuThrValValLeuLeuAlaValAlaCysValLeuLeuLe 180
||||| 111 111 111 111 111 111 111 111 111 111
432 GCCATTGTGACTGTCATCTCTGCTGTCATGGCTGCATGATTTCTTCCT 481
180 uThrSerAlaGlnLeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnL 197
||||| 111 111 111 111 111 111 111 111 111 111
482 AACCAAGTCCAGCTCGGCTGCACATATGGCAGCTGAGGAGGCAACACA 531
197 eu.LeuLeuGluValProProSerThrGluAspAlaArgSerCysGlnPh 213
||||| 111 111 111 111 111 111 111 111 111 111
532 TGTGTCCTCGAGAGACCC.....AGCCATTGCGGAGGTGCAGTTG 572
213 eProGluGluGluArg.....GlyGluArgSerAlaG 624
||||| 111 111 111 111 111 111 111 111 111 111
573 TCAAGCTGAGGATGCTTGGCTTCAGTCTCGGGGGGAGCGGGGGCGCA 622
224 luGlu 225
|||||
623 CGGAA 627
seq_name: gb_est45:AW300857

seq_documentation_block:
LOCUS AW300857 340 bp mRNA EST 18-JAN-2000
DEFINITION xk07c07.x1 NCI-CGAP Co20 Homo sapiens cDNA clone IMAGE:2666028 3'
similar to TR:095851 095851 TNF RECEPTOR SUPERFAMILY
ACTIVATION-INDUCIBLE PROTEIN. ; contains MER22.b1 TARI repetitive
element ;, mRNA sequence.
ACCESSION AW300857
VERSION AW300857.1 GI:6710534
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 340)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-femail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco

```

High quality sequence stop: 75.  
Location/Qualifiers  
1..340  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:2666028"  
/clone\_lib="NCI-CGAP-Co20"  
/tissue\_type="moderately differentiated adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Normalized to Cot 500. Average insert size 1.11kb.  
Normalized version of NCI-CGAP\_Col8. Library constructed  
by Life Technologies." 54 t 1 others

BASE COUNT 70 a 100 c 115 g 54 t 1 others  
ORIGIN

alignment\_scores:  
Quality: 608.00 Length: 113  
Ratio: 5.527 Gaps: 0  
Percent Similarity: 97.345 Percent Identity: 94.690

alignment\_block:  
US-09-512-363-2 x AW300857/rev ..

Align seg 1/1 to reverse of: AW300857 from: 1 to: 340

69 GluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProCys 85  
||||| 111 111 111 111 111 111 111 111 111 111  
340 GAGTGGAACTGCAATGTGTGCCACCTGAAATTCACCTGCCGAAGACCCCTG 291  
85 sCysThrThrCysArgHisHisProGlyGlnGlyValGln 102  
||||| 111 111 111 111 111 111 111 111 111 111  
290 CTCAGCACTGCGGGCAGCACCACT.TGTCCTCCAGCAGCGGGGTACAGT 242  
102 erGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerGly 118  
||||| 111 111 111 111 111 111 111 111 111 111  
241 CCCAGGGGAAATTCAGTTTGGCTTCCAGTGTATCGAGTGTGCTCGCGGG 192  
119 ThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCysTh 135  
||||| 111 111 111 111 111 111 111 111 111 111  
191 ACCTTCTCCGGGGCCACGAGGCCACTGCAAACTTGGACAGACTGCAC 142  
135 rGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAlaV 152  
||||| 111 111 111 111 111 111 111 111 111 111  
141 CCAGTTCGGGTTTCTCACTGTGTCTCCCTGGGAACAACCCACACACGCTG 92  
152 alCysValProGlySerProProAlaGluProLeuGlyTrpLeuThrVal 168  
||||| 111 111 111 111 111 111 111 111 111 111  
91 TGTGCGTCCCGAGGTCCTCCCGCGCAGCGGCTTGGGTGGTGCACCGTC 42  
169 ValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThr 181  
||||| 111 111 111 111 111 111 111 111 111 111  
41 GTCTCTCTGCGGCTGGCGCGCTGCTGCTCTCTCTGACC 3

seq\_name: gb\_est83:BF117994

seq\_documentation\_block:  
LOCUS BF117994 606 bp mRNA EST 29-DEC-2000  
DEFINITION uz10e09.y1 NCI-CGAP\_Mam5 Mus musculus cDNA clone IMAGE:366860 5',  
similar to TR:035714 035714 GLUCOCORTICOID INDUCED TNFR FAMILY  
RELATED PROTEIN PRECURSOR. ;, mRNA sequence.  
ACCESSION BF117994  
VERSION BF117994.1 GI:10987470  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 606)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),



```

DEFINITION      uo63d10.y1 NCI-CGAP_Mam1 Mus musculus cDNA clone IMAGE:2647219 5'
                  similar to TR:O35714 O35714 GLUCOCORTICOID INDUCED TNFR FAMILY
                  RELATED PROTEIN PRECURSOR. ;, mRNA sequence.
ACCESSION       AW230423
VERSION         AW230423.1 GI:6559719
KEYWORDS        EST.
SOURCE          house mouse.
ORGANISM        Mus musculus
REFERENCE       1 (bases 1 to 644)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
JOURNAL         Unpublished (1997)
COMMENT        Other_ESTs: uo63d10.x1
                Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-remail.nih.gov
                Tissue Procurement: Gilbert Smith, Ph.D.
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                www-bio.llnl.gov/bbrp/image/image.html

MGI:1027671
Seq primer: -40RP from Gibco
High quality sequence stop: 425.
FEATURES        Location/Qualifiers
                1..644
                /organism="Mus musculus"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:2647219"
                /clone_lib="NCI-CGAP_Mam1"
                /tissue_type="tumor, biopsy sample"
                /dev_stage="3 months, virgin"
                /lab_host="DH10B"
                /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;
                Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"
BASE COUNT     141 a 173 c 183 g 145 t
ORIGIN
alignment_scores:
  Quality: 626.50      Length: 214
  Ratio: 3.867         Gaps: 3
  Percent Similarity: 75.701 Percent Identity: 52.336
alignment_block:
US-09-512-363-2 x AW230423 ..
Align seg 1/1 to: AW230423 from: 1 to: 644
3 GlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeuLe 19
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 AGGAGAAGCACTATGGGCGCATGGGCCATGCTGTATGGAGTCTCGATGCT 70
19 uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG 35
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
71 CTGTGTGTCGGACCTAGGTCACCGAGTAGTGTAGGAGCGCTGGCTGTG 120
35 1yProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCysArg 51
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 GCCTGGCAAGGTTGACAGACGGAGTGGCAACACACTGCTGCTCGAGC 170
52 ValHisThrThrArgCysCysArgAspTyrProGlyGluCysCysSe 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
171 CTGTATGCT.....CCAGGCAAGGAGGAGTCTCC 199

```

```

68 rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProc 85
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
200 AAAAGAAAGTGCATATGTGTACACACTGAGTACCACTGTGGAGACCTC 249
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
85 yScySthrThrCysArgHisHisProCysProGlyGlnGlnValGln 101
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
250 ATGCAAGATCTGCACAGCACTACCCCTGCCACACAGGCGGAGGTGGAG 299
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
102 SerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerG 118
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
300 TCTCAAGGGGATATGTGTGGCTTCGGGTGTGCTGCTGTCATGGG 349
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
118 yThrPheSerGlyCysHisGluGlyHisCysLysProThrThrAspCys 135
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
350 CACCTTCTCCGCGAGTGTGACGGTCTACTGCAGACTTTGGACCACTGT 399
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
135 hrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAla 151
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
400 CTGAGTTGGATTCTCACCATGTTCCCTGNGAACACAGACCAACATGCT 449
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
152 ValCysValProGlySerProAlaGluProLeuGlyTrpLeuThrVa 168
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
450 GTGTGCATCCGGAGCCACTGCCCACTGACCAATACGGCCATTGACTGT 499
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
168 lValLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnL 185
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
500 CATCTTCTGCTGTCATGGCTGCATGCAATTNTCTCTAACCACAGTCCAGC 549
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
185 euGlyLeuHisIleTrpGlnLeuArgLys..... 194
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
550 TCGGCTGCACATATGCCAGTGCAGGAGGCAACACATGTGTCTCGAGAG 599
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
195 ThrGlnLeuLeuGluValProSerThrGluAspAla 208
   |||:||||:||||:||||:||||:||||:||||:||||:||||:
600 ACCAGCAATTCGGGAGGTGCATTTGTCAGTCAAGATGCT 641

seq_name: gb_est80:BE850742

seq_documentation_block:
LOCUS      BE850742      609 bp      mRNA      EST      26-SEP-2000
DEFINITION ux01e06.y1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:3470242 5' similar to TR:O35714 O35714 GLUCOCORTICOID INDUCED
            TNFR FAMILY RELATED PROTEIN PRECURSOR. ;, mRNA sequence.
ACCESSION  BE850742
VERSION    BE850742.1 GI:10309101
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 609)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1389602
Seq primer: -40RP from Gibco
High quality sequence stop: 462.
FEATURES    Location/Qualifiers
            1..609
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="IMAGE:3470242"
            /clone_lib="Soares_thymus_2NbMT"
            /sex="male"
            /tissue_type="Thymus"
            /dev_stage="4 weeks"
            /lab_host="DH10B"

```



```
3  GlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeuLe 19
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
55 AGGAGAACCACTATGGGGGATGGGCGCATGCTGTATGGAGTCTCGATGCT 104
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
19  uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG 35
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
105 CTGTGTGCTGGAGCTAGTACAGCGAGTGTAGTGTAGGAGCCTGGCTGTG 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
35  lProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCysArg 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
155 GCCTGGCAAGTTTCAGAACGGAAGTGGCAACAACACTCGCTCTGCAGC 204
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
52  ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCys 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
205 CTGTATGCT.....CCAGCAAGGAGGAGCTGTCC 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
68  rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspPro 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
234 AAAGAAAGGTGCTATGTGTACACCTGAGTACCACCTGTGGAGACCTC 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
85  ysCysThrThrCysArgHisHisProCysProProGlyGlnGlyValGln 101
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
284 AGTGCAAGATCTGCAGCACTACCCCTGCCAACCCAGCCAGAGGTGGAG 333
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
102 SerGlnGlyLysSerPheGlyPheGlnCysIleAspCysAlaSerG 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
334 TCTCAAGGGGATATTGTGTGGCTTCGGGTGTGGCTGTGCCATGGG 383
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
118 yThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCys 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
384 CACCTTCTCCGAGGTCGTGACGGTCTCAGTGCAGACTTTGGACCACTGT 433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
135 hrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAla 151
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
434 CTCAGTTTGGATTTCTACCATGTTTCCCTGGGAACAGACCCCAATGCT 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
152 ValCysValProGlySerProProAlaGluProLeuGlyTrpLeuThr 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
484 GTGTGCATCCCGGAGCAGCTGCCCATGAGCAATACGCCATTTGACTGT 533
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
168 lValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGln 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
534 CATCTTCCTGGTATGGCTGATGCTGATGCTATTTCTTCTTAACACACAG 583
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 euGlyLeuHisIleTrpGlnLeuArgLys..... 194
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
584 TCGGCTGCACATATGGCAGCTGAGGAGGCAACACATGTCTCTCGAGAG 633
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
195 ThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSer 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
634 ACCACCCATTCCGGGAGGTGAGTGTCTCAGCTGAGGATGCTTGCAGCTT 683
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
211 sGlnPheProGluGluGluArgGlyGluArgSerAlaGluGlyLysGly 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
684 CCAGTTCCTGTAGGAGGACGCGGGGAGGAGACA...GAAGAAAGGTGTC 730
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
228 rGleuGlyAspLeuTrp 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
731 ATCTGGGGGTGCGGTGG 747
```

seq\_name: gb\_est89:BF539340

```
seq_documentation_block:
LOCUS      BF539340          953 bp      mRNA      EST      11-DEC-2000
DEFINITION 602049520F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4188724 5',
           mRNA sequence.
ACCESSION  BF539340
VERSION    BF539340.1  GI:11626721
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE  
1 (bases 1 to 953)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9513 row: h column: 05  
High quality sequence stop: 649.

FEATURES  
Location/Qualifiers  
1..953  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4188724"  
/clone\_lib="NCI\_CGAP\_SG2"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 212 a 235 c 274 g 232 t  
ORIGIN

alignment\_scores:  
Quality: 644.50 Length: 218  
Ratio: 3.859 Gaps: 3  
Percent Similarity: 76.606 Percent Identity: 54.587  
alignment\_block:  
US-09-512-363-2 x BF539340 ..  
Align seg 1/1 to: BF539340 from: 1 to: 953

```
13  LeuCysGlyLeuAlaLeuLeuCysAlaLeuSerLeuGlyGln...ArgPr 28
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6  CTGTATGGAGTCTCGATGCTCTGTGTGTGTGGACCTAGGTGAGCCGAGTGT 55
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
28  oThrGlyGlyProGlyCysGlyProGlyArgLeuLeuLeuGlyThrGlyT 45
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
56 AGTTGAGGAGCCTGGCTGTGGCCCTGGCAAGGTTTCAGAACGGAAGTGCA 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
45 hrAspAlaArgCysCysArgValHisThrThrArgCysCysArgAspTyr 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
106 ACAACACTCGCTGTGCTGAGCCTGTATGCT..... 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 ProGlyGluGluCysCysSerGluTrpAspCysMetCysValGlnProG 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
135 CCAGCAAGGAGGACTGTCCAAAGAAAGAGGTGCATATGTGTACACCTGA 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
78  uPheHisCysGlyAspProCysCysThrThrCysArgHisHisProCys 95
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 GTACCACTGTGGAGACCTCAGTCAAGATCTGCAAGCACTACCCCTGCC 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
95  roProGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGln 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235 AACCAAGCCAGAGGTGGAGTCTCAAGGGGA.TATTGTGTGGCTTCGGG 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
112 CysTleAspCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCy 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
284 TGTGTTGCCGTGTCATGGGACACCTTCTCCGAGGTGCTGACGGTCACTG 333
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
128 sLysProTrpThrAspCysThrGlnPheGlyPheLeuThrValPhePro 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
334 CAGACTTTGGACCAACTCTTCTCAGTTTGGATTCTCACCATTGTTCCCTG 383
```

Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Murinae; Mus.

145 lyAsnLysThrHisAsnAlaValCysValProGlySerProProAlaGlu 161  
 |||||  
 384 GGAACAAGACCACTGCTGTGTCATCCCGGAGCCACTGCCACTGAG 433  
 |||||  
 162 ProLeuGlyTrpLeuThrValValLeuLeuAlaValAlaAlaCysValLe 178  
 |||||  
 434 CAATACGGCCATTGTCATGCTGCTGTCATGCTGTCATGCTGCTGCT 483  
 |||||  
 178 uLeuLeuThrSerAlaGlnLeuGlyLeuHisIleTrpGlnLeuArgLys. 194  
 ::::|  
 484 CTTCTTAACACACTCCAGCTCGCGCTGCACATATGGCAGCTGAGGAGCC 533  
 |||||  
 195 .....ThrGlnLeuLeuLeuGluValProProSer 204  
 |||||  
 534 AACACATGTGTCTCGAGAGACCCAGCATTCCGCGAGGTGCAGTTGCA 583  
 |||||  
 205 ThrGluAspAlaArgSerCysGlnPheProGluGluGluArgGlyGluAr 221  
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 RELATED PROTEIN PRECURSOR. ;, mRNA sequence.  
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 VERSION AW230447.1 GI:6559743  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 659)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Other ESTs: uo63f10.x1  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Clone Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/dbrrp/image/image.html](http://www-bio.llnl.gov/dbrrp/image/image.html)

MGI:1027695

Seq primer: -40RP from Gibco  
 High quality sequence stop: 434.

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 Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH"

BASE COUNT

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 LOCUS AW230423

644 bp mRNA EST

10-DEC-1999

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 300 TCTCAAGGGATATTGTTGCTTCGGTGTGTTGCCCTGTGCCATGGG 349  
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seq\_name: gb\_est44:AW230423

seq\_documentation\_block:

LOCUS AW230423

644 bp

mRNA

EST

10-DEC-1999



OM of: US-09-512-363-2 to: EST:\* out\_format : pfs

Date: Sep 4, 2001 3:53 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MINMATCH=0.100 -LOOPCL=0.000 -LOPEXT=0.000 -QAPOP=4.500  
-QAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blotsum62 -TRANS=human40.cdi  
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Search information block:

Query: US-09-512-363-2

Query length: 234

Database: EST:\*

Database sequences: 10228115

Database length: 431459454

Search time (sec): 630.590000

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gb_est89:BF539340	+	644.50	940.71	2.8e-43	933	! BF539340 602049520F1 NCI_CGAP_S
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gb_est73:BE374685	+	608.50	890.91	1.7e-40	689	! BE374685 601224187F1 NCI_CGAP_M
gb_est45:AW300857	-	608.00	897.51	7.1e-41	340	! AW300857 xk07c07.x1 NCI_CGAP_Cc
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VERSION AI923712.1 GI:56595676  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 650)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
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Eco RI adaptors (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of the modified  
pT7T3 vector. Library went through one round of  
normalization. Library constructed by Bento Soares and M.  
Fatima Bonaldo."

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seq\_documentation\_block:

; Sequence 1, Application US/08195967

; Patent No. 6242566

; GENERAL INFORMATION:

; APPLICANT: Godfrey, Wayne

; APPLICANT: Engleman, Edgar G.

; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Hourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

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ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,967
FILING DATE: 10-FEB-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05490A-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 15..845
OTHER INFORMATION: /standard_name= "ACT-4 cDNA"
US-08-195-967-1
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Quality: 168.50 Length: 253

Ratio: 1.518 Gaps: 8

Percent similarity: 43.874 Percent identity: 25.692

alignment\_block:

US-09-512-363-2 x US-08-195-967-1

Align seg 1/1 to: US-08-195-967-1 from: 1 to: 1057

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26 lnArgProThrGlyGlyPro.GlyCysGlyProGlyArgLeuLeuG1 42

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126 AGCAACGACCGGTGCTGCCAGAGTGCAGGCCA.....GG 160

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; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; CLONE: MOX40Fc MuteIn
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1317
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US-08-494-574-10

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US-09-512-363-2 x US-08-494-574-10 ..

Align seg 1/1 to: US-08-494-574-10 from: 1 to: 1317

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    16  CAGCAGCCACACACACACACACACACACACACACACACACACAC 44
    42  y.....ThrGlyThrAspAlaArg.....CysCysArgValHisThr. 54
    |      |||:|||||:|||||:|||||:|||||:|||||:|||||
    45  ACTCACACTTGGAGTTACAGCAGCGCGCTCAACTGTGTTAAACATACCT 94
    55  .....ThrArgCysCysArgAsp....TyrProGly.....63
    95  ACCCCAGTGGTCAACAAGTGTGTCGTGAGTGCAGCCAGCCCATGTATG 144
    64  ...GluGluCysCysSerGluTrpAspCysMetCysValGlnProGluPh 79
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
    145  GTCAACCGCTGTGATCATACACAGGATACCTCTATGT.....180
    79  eHisCysGlyAspProCys.....85
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    181  .....CATCCGTGTGAGACTGGCTTCTACAAATGAAGCTGTCAATT 220
    86  .....CysThrThrCysArgHisPro.....93
    |||:|||||:|||||:|||||:|||||:|||||:|||||
    221  ATGATACCTGCAACAGAGTGTACACAGTGAACCATCGAAGTGAAGTAA 270
    94  .....CysProPr 96
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    271  CTCACAGCAANTTGCACACTACTCAGGATCTGTCTGCAGATGTGACCC 320
    96  oGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysI 113
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    113  leAspCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLys 129
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    371  TTCCTCTGCCCTCTCGCCACTTCTCTCCAGGCAACACACAGGCTGCAAG 420

130  ProTrpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAs 146
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
    421  CCCTGGACCAATTGTACCTTATCTGGAAGCAGACCCGCCACCCAGCCAG 470
    146  nLysThrHisAsnAlaValCysValProGlySerProProAlaGluProL 163
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
    471  TGACAGCTTGGACGACGCTGT.....GAGGACA 499
    163  euGlyTrpLeuThrValValLeuLeuAlaValAlaAlaCysValLeuLeu 179
    :|||:|||||:|||||:|||||:|||||:|||||:|||||
    500  GAGCCTCTCTGGCCACACTGCTCTGGGAGACCCAGCGCCCTACATTGAG 549
    180  LeuThrSerAlaGlnLeuGlyLeuHisIleTrp.....GlnLe 192
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    550  CCAACCACTGTCCAA...TCCACACACAGCTCTGGCCAGGACTTCTGAGTT 596
    192  uArgLysThrGlnLeuLeuLeuGluValProProSer.....ThrG 206
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    597  GCCCTCTACACCCACCTTGTGGAG...CCAGATCTTGTGACAAACTC 643
    206  luAspAlaArgSerCysGlnPheProGluGlu 217
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    644  ACACATGCCACCGTGCACACCACTGAAGCCGAG 678

seq_name: /cgn2_6/ptodata/1/lna/5A_COMB.seq:US-08-192-480A-1

seq_documentation_block:
; Sequence 1, Application US/08192480A
; Patent No. 5759546
; GENERAL INFORMATION:
; APPLICANT: Andrew D. Weinberg and Arthur A.
; APPLICANT: Vandenberg
; TITLE OF INVENTION: TREATMENT OF CD4 T-CELL
; TITLE OF INVENTION: MEDIATED CONDITIONS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Polley, Esq.
; ADDRESSEE: Klarquist Sparkman Campbell
; ADDRESSEE: Leigh & Whinston
; STREET: 121 S.W. Salmon Street, Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,480A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard J. Polley, Esq.
; REGISTRATION NUMBER: 28,107
; REFERENCE/DOCKET NUMBER: 4282-38649
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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125 GluGlyHisCysLysProThrPheGlnPheGlyPheLeuTh 141
507 CQTGGCATCTGTCACCCCTGGACAACTCTTCTTGGATGGAAGTCTGT 556
141 rValPheProGlyAsnLysThrHisAsnAlaValCysValProGly. 156
557 GCTTGTGAATGGACGACGAGGAGGACGTGTCTGTGGACCATCTCCAG 606
157 .....SerProProAla..... 160
607 CGGACCTCTCTCGGGAGCATCTCTGTGACCCGCTGCCCCTGCGAGA 656
161 GluProLeuGlyTrpLeuThrValVal.....LeuLeuAlaValAla 175
657 GAGCCAGGACACTCTCCGAGATCATCTCTTCTTCTTGGCTGACGTC 706
175 aCysValLeuLeuLeuThrSerAlaGlnLeuGlyHis.....I 189
707 GACTGGTGTGCTTCTCTCTGTTCTTCTCAGGCTCCGTTCTCTGTGTG 756
189 leTrpGlnLeuArgLysThrGlnLeuLeuGluValProPro..... 203
757 TTAACGGGGCAGAGAAGAACTCTCTATATATTCACAAACCATTTATG 806
204 .....SerThrGluAspAlaArgSerCysGlnPhePr 214
807 AGACAGGACATAAATACTACTCAAGAGGAAGTGGCTGTAGCTGCGATTCC 856
214 oGluGluGluArgGly 219
857 AGAAGAAGAAGAAGGA 872

seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-816-605-1

seq_documentation_block:
; Sequence 1, Application US/08816605
; Patent No. 5874240
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816.605
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PP254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 946 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..780
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 124..177
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 178..780
US-08-816-605-1

alignment_scores:
Quality: 194.00 Length: 199
Ratio: 1.940 Gaps: 10
Percent Similarity: 50.251 Percent Identity: 31.156

alignment_block:
US-09-512-363-2 x US-08-816-605-1 ..

Align seg 1/1 to: US-08-816-605-1 from: 1 to: 946

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68 r.....GluTrpAspCysMetCysValGlnProGluPheHisC 81
255 CACCAGCAATGCAGAGTGTACTGC.....ACTCCAGGGTTTCACT 295
81 ysGlyAspProCysCysThrThrCysArgHisHisProCysProProGly 97
296 GCCTGGGGGAGGATGCAGCATGTGT...GAACAGGATTGTAACAAGGT 342
98 GlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAs 114
343 CAAGAACTGACAAAAAAGGT.....TCTAAAGA 371
114 pCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysProT 131
372 CTGTTGCTTGGGACATTTACGATCAGAAAGTGGCATCTGTGCGACCT 421
131 rpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLys 147
422 GGACAAACTGTTCTTTGGATGGAAGTCTGTGTCGTGTAATGGGACGAAG 471
148 ThrHisAsnAlaValCysValProGlySer..... 157
472 GAGAGGGACGTGTCTGTGGACCATCTTCAGCCGACCTCTCTCCGGAGC 521
158 .....ProProAla.....GluProLeuGlyTrpLeuT 167
522 ATCTCTGTGACCCCGCTGCCCTGCGAGAGAGCCGAGGACACTCTCCGC 571
167 hrValVal.....LeuLeuAlaValAlaLacCysValLeuLeuLeuThr 181
572 AGATCATCTCTCTTCTTCTTGGCTGAGTGCAGTGCCTGTCTCTCTCTG 621
182 SerAlaGlnLeuGlyLeuHis.....IleTrpGlnLeuArgLysTh 195
622 CTGTTCTTCTCAGCTCCGTTTCTCTGTTTAAACGGGCGAGAAGAA 671
195 rGlnLeuLeuLeuGluValProPro.....S 204
672 ACTCTGTATATATTCAAACAAACCATTTATGAGACCACTACAACTACTC 721
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722 AAGAGGAGAGTGGCTGTAGCTGCCGATTTCCAGAGAAGAAGAAGGA 768

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; Sequence 10, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: MOX40Fc Mutein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1317
; US-08-097-827-10
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alignment_scores:
  Quality: 175.50      Length: 245
  Ratio: 1.610        Gaps: 14
  Percent Similarity: 44.490  Percent Identity: 27.347

alignment_block:
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  Align seg 1/1 to: US-08-097-827-10 from: 1 to: 1317

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16 CAGCAGCCACCA.....GCCCTTCTGCTGGTGG 44
42 Y.....ThrGlyThrAspAlaArg.....CysCysArgValHisThr. 54
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45 ACTCACACTGGAGTTACAGCAAGCGGCTCACTGTGTTAAACATACCT 94
55 .....ThrArgCysCysArgAsp...TyrProGly..... 63
95 ACCCCAGTGGTTCACAAGTGTGCTGAGTCCAGCCAGCGCATGGTATG 144
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321 AGGCACCCCAACCTCGCAGGACAGCGGCTACAAGCTTGGAGTTGACTGTG 370
113 leAspCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLys 129
371 TTCCCTGCCCTCCTGGCCACTTTTCTCCAGGCACACCAACCCAGCCTGCAAG 420
130 ProTrpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAs 146
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146 nlyThrHisAsnAlaValCysValProGlySerProProAlaGluProL 163
471 TGACAGCTTGGACGAGTCTGT.....GAGGACA 499
163 euGlyTrpLeuThrValValLeuLeuAlaValAlaCysValLeuLeu 179
500 GAAGCCTCTCTGGCCACACTGTCTGGAGAGCCAGCCGCTTACATTCAGG 549
180 LeuThrSerAlaGlnLeuGlyLeuHisIleTrp.....GlnLe 192
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192 uArgLysThrGlnLeuLeuLeuGluValProProSer.....ThrG 206
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206 luAspAlaArgSerCysGlnPheProGluGluGlu 217
644 ACACATGCCACCCGTCGCCAGCACCTGAAGCCGAG 678
seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-494-574-10

seq_documentation_block:
; Sequence 10, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
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125 GluGlyHisCysLysProTrpThrAspCysThrGlnPheGlyPheLeuTh 141
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161 GluProLeuGlyTrpLeuThrVal.....LeuLeuAlaValAlaAl 175
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seq\_documentation\_block:

; Sequence 7, Application PC/TUS9603965

; GENERAL INFORMATION:

; APPLICANT: Kwon, Byoung Se

; APPLICANT: Kang, Chang-Yuil

; TITLE OF INVENTION: Monoclonal antibody against human

; TITLE OF INVENTION: receptor 4-1BB

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Barnard, Brown & Michaels

; STREET: 306 East State Street, Suite 220

; CITY: Ithaca

; STATE: NY

; COUNTRY: USA

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ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,369
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: KW05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 838 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: H4-1BB #1
DEVELOPMENTAL STAGE: Differentiated T-cell
CELL TYPE: Lymphocyte
FEATURE:
NAME/KEY: CDS
LOCATION: 41..805
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Quality: 197.00 Length: 222  
Ratio: 1.807 Gaps: 12  
Percent Similarity: 49.099 Percent Identity: 30.180

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Align seg 1/1 to: PCT-US96-03965-7 from: 1 to: 838

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331 CATCTGCAGAGTG.....TGTCAGGCTATTTCAGGTTCAAGA 368
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65 luCysCysSerGluTrp.....AspCysMetCysValGlnProGlu 78
111 |||||
369 ACTTTTGTCTCTCCCAACACGCGAGTGTGAGTGCATTGAA...GGA 415
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79 PheHisCysGlyAspProCysCysThrThrCysArgHisProCysPr 95
111 |||||
416 TTCCCATTTGTTGGGCGCAGTGCACCATGT...GAAAAGAGCTGCAG 462
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95 oProGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnC 112
111 |||||
463 GCCTGCCAGGAGCTAACCAAGCAGGGT.....T 491
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112 ysileAspCysAlaSerGlyThrPheSerGlyGlyHis...GluGlyHis 127
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492 GCAAAACCTGTAGCTGGGAACATTAATGACCAAGACGGTACTGCGCTC 541
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128 CysLysProTrpThrAspCysThrGlnPheGlyPheLeuThrValPhePr 144
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542 TGTGACACCTGCGACGAACGTCTCTAGACGGAAGTCTGTGCTTAAGAC 591
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144 OGlyAsnLysThrHisAsnAlaValCysValPro..... 155
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592 CGGGACCGAGGAAGGACGTGTGTGTGGACCCCTGTGTGAGCTTCT 641
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162 ProLeuGlyTrpLeuThrValValLeuLeuAlaValAlaAlaCysValle 178
111 |||||
692 TCCTTCGAGGCTCTTACCTTGTCTGCGCGCTGACATCGCTTGTGCTGT 741
111 |||||
178 uLeuLeuThrSerAlaGlnLeuGlyLeuHisIle.....TrpGlnLeuA 193
111 |||||
742 GGCCCTGATCTTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 791
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193 rGlyThrGlnLeuLeuValPro..... 202
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; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: mu4-1BB
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; NAME/KEY: CDS
; LOCATION: 1..768
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; US-08-236-918A-5
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## alignment\_block:

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1 APPLICATION NUMBER: PCT/US94/10457
2 FILING DATE:
3 CLASSIFICATION:
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: 08/012,269
6 FILING DATE: 2/1/93
7 APPLICATION DATA:
8 APPLICATION NUMBER: 07/922,996
9 FILING DATE: 7/30/92
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 07/267,577
12 FILING DATE: 11/7/88
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Michaels, Christopher A.
15 REGISTRATION NUMBER: 34,390
16 REFERENCE/DOCKET NUMBER: kwnh41bb
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 607-273-1711
19 TELEFAX: 607-273-2609
20 TELEX:
21 INFORMATION FOR SEQ ID NO: 1 :
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 838
24 TYPE: nucleic acid
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26 TOPOLOGY: linear
27 MOLECULE TYPE: cDNA to mRNA
28 HYPOTHEICAL: NO
29 ANTI-SENSE: NO
30 FRAGMENT TYPE: n/a
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32 ORGANISM: Human
33 STRAIN:
34 INDIVIDUAL ISOLATE: H4-1BB #1
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36 HAPLOTYPE:
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39 CELL LINE:
40 ORGANELLE:
41 IMMEDIATE SOURCE:
42 LIBRARY: cDNA library
43 CLONE:
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48 FEATURE:
49 NAME/KEY: H4-1BB
50 LOCATION:
51 IDENTIFICATION METHOD: Similarity to mouse 4-1BB and other
52 IDENTIFICATION METHOD: members of NGFR superfamily
53 OTHER INFORMATION:
54 PUBLICATION INFORMATION:
55 AUTHORS: Kwon, B.S., and Weissman, S.M.
56 TITLE: cDNA sequences of two inducible T-cell genes
57 JOURNAL: Proc. Natl. Acad. Sci. USA
58 VOLUME: 86
59 ISSUE:
60 PAGES: 1963-1967
61 RELEVANT RESIDUES IN SEQ ID NO: all
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; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
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; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
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; TOPOLOGY: linear
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; NAME/KEY: CDS
; LOCATION: 68..751
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Date: Sep 4, 2001 3:55 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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Search information block:

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seq\_documentation\_block:

Sequence 3, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION/DOCKET NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1006 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
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US-08-911-423-3

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; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
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; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911.423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023.419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027.901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-911-423-5
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alignment_scores:
Quality: 1075.50      Length: 241
Ratio: 5.487          Gaps: 1
Percent Similarity: 81.328      Percent Identity: 76.349
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alignment\_block:

US-09-512-363-2 x US-08-911-423-5 ..

Align seg 1/1 to: US-08-911-423-5 from: 1 to: 723

```
1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17
|||||
1 ATGGCNCARCAAYGGNGCNCATGGGNCNTTYMGNGCNYTNTGTYGGNTGCC 50
|||||
17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34
|||||
51 NYTNTNTGTCGNTNWSYNTNGGNCARMGNCNCACNGGNGCNCNGNT 100
|||||
34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50
|||||
101 GYGGCNCNGNMGNNTNTNTNGGNCACNGGNCACGAYGCNNMGNTGYTGY 150
|||||
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysC 67
|||||
151 MNGTNCAYACNACNMGNNTGYTYMGNGAYTAYCCNGGNGARGARTGYTG 200
|||||
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84
|||||
201 YWSNGARTGGGATGYATGTGTGTCARCCNGARTTYCAYTGYGGNGAYC 250
|||||
84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100
|||||
251 CNTGYTGACNACNTGYMGNCAYCAYCCNTGYCCNCNGGNCARGNGNTN 300
|||||
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
|||||
301 CARWSNCARGGNAARTTWSNTTYGNTTYCARTGYATHGAYTGYGCNWS 350
|||||
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Db 22 LCGLALL 28

## RESULT 14

B83642

hypothetical protein PA0028 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C&gt;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: B83642

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: AB2950; MUID:20437337

A:Accession: B83642

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-200 &lt;STO&gt;

A:Cross-references: GB:AE004442; GB:AE004091; NID:g9945843; PIDN:AAG03418.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0028

Search completed: September 5, 2001, 09:47:28  
Job time: 69 sec

## Query Match

Best Local Similarity 3.0%; Score 7; DB 2; Length 200;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 GERSAEE 225

||||||

Db 156 GERSAEE 162

## RESULT 15

E69961

N-acetylmuramoyl-L-alanine amidase homolog yqiI - Bacillus subtilis

C:Species: Bacillus subtilis

C&gt;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999

C:Accession: E69961

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertea

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Kotter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wilpat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbato, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033

A:Accession: E69961

A&gt;Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-206 &lt;KUN&gt;

A:Cross-references: GB:Z99116; GB:AL009126; NID:g2634723; PIDN:CAB14350.1; PID:el185687;

A:Experimental source: strain 168

C:Genetics:

A:Gene: yqiI

## Query Match

Best Local Similarity 3.0%; Score 7; DB 2; Length 206;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ALCGLAL 18

||||||

Db 9 ALCGLAL 15

---

nd with high affinity to fibronectin.

C:Genetics:  
A:Gene: GDB:GSN  
A:Cross-references: GDB:120019; OMIM:105120; OMIM:137350  
A:Map position: 9q33-q33  
A:Introns: 48/3; 117/1  
C:Superfamily: gelsolin; gelsolin repeat homology  
C:Keywords: actin binding; alternative splicing; amyloid; calcium; duplication  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-782/Product: gelsolin, plasma #status experimental <MAT1>  
F:51-176/Domain: actin-severing #status predicted <SEV>  
F:53-782/Product: gelsolin, cytosolic #status experimental <MAT2>  
F:66-397/Domain: gelsolin repeat homology <GEL1>  
F:123-126/Region: actin-actin interfilament contact  
F:434-782/Domain: calcium-sensitive, actin binding #status predicted <ACT>  
F:445-764/Domain: gelsolin repeat homology <GEL2>

Query Match 3.4%; Score 8; DB 1; Length 782;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ALLCALSL 24

Db 9 ALLCALSL 16

RESULT 6

I48349  
fibronectin - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
C:Accession: I48349; S33445  
R:Polly, P.; Nicholson, R.C.  
Gene 137, 353-354, 1993  
A:Title: Sequence of the mouse fibronectin-encoding gene promoter region.  
A:Reference number: I48349; MUID:94131313  
A:Accession: I48349  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-28 <RES>  
A:Cross-references: EMBL:222729; NID:g297911; PIDN:CAA80422.1; PID:g297912  
R:Polly, P.; Nicholson, R.C.  
submitted to the EMBL Data Library, May 1993  
A:Description: Nucleotide sequence of the murine fibronectin gene promoter region.  
A:Reference number: S33445  
A:Accession: S33445  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-27 <POL>  
A:Cross-references: EMBL:222729  
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat

Query Match 3.0%; Score 7; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 GPGRLLL 41

Db 6 GPGRLLL 12

RESULT 7

A83044  
hypothetical protein PA4823 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: A83044  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.  
A:Reference number: A82950; MUID:20437337  
A:Accession: A83044  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-69 <STO>  
A:Cross-references: GB:AE004895; GB:AE004091; NID:g9951083; PIDN:AAG08208.1; GSPDB:GN000146  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4823

Query Match 3.0%; Score 7; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RALCGLA 17

Db 13 RALCGLA 19

RESULT 8

A86860  
hypothetical protein ytfA [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: A86860  
R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehlen, J.; et al.  
Genome Res. in press, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium.  
A:Reference number: A86860  
A:Accession: A86860  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-92 <STO>  
A:Cross-references: GB:AE005176; NID:g12724914; PIDN:AAK05979.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: ytfA

Query Match 3.0%; Score 7; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLLAVA 174

Db 80 VLLAVA 86

RESULT 9

B25429  
T-cell receptor beta chain precursor V region (SJL73) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 30-May-1997  
C:Accession: B25429  
R:Behlke, M.A.; Chou, H.S.; Huppi, K.; Loh, D.Y.  
Proc. Natl. Acad. Sci. U.S.A. 83, 767-771, 1986  
A:Title: Murine T-cell receptor mutants with deletions of beta-chain variable region  
A:Reference number: A94132; MUID:86121021  
A:Accession: B25429  
A:Molecule type: mRNA  
A:Residues: 1-120 <BEH>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor  
F:11-120/Product: T-cell receptor beta chain V region SJL73 #status predicted <MAT>

Query Match 3.0%; Score 7; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GPGCGPG 37

Db 5 GPCCGPG 11  
|||||||

## RESULT 10

A71173  
hypothetical protein PH0581 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000  
C:Accession: A71173  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yanazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A:Reference number: A71000; MUID:98344137  
A:Accession: A71173  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-133 <KAW>  
A:Cross-references: GB:AP000002; NID:g3236129; PIDN:BAA29670.1; PID:g3256987  
A:Experimental source: strain OT3  
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C:Genetics:  
A:Gene: PH0581  
C:Superfamily: hypothetical protein MJ1081

Query Match 3.0%; Score 7; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GRLLGT 43  
|||||||  
Db 103 GRLLGT 109

## RESULT 11

G75053  
hypothetical protein PAB0941 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C:Accession: G75053  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
A:Reference number: A75001  
A:Accession: G75053  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-133 <KAW>  
A:Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50324.1; PID:g545883  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB0941  
C:Superfamily: hypothetical protein MJ1081

Query Match 3.0%; Score 7; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GRLLGT 43  
|||||||  
Db 103 GRLLGT 109

## RESULT 12

UTCAB  
gonadotropin beta chain precursor - common carp  
C:Species: Cyprinus carpio (common carp)  
C>Date: 31-Aug-1979 #sequence\_revision 16-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S29677; S29678; J70462; A01504  
R:Chang, Y.S.; Huang, F.L.; Lo, T.B.

submitted to the EMBL Data Library, May 1991  
A:Reference number: S29677  
A:Accession: S29677  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-144 <CHI>  
A:Cross-references: EMBL:X59888; NID:g62619; PIDN:CAA42542.1; PID:g62620  
A:Accession: S29678  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-144 <CHA>  
A:Cross-references: EMBL:X59889; NID:g62621; PIDN:CAA42543.1; PID:g62622  
R:Chang, Y.S.; Huang, C.J.; Huang, F.L.; Lo, T.B.  
Int. J. Pept. Protein Res. 32, 556-564, 1988  
A:Title: Primary structures of carp gonadotropin subunits deduced from cDNA nucleotid  
A:Reference number: J70462; MUID:89233593  
A:Accession: J70462  
A:Molecule type: mRNA  
A:Residues: 1-144 <CH2>  
R:Joilles, J.; Burzawa-Gerard, E.; Fontaine, Y.A.; Joilles, P.  
Biochimie 59, 893-898, 1977  
A:Title: The evolution of gonadotropins: some molecular data concerning a non-mammali  
A:Reference number: A90673; MUID:78124308  
A:Accession: A01504  
A:Molecule type: protein  
A:Residues: 28-36, 'X', 38-53; 141-142 <JOL>  
C:Genetics:  
A:Introns: 6/2; 65/3  
A:Superfamily: pituitary glycoprotein hormone beta chain  
C:Keywords: glycoprotein; pituitary  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-117/Product: gonadotropin beta chain #status predicted <MAT>  
F:33-58,47-81,50-112,62-134,96-124,114-117/Disulfide bonds: #status predicted  
F:37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.0%; Score 7; DB 1; Length 144;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 VVLLAVA 174  
|||||||  
Db 19 VVLLAVA 25

## RESULT 13

G83342  
hypothetical protein PA2436 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: G83342  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A:Reference number: A82950; MUID:20437337  
A:Accession: G83342  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-144 <STO>  
A:Cross-references: GB:AE004670; GB:AE004091; NID:g9948470; PIDN:AAG05824.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA2436

Query Match 3.0%; Score 7; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LCGLALL 19  
|||||||

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:19 ; Search time 17.09 Seconds  
(without alignments)  
1042.999 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 234  
Sequence: 1 MAQHGAMGAFRALCGALLC.....EEERGSAAEKRLGDLWV 234

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_68:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.4	215	2 T33566	hypothetical prote
2	8	3.4	241	2 E70470	conserved hypothet
3	8	3.4	411	2 S61245	probable virion gl
4	8	3.4	509	2 H70597	probable membrane
5	8	3.4	782	1 FAHUP	gelosin precursor
6	7	3.0	28	2 I48349	fibronectin - mous
7	7	3.0	69	2 A83044	hypothetical prote
8	7	3.0	92	2 A86860	hypothetical prote
9	7	3.0	120	2 B25429	T-cell receptor be
10	7	3.0	133	2 A71173	hypothetical prote
11	7	3.0	133	2 G75053	hypothetical prote
12	7	3.0	144	1 UTCAB	gonadotropin beta
13	7	3.0	144	2 G83342	hypothetical prote
14	7	3.0	200	2 B83642	hypothetical prote
15	7	3.0	206	2 E69961	N-acetylmutamoyl-L
16	7	3.0	213	2 G75303	conserved hypothet
17	7	3.0	232	2 S58353	CD1b protein - she
18	7	3.0	256	2 D69845	thiamin biosynthes
19	7	3.0	288	2 B42424	chitinase (EC 3.2.
20	7	3.0	272	2 G75291	guanylate kinase -
21	7	3.0	274	2 B45887	leukocyte differen
22	7	3.0	286	2 S07533	puff II/9A-2 prote
23	7	3.0	286	2 S07532	puff II/9-1 protei
24	7	3.0	288	2 G75613	thiamin biosynthes
25	7	3.0	297	2 I38517	syntaxin - human
26	7	3.0	297	2 S52726	syntaxin-4 - human
27	7	3.0	320	2 T35265	probable D-amino a
28	7	3.0	320	2 T36062	probable ABC-type
29	7	3.0	324	2 S51001	transforming prote

30 7 3.0 325 2 D83366 probable transcrip  
31 7 3.0 332 2 S63660 NADH dehydrogenase  
32 7 3.0 333 2 S47246 gene CDI protein -  
33 7 3.0 335 1 HLHUR3 T-cell surface gly  
34 7 3.0 350 2 T03485 ornithine cyclodea  
35 7 3.0 352 2 S76078 hypothetical prote  
36 7 3.0 354 2 G75548 ABC transporter, A  
37 7 3.0 359 2 A56549 cell-cell signalin  
38 7 3.0 371 2 T20093 hypothetical prote  
39 7 3.0 376 2 T35085 hypothetical prote  
40 7 3.0 377 2 G71341 conserved hypothet  
41 7 3.0 401 1 A36961 pilin biogenesis p  
42 7 3.0 407 2 E81914 probable transmem  
43 7 3.0 426 2 F81187 glucose/galactose  
44 7 3.0 440 2 A83435 ATP synthase in ty  
45 7 3.0 447 2 S37048 cysteine proteinas

ALIGNMENTS

RESULT 1

T33566  
hypothetical protein R160.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T33566  
R:Nelson, J.; Gattung, S.  
Submitted to the EMBL Data Library, October 1998  
A:Description: The sequence of C. elegans cosmid R160.  
A:Reference number: Z21370  
A:Accession: T33566  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-215 <NE>  
A:Cross-references: EMBL:AF099001; PIDN:AAC68733.1; GSPDB:GN00028; CESP:R160.6  
A:Experimental source: strain Bristol N2; clone R160  
C:Genetics:  
A:Gene: CESP:R160.6  
A:Map position: X  
A:Introns: 31/2; 74/1; 96/2  
C:Superfamily: Caenorhabditis elegans hypothetical protein R160.6

Query Match 3.4%; Score 8; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 VLLAVAAC 176  
| | | | | | | |  
Db 24 VLLAVAAC 31

RESULT 2

E70470  
conserved hypothetical protein aq\_1986 - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 18-Aug-2000  
C:Accession: E70470  
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666  
A:Accession: E70470  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-241 <AAQ>  
A:Cross-references: GB:AE000766; NID:q2984216; PIDN:AAC07762.1; PID:q2984233; GB:AE00  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: aq\_1986  
C:Superfamily: conserved hypothetical protein aq\_1986

Query Match 3.4%; Score 8; DB 2; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ALLCALSL 24  
 |||||  
 Db 38 ALLCALSL 45

## RESULT 3

S61245 probable virion glycoprotein M (gm) - bovine herpesvirus 1

C:Species: bovine herpesvirus 1  
 C:Date: 18-Sep-1997 #sequence\_revision 18-Sep-1997 #text\_change 26-Aug-1999  
 C:Accession: S61245  
 R:Vleck, C.; Benes, V.; Lu, Z.; Kutish, G.F.; Paces, V.; Rock, D.; Letchworth, G.J.; Sch  
 submitted to the EMBL Data Library, January 1995  
 A:Description: Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus  
 A:Reference number: S61233  
 A:Accession: S61245  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-411 <VLC>  
 A:Cross-references: EMBL:Z48053; NID:g971311; PIDN:CAA88123.1; PID:g971324  
 C:Superfamily: herpesvirus 51K protein

Query Match 3.4%; Score 8; DB 2; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VVLLAVAA 175  
 |||||  
 Db 93 VVLLAVAA 100

## RESULT 4

H70597 probable membrane protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis  
 C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
 C:Accession: H70597  
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987  
 A:Accession: H70597  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-509 <COL>  
 A:Cross-references: GB:Z94121; GB:ALL23456; NID:g3261736; PIDN:CAB08087.1; PID:e312290;  
 A:Experimental source: strain H37RV  
 C:Genetics:  
 A:Gene: RV3887C

Query Match 3.4%; Score 8; DB 2; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 9.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VVLLAVAA 175  
 |||||  
 Db 205 VVLLAVAA 212

## RESULT 5

FAHUP gelsolin precursor, plasma [validated] - human

N:Alternate names: actin-depolymerizing factor; brevini  
 N:Contains: amyloid protein, I2K; gelsolin, cytosolic  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 08-Dec-2000  
 C:Accession: A03011; A38797; S03073; A60849; A36029; A61263; A34137  
 R:Kwiatkowski, D.J.; Stossel, T.P.; Orkin, S.H.; Mole, J.E.; Colten, H.R.; Yin, H.L.  
 Nature 323, 455-458, 1986  
 A:Title: Plasma and cytoplasmic gelsolins are encoded by a single gene and contain a  
 A:Reference number: A93383; MUID:87014807  
 A:Accession: A03011  
 A:Molecule type: mRNA  
 A:Residues: 1-782 <KWI>  
 A:Cross-references: EMBL:X04412; NID:g35447; PIDN:CAA28000.1; PID:g736249  
 A:Accession: A38797  
 A:Molecule type: protein  
 A:Residues: 28-52; 178-194, 'XX', 197; 279-290, 'S', 292-294, 'XX', 297-303; 434-449, 'XX', 452-  
 R:Kwiatkowski, D.J.; Wehl, R.; Yin, H.L.  
 J. Cell Biol. 106, 375-384, 1988  
 A:Title: Genomic organization and biosynthesis of secreted and cytoplasmic forms of g  
 A:Reference number: S03073; MUID:88115587  
 A:Accession: S03073  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-116 <KW3>  
 A:Cross-references: EMBL:X07065  
 A:Note: 1-Met is the initiator for plasma gelsolin. 52-Met is the initiator for cyto  
 R:Bryan, J.; Hwo, S.  
 J. Cell Biol. 102, 1439-1446, 1986  
 A:Title: Definition of an N-terminal actin-binding domain and a C-terminal Ca(2+) reg  
 A:Reference number: A60849; MUID:86168493  
 A:Accession: A60849  
 A:Molecule type: protein  
 A:Residues: 'X', 52-55, 'X', 57-59, 'X', 61-62 <BRV>  
 R:Vandekerckhove, J.; Bauw, G.; Vancompernelle, K.; Honore, B.; Celis, J.  
 J. Cell Biol. 111, 95-102, 1990  
 A:Title: Comparative two-dimensional gel analysis and microsequencing identifies gels  
 A:Reference number: A36029; MUID:90307803  
 A:Accession: A36029  
 A:Molecule type: protein  
 A:Residues: 'XX', 150-153, 'X', 155, 'X', 157-159; 486-492, 'X', 494-498, 'X', 500, 'X', 628-641,  
 R:Maury, C.P.J.  
 J. Clin. Invest. 87, 1195-1199, 1991  
 A:Title: Gelsolin-related amyloidosis. Identification of the amyloid protein in Finni  
 A:Reference number: A61263; MUID:91185597  
 A:Accession: A61263  
 A:Molecule type: protein  
 A:Residues: 200-213, 'N', 215-270 <MAU>  
 A:Experimental source: familial amyloid polynuropathy (Finnish-type) heart and kidne  
 A:Note: the substitution of Asn for 214-Asp causes disease  
 R:Haltia, M.; Prelli, F.; Ghiso, J.; Kiuru, S.; Somer, H.; Palo, J.; Frangione, B.  
 Biochem. Biophys. Res. Commun. 167, 927-932, 1990  
 A:Title: Amyloid protein in familial amyloidosis (Finnish type) is homologous to gels  
 A:Reference number: A34562; MUID:90211339  
 A:Accession: A34562  
 A:Molecule type: protein  
 A:Residues: 200-214 <HAL>  
 A:Experimental source: diseased kidney, familial amyloidosis (Finnish type)  
 R:Lind, S.E.; Janney, P.A.  
 J. Biol. Chem. 259, 13262-13266, 1984  
 A:Title: Human plasma gelsolin binds to fibronectin.  
 A:Reference number: A92450; MUID:85030446  
 A:Contents: annotation; fibronectin binding  
 R:Maury, C.P.J.; Alli, K.; Baumann, M.  
 FEBS Lett. 260, 85-87, 1990  
 A:Title: Finnish hereditary amyloidosis. Amino acid sequence homology between the amy  
 A:Reference number: A34137; MUID:90127414  
 A:Accession: A34137  
 A:Molecule type: protein  
 A:Residues: 235-237; 240-252; 258-269 <MA2>  
 A:Experimental source: kidney, Finnish hereditary amyloidosis patient  
 C:Comment: Gelsolin is a calcium-regulated, actin-modulating protein that binds to th  
 can promote the assembly of monomers into filaments (nucleation) as well as sever fil  
 C:Comment: A single gene encodes two forms of gelsolin; one remains associated with t

SQ SEQUENCE 335 AA; 37717 MW; EA041C1C45A5777F CRC64;

Query Match 3.0%; Score 7; DB 1; Length 335;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 GPGRLLL 41  
| | | | |  
Db 216 GPGRLLL 222

## RESULT 15

WN5A\_AMBME  
ID WN5A\_AMBME STANDARD; PRT; 359 AA.  
AC Q06442;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE WNT-5A PROTEIN PRECURSOR.  
GN WNT-5A.  
OS Ambystoma mexicanum (Axolotl).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;  
OC Ambystoma.  
OX NCBI\_TaxID=8296;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=93183769; PubMed=8443107;

RA Busse U., Seguin C.;  
RT "Isolation of cDNAs for two closely related members of the axolotl  
Wnt family, Awnt-5A and Awnt-5B, and analysis of their expression  
during development.";  
RL Mech. Dev. 40:63-72(1993).

CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING  
MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF  
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.

CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE  
EXTRACELLULAR MATRIX.

CC -!- TISSUE SPECIFICITY: NEUROECTODERMAL AND NON-NEUROECTODERMAL  
TISSUES.

CC -!- DEVELOPMENTAL STAGE: ABUNDANT IN THE BLASTULA UNTIL GASTRULATION,  
BARELY DETECTABLE DURING GASTRULATION, AND INCREASE AGAIN DURING  
NEURULATION. DETECTED THROUGHOUT THE REMAINING DEVELOPMENT AND IN  
HATCHED LARVAE.

CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----

CC EMBL: Z14047; CAA78415.1; -

DR PIR: S24999; S24999.

DR InterPro: IPR000970; -

DR Pfam: PF00110; wnt; 1.

DR PROSITE: PS00246; WNT1; 1.

KW Developmental protein; Glycoprotein; Signal.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 359 WNT-5A PROTEIN.

FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 359 AA; 40116 MW; 533FEB0414DAA14 CRC64;

## Query Match

Best Local Similarity 3.0%; Score 7; DB 1; Length 359;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LALLCAL 22  
| | | | |  
Db 10 LALLCAL 16

Search completed: September 5, 2001, 09:48:13  
Job time: 113 sec





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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=95094925; PubMed=8001672;
RA Metzger R., Bader M., Ludwig T., Berberich C., Bunnemann B.,
RA Ganten D.;
RT "Expression of the mouse and rat mas proto-oncogene in the brain and
RT peripheral tissues.";
RL FEBS Lett. 357:27-32(1995).
[2]
RN SEQUENCE OF 1-25 FROM N.A.
RP STRAIN=BCBA; TISSUE=Testis;
RX MEDLINE=97422605; PubMed=9268631;
RA Schweifer N., Valk P.J., Delwel R., Cox R., Francis F.,
RA Meier-Ewert S., Lehrach H., Barlow D.P.;
RT "Characterization of the C3 YAC contig from proximal mouse chromosome
RT 17 and analysis of allelic expression of genes flanking the imprinted
RL Igf2r gene.";
RL Genomics 43:285-297(1997).
CC -1- FUNCTION: NOT KNOWN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR ANGIOTENSIN
CC II.
-----
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-----
DR EMBL: X67735; CAA47964.1; -
DR EMBL: U96273; AAB69120.1; -
DR PIR: S29619; S29619.
DR GCRDB: GCR_0660; -
DR GCRDB: GCR_2448; -
DR MGD: MGI:96918; Mas1.
DR InterPro: IPR000276; -
DR InterPro: IPR000820; -
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00533; MASONCOGENE.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Proto-oncogene.
FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 127 3 (POTENTIAL).
FT DOMAIN 128 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 171 4 (POTENTIAL).
FT DOMAIN 172 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 205 5 (POTENTIAL).
FT DOMAIN 206 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 6 (POTENTIAL).
FT DOMAIN 245 262 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 263 283 7 (POTENTIAL).
FT DOMAIN 284 324 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 325 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19 19 S -> I (IN REF. 2).
FT SEQUENCE 324 AA; 36904 MW; 24F4AB7299E6016F CRC64;
Query Match 3.0%; Score 7; DB 1; Length 324;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 17 ALLCALLS 23
DB 153 ALLCALLS 159
RESULT 12
CIBL_SHEEP
ID CIBL_SHEEP STANDARD; PRT; 333 AA.
AC Q28565;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE T-CELL SURFACE GLYCOPROTEIN CD1B-1 PRECURSOR (CD1B-1 ANTIGEN)
DE (SCD1A25).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal thymocytes;
RX MEDLINE=96269982; PubMed=8662069;
RA Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
RL Immunogenetics 44:86-96(1996).
CC -1- FUNCTION: NOT KNOWN.
CC -1- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: Z36890; CAA85359.1; -
DR HSSP: P11609; 1CD1.
DR InterPro: IPR003006; -
DR Pfam: PF00047; Ig; 1.
KW Glycoprotein; Signal; Immunoglobulin domain; Transmembrane;
KW Multigene family.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 333 T-CELL SURFACE GLYCOPROTEIN CD1B-1.
FT DOMAIN 19 302 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 303 323 POTENTIAL.
FT DOMAIN 324 333 CYTOPLASMIC (POTENTIAL).
FT DISULFID 120 184 BY SIMILARITY.
FT DISULFID 224 279 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 333 AA; 37136 MW; 0144767E2525509 CRC64;
Query Match 3.0%; Score 7; DB 1; Length 333;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 35 GPGRLLL 41
DB 216 GPGRLLL 222
RESULT 13
CIB2_SHEEP
ID CIB2_SHEEP STANDARD; PRT; 333 AA.
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AC 029422;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DE T-CELL SURFACE GLYCOPROTEIN CD1B-2 ANTIGEN  
 DE (SCD1B-42) (ANTIGEN IAH-CC14).  
 OS Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 CC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96269982; PubMed=8662069;  
 RX Fergusson E.E., Dutia B.M., Hein W.R., Hopkins J.;  
 RT "The sheep CD1 gene family contains at least four CD1B homologues.";  
 RL Immunogenetics 44:86-96(1996).  
 RN [2]  
 RP SEQUENCE OF 21-33.  
 RX MEDLINE=99115506; PubMed=9914336;  
 RA Rhind S.M., Hopkins J., Dutia B.M.;  
 RT "Amino-terminal sequencing of sheep CD1 antigens and identification of  
 a sheep CD1B gene.";  
 RL Immunogenetics 49:225-230(1999).  
 CC -!- FUNCTION: NOT KNOWN.  
 CC -!- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY  
 SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
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 CC  
 DR EMBL; Z36891; CAA85360.1; -;  
 DR HSP; P11609; 1CD1.  
 DR InterPro; IPR003006; -;  
 DR Pfam; PF00047; 1g; 1.  
 KW Glycoprotein; Signal; Immunoglobulin domain; Transmembrane;  
 KW Multigene family.  
 FT SIGNAL 1 20  
 FT CHAIN 21 333 T-CELL SURFACE GLYCOPROTEIN CD1B-2.  
 FT DOMAIN 21 302 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 303 323 POTENTIAL.  
 FT DOMAIN 324 333 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 120 184 BY SIMILARITY.  
 FT DISULFID 224 279 BY SIMILARITY.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 333 AA; 37039 MW; 861BAE9617DB9BA1 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 35 GPGRLL 41  
 Db 216 GPGRLL 222  
 |||||  
 RESULT 14  
 CD1B\_HUMAN  
 ID CD1B\_HUMAN STANDARD; PRT; 335 AA.  
 AC P15813; Q9Y5M4;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE T-CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1).  
 GN CD1D.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89196496; PubMed=2467814;  
 RA Calabi F., Jarvis J.M., Martin L., Milstein C.;  
 RT "Two classes of CD1 genes.";  
 RL Eur. J. Immunol. 19:285-292(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89098892; PubMed=2463622;  
 RA Balk S.P., Bleicher P.A., Terhorst C.;  
 RT "Isolation and characterization of a cDNA and gene coding for a  
 fourth CD1 molecule.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:252-256(1989).  
 RN [3]  
 RP SEQUENCE OF 19-109 FROM N.A., AND VARIANT SER-64.  
 RX MEDLINE=99416841; PubMed=10488738;  
 RA Han M., Hannick L.I., DiBrino M., Robinson M.A.;  
 RT "Polymorphism of human CD1 genes.";  
 RL Tissue Antigens 54:122-127(1999).  
 CC -!- FUNCTION: NOT KNOWN.  
 CC -!- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED ON CORTICAL THYMOCYTES, ON CERTAIN  
 T-CELL LEUKEMIAS, AND IN VARIOUS OTHER TISSUES.  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC -!- DATABASE: NAME-PROW; NOTE-CD guide CD1 entry;  
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd1.htm".  
 CC  
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 CC  
 DR EMBL; L38820; AAA59672.1; -;  
 DR EMBL; L38815; AAA59672.1; JOINED.  
 DR EMBL; L38817; AAA59672.1; JOINED.  
 DR EMBL; L38816; AAA59672.1; JOINED.  
 DR EMBL; L38818; AAA59672.1; JOINED.  
 DR EMBL; L38819; AAA59672.1; JOINED.  
 DR EMBL; X14974; CAA33099.1; -;  
 DR EMBL; J04142; AAA59673.1; -;  
 DR EMBL; AF143668; AAD37581.1; -;  
 DR PIR; S07715; HLHUR3.  
 DR PIR; A32217; A32217.  
 DR HSP; P11609; 1CD1.  
 DR MIM; 188410; -;  
 DR InterPro; IPR003006; -;  
 DR Pfam; PF00047; 1g; 1.  
 KW Glycoprotein; Signal; Transmembrane; Immunoglobulin domain;  
 KW Multigene family; Polymorphism.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 335 T-CELL SURFACE GLYCOPROTEIN CD1D.  
 FT DOMAIN 20 301 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 302 322 POTENTIAL.  
 FT DOMAIN 323 335 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 120 184 BY SIMILARITY.  
 FT DISULFID 224 279 BY SIMILARITY.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 64 64 T -> S.  
 /FTID=VAR\_010211.

DR Pfam: PF00187; chitin\_binding; 1.  
 DR PROSITE; PS00026; CHITIN\_BINDING; 1.  
 DR PROSITE; PS00773; CHITINASE\_19; 1.  
 DR PROSITE; PS00774; CHITINASE\_19; 2; 1.  
 KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;  
 KW Multigene family.  
 FT SIGNAL 1  
 FT CHAIN <1 20 POTENTIAL.  
 FT DOMAIN 21 269 ENDOCHITININASE B.  
 FT CHAIN 21 269 CHITIN\_BINDING (BY SIMILARITY).  
 FT DOMAIN 58 66 HINGE REGION (GLY-RICH).  
 FT DOMAIN 67 269 CATALYTIC.  
 FT DISULFID 23 31 BY SIMILARITY.  
 FT DISULFID 25 37 BY SIMILARITY.  
 FT DISULFID 30 44 BY SIMILARITY.  
 FT DISULFID 48 53 BY SIMILARITY.  
 SQ SEQUENCE 269 AA; 28166 MW; 3D38B1BAD75DE8F CRC64;

Query Match 3.0%; Score 7; DB 1; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GLALLCA 21  
 Db 7 GLALLCA 13

RESULT 7  
 CDID\_SYLFL STANDARD; PRT; 275 AA.  
 AC P23043;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE T-CELL SURFACE GLYCOPROTEIN CDID (LEUCOCYTE DIFFERENTIATION-LIKE  
 DE ANTIGEN TA) (FRAGMENT).  
 GN CD1.  
 OS Sylvilagus floridanus (Cottontail rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Sylvilagus.  
 OX NCBI\_TaxID=9986;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE-90035137; PubMed-2478462;  
 RA Calabi F., Belt K.T., Yu C.Y., Bradbury A., Mandy W.J., Milstein C.;  
 RT "The rabbit CD1 and the evolutionary conservation of the CD1 gene  
 family.";  
 RL Immunogenetics 30:370-377(1989).  
 CC -1- FUNCTION: NOT KNOWN.  
 CC -1- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON CORTICAL THYMOCYTES, ON CERTAIN  
 CC T-CELL LEUKEMIAS, AND IN VARIOUS OTHER TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M26249; AAA31197.1; -.  
 DR HSSP; P11609; 1CD1.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; ig; 1.  
 KW Glycoprotein; Immunoglobulin domain; Multigene family.  
 FT SIGNAL 1  
 FT CHAIN 99 163 BY SIMILARITY.  
 FT DISULFID 203 258 BY SIMILARITY.  
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 275 275  
 SQ SEQUENCE 275 AA; 31047 MW; 8E7232CD5C0C31F4 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 275;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 GPGRLL 41  
 Db 195 GPGRLL 201

RESULT 8  
 PU91\_SCICO STANDARD; PRT; 286 AA.  
 ID PU91\_SCICO  
 AC P22311;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE PUFF II/9-1 PROTEIN PRECURSOR.  
 GN II/9-1.  
 OS Sclara coprophila (Fungus gnat).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Scleroidea;  
 OC Scleridae; Bradysia.  
 OX NCBI\_TaxID=38358;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=6980;  
 RX MEDLINE-90133907; PubMed-2614832;  
 RA Dibratolomeis S.M., Gerbi S.A.;  
 RT "Molecular characterization of DNA puff II/9A genes in Sclara  
 RT coprophila.";  
 RL J. Mol. Biol. 210:531-540(1989).  
 CC -1- MISCELLANEOUS: THE DNA PUFF II/9 PROTEINS HAVE A PROPOSED  
 CC INTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTERMOLECULAR  
 CC DISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUES IN POSITION  
 CC D OF THE HEPTAD REPEAT.  
 CC -1- SIMILARITY: 76% IDENTICAL TO THE PUFF II/9-2 PROTEIN.  
 CC -----  
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 CC -----  
 DR EMBL; X51680; CAA35983.1; -.  
 DR PIR; S07532; S07532.  
 KW Signal; Coiled coil; Glycoprotein.  
 FT SIGNAL 1 219 OR 21 (POTENTIAL).  
 FT CHAIN 720 286 PUFF II/9-1 PROTEIN.  
 FT DOMAIN 61 235 HELICAL (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 286 AA; 32034 MW; AAG7B55F191B1D CRC64;

Query Match 3.0%; Score 7; DB 1; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 LTVVLLA 172  
 Db 7 LTVVLLA 13

RESULT 9  
 PU92\_SCICO

ID PU92\_SCICO STANDARD; PRT; 286 AA.  
 AC P22312;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE PUFF II/9-2 PROTEIN PRECURSOR.  
 GN II/9-2.  
 OS Sclara coprophila (Fungus gnat).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Scleroidea;  
 OC Scleridae; Bradysia.  
 OX NCBI\_TaxID=38358;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=6980;  
 RX MEDLINE=90133907; PubMed=2614832;  
 RA Dibartolomeis S.M., Gerbi S.A.;  
 RT "Molecular characterization of DNA puff II/9A genes in Sclara  
 coprophila.";  
 RL J. Mol. Biol. 210:531-540(1989).  
 CC -!- MISCELLANEOUS: THE DNA PUFF II/9 PROTEINS HAVE A PROPOSED  
 INTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTERMOLECULAR  
 DISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUES IN POSITION  
 D OF THE HEPTAD REPEAT.  
 CC -!- SIMILARITY: 76% IDENTICAL TO THE PUFF II/9-1 PROTEIN.  
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 CC -----  
 DR EMBL; X51679; CAA35982.1; -.  
 DR PIR; S07533; S07533.  
 KW Signal; Coiled coil; Glycoprotein.  
 FT SIGNAL 1 219 OR 21 (POTENTIAL).  
 FT CHAIN 220 286 PUFF II/9-2 PROTEIN.  
 FT DOMAIN 61 235 HELICAL (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 286 AA; 32621 MW; 720AC8CCC22A869C CRC64;  
  
 Query Match 3.0%; Score 7; DB 1; Length 286;  
 Best Local Similarity 100.08; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 166 LRVVLLA 172  
 Db | | | | | | |  
 7 LRVVLLA 13  
  
 RESULT 10  
 ID STX4\_HUMAN STANDARD; PRT; 297 AA.  
 AC Q12846; Q15525;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE SYNTAXIN 4.  
 GN STX4A OR STX4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=94266173; PubMed=8206394;  
 RA Li H., Hodge D.R., Pei G.K., Seth A.;  
 RT "Isolation and sequence analysis of the human syntaxin-encoding  
 gene.";

Gene 143:303-304(1994).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Skeletal muscle;  
 RX MEDLINE=96332494; PubMed=8760387;  
 RA Jagadeish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,  
 Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,  
 Frenkel M.J., Ward C.W.;  
 RA "Insulin-responsive tissues contain the core complex protein SNAP-25  
 (syntaxin-associated protein 25) A and B isoforms in addition to  
 syntaxin 4 and synaptobrevins 1 and 2.";  
 RL Biochem. J. 317:945-954(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Periphereal blood neutrophils;  
 RA Nabokina S., Lazo P.A., Mollinedo F.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lens epithelium;  
 RA Rae J.L., Shepard A.R.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: POTENTIALLY INVOLVED IN DOCKING OF SYNAPTIC VESICLES  
 AT PRESYNAPTIC ACTIVE ZONES.  
 CC -!- SIMILARITY: BELONGS TO THE SYNTAXIN/EPIMORPHIN FAMILY.  
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 CC -----  
 DR EMBL; U07158; AAA20967.1; -.  
 DR EMBL; X85784; CAA59769.1; -.  
 DR EMBL; AJ000541; CAA04174.1; -.  
 DR EMBL; AF026007; AAB88810.1; -.  
 DR HSP; P32851; LBR0.  
 DR MIM; 186591; -.  
 DR InterPro; IPR000017; -.  
 DR Pfam; PF00804; Syntaxin; 1.  
 DR PROSITE; PS00914; SYNTAXIN; 1.  
 KW Neurotransmitter transport; Coiled coil; Transmembrane.  
 FT DOMAIN 43 163 COILED COIL (POTENTIAL).  
 FT TRANSMEM 199 222 COILED COIL (POTENTIAL).  
 FT TRANSMEM 276 296 POTENTIAL.  
 FT CONFLICT 174 174 E -> D (IN REF. 1).  
 FT CONFLICT 269 269 A -> V (IN REF. 1).  
 SQ SEQUENCE 297 AA; 34180 MW; 5084FD1C49A86BAA CRC64;  
  
 Query Match 3.0%; Score 7; DB 1; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 167 TVVLLAV 173  
 Db | | | | | | |  
 283 TVVLLAV 289  
  
 RESULT 11  
 ID MAS\_MOUSE STANDARD; PRT; 324 AA.  
 AC P30554; O35944;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE MAS PROTO-ONCOGENE.  
 GN MAS1 OR MAS-1 OR MAS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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FT REPEAT 326 334 MOTIF B.
FT REPEAT 342 358 MOTIF A.
FT REPEAT 382 393 MOTIF C.
FT DOMAIN 434 555 2A.
FT REPEAT 468 476 MOTIF B.
FT REPEAT 490 506 MOTIF A.
FT REPEAT 528 539 MOTIF C.
FT DOMAIN 556 661 2B.
FT REPEAT 588 596 MOTIF B.
FT REPEAT 602 618 MOTIF A.
FT REPEAT 634 645 MOTIF C.
FT DOMAIN 662 782 2C.
FT REPEAT 693 701 MOTIF B.
FT REPEAT 707 723 MOTIF A.
FT REPEAT 749 761 MOTIF C.
FT DOMAIN 162 169 POLYPHOSPHOSINOSITIDE BINDING (BY SIMILARITY).
FT DOMAIN 188 196 POLYPHOSPHOSINOSITIDE BINDING (BY SIMILARITY).
FT DISULFID 215 228 IN PLASMA FORM ONLY.
FT VARIANT 214 214 D -> N (IN FAF).
FT VARIANT 214 214 /FTID=VAR_007718.
FT FT D -> Y (IN FAF).
FT FT /FTID=VAR_007719.
SQ SEQUENCE 782 AA; 85697 MW; 8CEBC52257A160F7 CRC64;

Query Match 3.4%; Score 8; DB 1; Length 782;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ALLCALS 24
Db 9 ALLCALS 16
|||||||

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RESULT 3
GTH2_CYPCA STANDARD; PRT; 144 AA.
AC P01235;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GONADOTROPIN BETA-II CHAIN PRECURSOR (GTH-II-BETA) (LUTEINIZING HORMONE-LIKE GTH)
DE HORMONE-LIKE GTH
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89233593; PubMed=3246480;
RA Chang Y.S., Huang C.-J., Huang F.-L., Lo T.-B.;
RT "Primary structures of carp gonadotropin subunits deduced from cDNA nucleotide sequences";
RL Int. J. Pept. Protein Res. 32:556-564(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Chang Y.S., Huang F.-L., Lo T.-B.;
RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 28-53 AND 141-142.
RX MEDLINE=78124308; PubMed=607993;
RA Jolles J., Burzawa-Gerard E., Fontaine Y.-A., Jolles P.;
RT "The evolution of gonadotropins: some molecular data concerning a non-mammalian pituitary gonadotropin, the hormone from a teleost fish (Cyprinus carpio L.)";
RL Biochimie 59:893-898(1977).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.

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CC -----
CC EMBL; X59888; CAA42542.1; -
CC EMBL; X59889; CAA42543.1; -
CC PIR; S29677; S29677.
CC PIR; S29678; S29678.
CC PIR; A01504; UTCAB.
CC PIR; J0462; J0462.
CC HSP; P01233; 1HRP.
CC InterPro; IPR000359; -
CC InterPro; IPR001545; -
CC InterPro; IPR002400; -
CC Pfam; PF00007; Cys_knot; 1.
CC PRINTS; PR00438; GFCYSKNOT
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 27
FT CHAIN 28 142 GONADOTROPIN BETA-II CHAIN.
FT PROPEP 143 144
FT DISULFID 33 81 BY SIMILARITY.
FT DISULFID 47 96 BY SIMILARITY.
FT DISULFID 50 134 BY SIMILARITY.
FT DISULFID 58 112 BY SIMILARITY.
FT DISULFID 62 114 BY SIMILARITY.
FT DISULFID 117 124 BY SIMILARITY.
FT CARBOHYD 37 37 N-LINKED (GLCNAC...) (PROBABLE).
SQ SEQUENCE 144 AA; 16039 MW; 854FE80D4A39DCF8 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLLAVA 174
Db 19 VLLAVA 25
|||||||

RESULT 4
YQII_BACSU STANDARD; PRT; 206 AA.
AC P54525; P54526; O32017;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 22.2 KDA PROTEIN IN SPOOA-MMGA INTERGENIC REGION.
GN YQII.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,
RA Sato T., Takeuchi M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY 3.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO

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CC -----  
DR EMBL; D84432; BAA12584.1; ALT\_FRAME.  
DR EMBL; D84432; BAA12585.1; ALT\_FRAME.  
DR EMBL; Z99116; CABI4350.1; -.  
DR Subtilisin; BGI1717; YqII.  
DR InterPro; IPR002508; -.  
DR Pfam; PF01520; Amidase\_3; 1.  
KW Hypothetical protein; Hydrolase.  
FT CONFLICT 170 170 E -> D (IN REF. 1).  
SQ SEQUENCE 206 AA; 22235 MW; B0950FA7E4D12D1E CRC64;  
  
Query Match 3.0%; Score 7; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 ALCGLAL 18  
Db 9 ALCGLAL 15  
|||||  
  
RESULT 5  
CIB3\_SHEEP STANDARD; PRT; 232 AA.  
AC P80943;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE T-CELL SURFACE GLYCOPROTEIN CD1B-3 (CD1B-3 ANTIGEN) (SCDIT10)  
DE (FRAGMENT).  
OS Ovis aries (Sheep).  
CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
CC Bovidae; Caprinae; Ovis.  
CC NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal thymocytes;  
RA MEDLINE=96269982; PubMed=8662069;  
RX Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;  
RT "The sheep CD1 gene family contains at least four CD1B homologues.";  
RL Immunogenetics 44:86-96(1996).  
CC -|- FUNCTION: NOT KNOWN.  
CC -|- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY  
CC SIMILARITY).  
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
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CC -----  
DR EMBL; X90567; CAA62187.1; -.  
DR HSSP; P11609; 1CD1.  
DR InterPro; IPR003006; -.  
DR Pfam; PF00047; Ig\_1.  
KW Glycoprotein; Immunoglobulin domain; Transmembrane; Multigene family.  
FT NON\_TER 1 201  
FT DOMAIN <1 201 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 202 222  
Pfam; PF00182; Glyco\_hydro\_19; 1.

FT DOMAIN 223 232 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 19 83 BY SIMILARITY.  
FT DISULFID 123 178 BY SIMILARITY.  
FT CARBOHYD 45 45 N-LINKED (GLCNAC... (POTENTIAL).  
SQ SEQUENCE 232 AA; 26023 MW; C96DB93840B56158 CRC64;  
  
Query Match 3.0%; Score 7; DB 1; Length 232;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 35 GPGRLLL 41  
Db 115 GPGRLLL 121  
|||||  
  
RESULT 6  
CHIB\_MAIZE STANDARD; PRT; 269 AA.  
ID CHIB\_MAIZE AC P29023;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE ENDOCHITINASE B PRECURSOR (EC 3.2.1.14) (SEED CHITINASE B) (FRAGMENT).  
OS Zea mays (Maize).  
CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
CC Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;  
CC Andropogoneae; Zea.  
CC NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Seed;  
RX MEDLINE=92202208; PubMed=1551872;  
RA Huynh O.K., Hironaka C.M., Levine E.B., Smith C.E., Borgmeyer J.R.,  
RA Shah D.M.;  
RT "Antifungal proteins from plants. Purification, molecular cloning,  
RT and antifungal properties of chitinases from maize seed.";  
RL J. Biol. Chem. 267:6635-6640(1992).  
RN [2]  
RP SEQUENCE OF 169-184.  
RC TISSUE=Seed;  
RX MEDLINE=92156129; PubMed=1740436;  
RA Verburg J.G., Smith C.E., Lisek C.A., Huynh O.K.;  
RT "Identification of an essential tyrosine residue in the catalytic  
RT site of a chitinase isolated from Zea mays that is selectively  
RT modified during inactivation with  
RT 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide.";  
RL J. Biol. Chem. 267:3886-3893(1992).  
CC -|- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN  
CC CONTAINING FUNGAL PATHOGENS.  
CC -|- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF  
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.  
CC -|- MISCELLANEOUS: MAIZE CHITINASE B SEEMS TO BE LESS ACTIVE THAN  
CC CHITINASE A.  
CC -|- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO  
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL  
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL  
CC HYDROLASES).  
CC -----  
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CC -----  
DR EMBL; M84165; AAA33445.1; -.  
DR HSSP; P02877; 1HEV.  
DR MaizeDB; Z5130; -.  
DR InterPro; IPR000726; -.  
DR InterPro; IPR001002; -.  
DR Pfam; PF00182; Glyco\_hydro\_19; 1.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:20 ; Search time 10.37 Seconds  
(without alignments)  
772.978 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 234  
Sequence: 1 MAQHGAMGAFRALCGLALLC.....EEEGERSAEKRGRLDLMV 234

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.4	411	1 VGLM_HSVBC	P52370 bovine herp
2	8	3.4	782	1 GELS_HUMAN	P06396 homo sapien
3	7	3.0	144	1 Q1235_CYPCA	P01235 cyprinus ca
4	7	3.0	206	1 YQ11_BACSU	P54525 bacillus su
5	7	3.0	232	1 C1B3_SHEEP	P80943 ovis aries
6	7	3.0	269	1 CHIB_MAIZE	P29023 zea mays (m
7	7	3.0	275	1 CD1D_SYLFL	P23043 syviliagus
8	7	3.0	286	1 PU91_SCICO	P22311 scilara copr
9	7	3.0	286	1 PU92_SCICO	P22312 scilara copr
10	7	3.0	297	1 STX4_HUMAN	Q12846 homo sapien
11	7	3.0	324	1 MAS_MOUSE	P30554 mus musculu
12	7	3.0	333	1 C1B1_SHEEP	Q28585 ovis aries
13	7	3.0	333	1 C1B2_SHEEP	Q29422 ovis aries
14	7	3.0	335	1 CD1D_HUMAN	P15813 homo sapien
15	7	3.0	359	1 WN5A_AMBME	Q06442 ambystoma m
16	7	3.0	401	1 PILC_PSEPU	P36641 pseudomonas
17	7	3.0	508	1 VGLG_IHNV	P07923 infectious
18	7	3.0	524	1 VGLG_CHRV	P13180 candidura
19	7	3.0	555	1 NUSM_CANPA	P48919 candida par
20	7	3.0	598	1 NUSM_BRALA	Q79422 branchiosto
21	7	3.0	599	1 NUSM_BRAFL	Q47430 branchiosto
22	7	3.0	600	1 NUSM_METSE	Q35099 metridium s
23	7	3.0	603	1 NUSM_GORGO	P03917 gorilla gor
24	7	3.0	603	1 NUSM_HUMAN	P03915 homo sapien
25	7	3.0	603	1 NUSM_HYLLA	P03919 hylobates l
26	7	3.0	603	1 NUSM_PANPA	P03916 pan paniscu
27	7	3.0	603	1 NUSM_PANTR	Q35648 pan troglod
28	7	3.0	603	1 NUSM_PONPA	P32699 pongo pygma
29	7	3.0	603	1 NUSM_PONPY	P03918 pongo pygma
30	7	3.0	611	1 AFAM_MOUSE	O89020 mus musculu
31	7	3.0	641	1 NUSM_ALIMA	P50365 allomyces m
32	7	3.0	653	1 CCMF_RHOCA	Q00500 rhodobacter
33	7	3.0	666	1 NUSM_CHOCR	P48920 chondrus cr

34	7	3.0	675	1 NUSM_ACACA	Q37372 acanthamoeb
35	7	3.0	713	1 CADD_HUMAN	P55290 homo sapien
36	7	3.0	750	1 YD33_MYCPN	P75445 mycoplasma
37	7	3.0	757	1 COMP_HUMAN	P49747 homo sapien
38	7	3.0	830	1 YJG2_YEAST	P40367 saccharomyc
39	7	3.0	1248	1 SYJ2_RAT	O55207 rattus norv
40	7	3.0	1443	1 SYJ2_HUMAN	O15056 homo sapien
41	7	3.0	1469	1 DP27_CAEEL	P48996 caenorhabdi
42	7	3.0	2477	1 FINC_MOUSE	P11276 mus musculu
43	7	3.0	2477	1 FINC_RAT	P04937 rattus norv
44	6	2.6	71	1 NXLB_PSETE	P13495 pseudonaja
45	6	2.6	73	1 VF09_ORFNP2	P52586 orf virus (

ALIGNMENTS

RESULT 1  
VGLM\_HSVBC  
ID VGLM\_HSVBC STANDARD: PRT: 411 AA.  
AC P52370:  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE GLYCOPROTEIN M.  
GN GM OR UL10.  
OS Bovine herpesvirus type 1 (strain Cooper).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_TaxID=10323;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95313343; PubMed=7793062;  
RA Vleck C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,  
RA Letchworth G.J., Schwyzler M.;  
RT "Nucleotide sequence analysis of a 30-kb region of the bovine  
herpesvirus 1 genome which exhibits a collinear gene arrangement with  
the UL21 to UL4 genes of herpes simplex virus.";  
RL Virology 210:100-108(1995)  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN M.  
CC -----  
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CC -----  
CC EMBL: Z48053; CAA88123.1; -.  
DR InterPro: IPR000785; -.  
DR Pfam: PF01528; Herpes\_glycop; 1.  
DR PRINTS: PR00333; HSVINTEGRLMP.  
KW Transmembrane; Glycoprotein.  
FT TRANSMEM 14 34 POTENTIAL.  
FT TRANSMEM 89 109 POTENTIAL.  
FT TRANSMEM 133 153 POTENTIAL.  
FT TRANSMEM 159 179 POTENTIAL.  
FT TRANSMEM 213 233 POTENTIAL.  
FT TRANSMEM 249 269 POTENTIAL.  
FT TRANSMEM 277 297 POTENTIAL.  
FT TRANSMEM 318 338 POTENTIAL.  
FT CARBOHYD 57 57 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 411 AA; 43029 MW; 20F156DA9F40158C CRC64;

Query Match 3.4%; Score 8; DB 1; Length 411;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 168 VYLLAVAA 175  
|||||||

DB 93 VVLLAVAA 100

RESULT 2

GELS\_HUMAN

ID GELS\_HUMAN STANDARD; PRT; 782 AA.

AC P06396;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF)

DE (BREVIN) (AGEL).

GN GSN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID:9606;

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE-87014807; PubMed-3020431;

RA Kwiatkowski D.J., Stossel T.P., Orkin S.H., Mole J.E., Colten H.R.,

RA Yin H.L.;

RT "Plasma and cytoplasmic gelsolins are encoded by a single gene and

RT contain a duplicated actin-binding domain.";

RL Nature 323:455-458(1986).

RN [2]

RN FIBRONECTIN BINDING.

RX MEDLINE-85030446; PubMed-6092370;

RA Lind S.E., Janmey P.A.;

RT "Human plasma gelsolin binds to fibronectin.";

RL J. Biol. Chem. 259:13262-13266(1984).

RN [3]

RN IDENTITY OF FAF AMYLOID PROTEIN WITH GELSOLIN.

RX MEDLINE-90211339; PubMed-2157434;

RA Haltia M., Prelli F., Ghiso J., Kluru S., Sommer H., Palo J.,

RA Frangione B.;

RT "Amyloid protein in familial amyloidosis (Finnish type) is homologous

RT to gelsolin, an actin-binding protein.";

RL Biochem. Biophys. Res. Commun. 167:927-932(1990).

RN [4]

RN IDENTITY OF FAF AMYLOID PROTEIN WITH GELSOLIN.

RX MEDLINE-90127414; PubMed-2153578;

RA Maury C.P.J., Ali K., Baumann M.;

RT "Finnish hereditary amyloidosis. Amino acid sequence homology between

RT the amyloid fibril protein and human plasma gelsoline.";

RL FEBS Lett. 260:85-87(1990).

RN [5]

RN DISULFIDE BOND.

RX MEDLINE-96312883; PubMed-8703941;

RA Wen D., Corina K., Chow E.P., Miller S., Janmey P.A., Pepinsky R.B.;

RT "The plasma and cytoplasmic forms of human gelsolin differ in

RT disulfide structure.";

RL Biochemistry 35:9700-9709(1996).

RN [6]

RN DISULFIDE BOND.

RX MEDLINE-97157527; PubMed-9003812;

RA Allen P.G.;

RT "Functional consequences of disulfide bond formation in gelsolin.";

RL FEBS Lett. 401:89-94(1997).

RN [7]

RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-503.

RX MEDLINE-93361115; PubMed-8395021;

RA McLaughlin P.J., Gooch J.T., Mannherz H.-G., Weeds A.G.;

RT "Structure of gelsolin segment I-actin complex and the mechanism of

RT filament severing.";

RL Nature 364:685-692(1993).

RN [8]

RN STRUCTURE BY NMR OF 177-196.

RX MEDLINE-96167246; PubMed-8599675;

RA Xian W., Vegners R., Janmey P.A., Braunlin W.H.;

RT "Spectroscopic studies of a phosphoinositide-binding peptide from

RT gelsolin: behavior in solutions of mixed solvent and anionic

RT micelles.";

Biophys. J. 69:2695-2702(1995).

[9]

RN VARIANT FAF ASN-214.

RX MEDLINE-91097517; PubMed-2176481;

RA Ghiso J., Haltia M., Prelli F., Novello J., Frangione B.;

RT "Gelsolin variant (Asn-187) in familial amyloidosis, Finnish type.";

RL Biochem. J. 272:827-830(1990).

RN [10]

RN VARIANTS FAF ASN-214 AND TYR-214.

RX MEDLINE-93265143; PubMed-1338910;

RA de la Chapelle A., Tolvanen R., Boysen G., Santavy J.,

RA Bleeker-Wagemakers L., Maury C.P.J., Kere J.;

RT "Gelsolin-derived familial amyloidosis caused by asparagine or

RT tyrosine substitution for aspartic acid at residue 187.";

RL Nat. Genet. 2:157-160(1992).

CC -!- FUNCTION: GELSOLIN IS A CALCIUM-REGULATED, ACTIN-MODULATING

CC PROTEIN THAT BINDS TO THE PLUS (OR BARBED) ENDS OF ACTIN MONOMERS

CC OR FILAMENTS, PREVENTING MONOMER EXCHANGE (END-BLOCKING OR

CC CAPPING). IT CAN PROMOTE THE ASSEMBLY OF MONOMERS INTO FILAMENTS

CC (NUCLEATION) AS WELL AS SEVER FILAMENTS ALREADY FORMED.

CC -!- SUBCELLULAR LOCATION: SECRETED (PLASMA FORM) AND CYTOPLASMIC.

CC -!- ALTERNATIVE PRODUCTS: PLASMA GELSOLIN AND CYTOPLASMIC GELSOLIN

CC ARE DERIVED FROM A SINGLE GENE BY ALTERNATE INITIATION SITES AND

CC DIFFERENTIAL SPLICING.

CC -!- TISSUE SPECIFICITY: PHAGOCYTTIC CELLS, PLATELETS, FIBROBLASTS,

CC NONMUSCLE CELLS, SMOOTH AND SKELETAL MUSCLE CELLS.

CC -!- DISEASE: DEFECTS IN GSN ARE THE CAUSE OF FAMILIAL AMYLOIDOSIS,

CC FINNISH TYPE (FAF), AN INHERITED FORM OF SYSTEMIC AMYLOIDOSIS

CC CLINICALLY CHARACTERIZED BY CRANIAL NEUROPATHY AND LATTICE CORNEAL

CC DYSTROPHY.

CC -!- MISCELLANEOUS: IN ADDITION TO ITS ROLE IN ACTIN REGULATION, THIS

CC PROTEIN IS KNOWN TO BIND WITH HIGH AFFINITY TO FIBRONECTIN.

CC -!- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.

CC

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CC EMBL; X04412; CAA28000.1; -

DR PIR; A03011; FAHUP.

DR PIR; A34137; A34137.

DR PIR; A34562; A34562.

DR PDB; 1SOL; 08-MAR-96.

DR MIM; 137350; -

DR MIM; 105120; -

DR InterPro; IPR001974; -

DR Pfam; PF00626; Gelsolin; 6.

DR PRINTS; PR00597; GELSOLIN.

KW Actin-binding; Repeat; Calcium; Alternative initiation; Signal;

KW Capping protein; Amyloid; Disease mutation; 3D-structure.

FT SIGNAL 1 27

FT CHAIN 28 782 GELSOLIN, PLASMA ISOFORM.

FT CHAIN 53 782 GELSOLIN, CYTOPLASMIC ISOFORM.

FT INIT\_MET 52 52 FOR CYTOPLASMIC ISOFORM.

FT DOMAIN 53 176 ACTIN-SEVERING (POTENTIAL).

FT DOMAIN 434 782 ACTIN-BINDING, CA-SENSITIVE (POTENTIAL).

FT SITE 123 126 ACTIN-ACTIN INTERFILAMENT CONTACT POINT.

FT REPEAT 57 416 1ST HALF.

FT DOMAIN 417 433 HINGE REGION.

FT REPEAT 434 782 2ND HALF.

FT DOMAIN 57 176 1A.

FT REPEAT 89 97 MOTIF B.

FT REPEAT 112 128 MOTIF A.

FT REPEAT 150 161 MOTIF C.

FT REPEAT 177 233 1B.

FT DOMAIN 210 218 MOTIF B.

FT REPEAT 224 240 MOTIF A.

FT REPEAT 263 274 MOTIF C.

FT DOMAIN 294 416 1C.



Search completed: September 4, 2001, 16:12:11  
Job time: 1108 sec

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Squires,  
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.  
Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649  
A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40:65-69; 136-141:300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A:Reference number: A35010; MUID:90110215  
A:Accession: B35010  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kuhnert, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of  
A:Reference number: I38094; MUID:95121934  
A:Accession: I38094  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:Cross-references: GDB:I25914; OMIM:191191  
A:Map position: lp36.2-lp36.2  
A:Introns: 26/3  
A:Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
F:1-22/Domain: duplication; glycoprotein; receptor; transmembrane protein  
F:23-416/Product: signal sequence #status predicted <SIG>  
F:40-76/Domain: tumor necrosis factor receptor 2 #status experimental <MAT>  
F:78-119/Domain: NGF receptor repeat homology <NG1>  
F:120-162/Domain: NGF receptor repeat homology <NG2>  
F:164-201/Domain: NGF receptor repeat homology <NG3>  
F:262-279/Domain: transmembrane #status predicted <TMN>  
F:280-461/Domain: intracellular #status predicted <INT>

F:171.193/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 12.3%; Score 119; DB 1; Length 461;  
Best Local Similarity 26.3%; Pred. No. 0.022;  
Matches 41; Conservative 14; Mismatches 63; Indels 38; Gaps 8;  
QY 34 CGPG---RLLLGGTGDARC-----CRVHTTRCCRDYPGBECCSEWD-- 71  
Db 57 CSPGQHAKEVCTKTSDFVCDSCEDSTYTQLWNWPECLSCGSRSSDOVEFQACTREQNR 116  
QY 72 -CMCVQPEFHC-----GDPCCTTCRHHPGPGGQVSGQKFSFGFCIDCASGTFSG-- 122  
Db 117 ICTC-RFGWYCALSKQSGRCALCAPLR--KCRPGFGVAPGCTETSDVVCVKPCAPGTFSTNT 173  
QY 123 GHEGCHKPWTDCQTFQGLTVFPNGKTHNAVCPGSP 158  
Db 174 SSTDICRPHOICN----VVAIPGNASMDAVCTSTSP 205  
RESULT 12  
B38634  
tumor necrosis factor receptor type 2 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
R:Accession: B38634; A40254; S54816  
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
A:Reference number: A38634; MUID:91187885  
A:Accession: B38634  
A:Molecule type: mRNA  
A:Residues: 1-474 <LEW>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f  
A:Reference number: A40254; MUID:91246168  
A:Accession: A40254  
A:Molecule type: mRNA  
A:Residues: 1-474 <GOO>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R:Kisssnerghis, M.; Follows, R.; Feldmann, M.; Chernajovsky, Y.  
submitted to the EMBL Data Library, May 1995  
A:Description: Characterization of the promoter region of the murine p75-TNF receptor  
A:Reference number: S54816  
A:Accession: S54816  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-22 <KTS>  
A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
F:Keywords: cytokine receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F:40-77/Domain: NGF receptor repeat homology <NG1>  
F:79-120/Domain: NGF receptor repeat homology <NG2>  
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 12.3%; Score 119; DB 2; Length 474;  
Best Local Similarity 31.0%; Pred. No. 0.023;  
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;  
QY 46 DARCCRVHTTRCCRDYPGBECCSEWDCMCVQPEFHCPCCTTC-RHHPCPPGGVSGQ 104  
Db 107 EIRACTKQKNRVCAACEAGRYCAL-----KTHSGS--CRQCMRLSKCGPGFGVASSR 155  
QY 105 KFSFGFCIDCASGTFSG--GHEGHCKPWTDCQTFGLTFVPPGNKTHNAVCPGSP 158  
Db 156 APNGNVLCACAPGTFSDTTSSTDVCRPHRICS-----ILAIPGNASTDAVCAPESP 207

RESULT 13  
A60771

B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)  
C>Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
EMBO J. 8, 1403-1410, 1989  
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A:Reference number: S04460; MUID:89356608  
A:Accession: S04460  
A:Molecule type: mRNA  
A:Residues: 1-277 <STA>  
A:CROSS-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851  
R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
A:Reference number: A60771; MUID:89093941  
A:Accession: A60771  
A:Molecule type: protein  
A:Residues: 21-50 <BRA>  
A:Experimental source: Burkitt lymphoma cell line Raji  
C:Genetics: GDB:CD40  
A:CROSS-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F:21-193/Domain: extracellular #status predicted <EXT>  
F:194-215/Domain: transmembrane #status predicted <TM>  
F:216-277/Domain: intracellular #status predicted <CYT>  
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.2%; Score 118.5; DB 2; Length 277;  
Best Local Similarity 27.7%; Pred. No. 0.017;  
Matches 36; Conservative 10; Mismatches 73; Indels 11; Gaps 5;

Qy 34 CGPGRLLGTGTDCRCRVHTTRCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 88  
|||  
Db 62 CGESELDFTWNRETHC---HQHKYCDPNLGRVQOKGTSETDTICTCEEGWHCTSEACES 118  
|||  
Qy 89 C-RHPCPPPGQGVQSGQKFSFGFICDASGTFSGGHEG--HCKPWTDTCTQFGFLTVPFG 145  
|||  
Db 119 CVLHRSCTSGFGVKQIATGVSDTICEPCPGVGFNSVSAFEKCHPWTSCETKDLVVOQAG 178  
|||

Qy 146 NKTHNAVCPV 155  
|||  
Db 179 TNKTDVVCVP 188  
|||

RESULT 14  
I54182

tumor necrosis factor receptor 2-related protein - human  
C:Species: Homo sapiens (man)  
C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
C:Accession: I54182  
R:Baens, M.; Chaifanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
Genomics 16, 214-218, 1993  
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequer  
A:Reference number: I54182; MUID:93252381  
A:Accession: I54182  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-435 <RES>  
A:CROSS-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762  
C:Genetics: GDB:LTBR  
A:Gene: GDB:LTBR  
A:CROSS-references: GDB:1230195; OMIM:600979  
A:Map position: 12p13.3-12p13.1

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 12.1%; Score 117; DB 2; Length 435;  
Best Local Similarity 25.6%; Pred. No. 0.031;  
Matches 42; Conservative 12; Mismatches 66; Indels 44; Gaps 10;  
Qy 34 CGPGRLLGTGTDCRCRVHTTRC-----CRDYPGEE-----C 66  
|||  
Db 62 CPP-----GTVVSARKSIRDTVTCATCAENSYNEHWNLTICQLCRPCDPVVMGLEIAIPC 116  
|||  
Qy 67 CS--EWDCMCVQPEPHCGDPC--CTTCR-HHPCPPGQGVQSGQKFSFG-FQCIDCASGTF 120  
|||  
Db 117 TSKRKTQCR-C-OPGMFCAAWALECTHCELLSDCPGTAEALKEVKGNNHCVPCKAGHF 175  
|||  
Qy 121 --SGGHECHCKPWTDTCTQFGFLTVPFGNKTTHNAVCPGSPPAEP 162  
|||  
Db 176 QNTSSPSARCOPHTRCENQGLVEAAPGTAQSDTTC---KNPLEP 216  
|||

RESULT 15  
A33837

insulin-like growth factor I receptor precursor - rat  
N:Contains: insulin-like growth factor I alpha chain; insulin-like growth factor I be  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 16-Mar-1990 #sequence\_revision 03-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: JC2461; A33837; PC1131  
R:Pedrini, M.T.; Giorgino, F.; Smith, R.J.  
Biochem. Biophys. Res. Commun. 202, 1038-1046, 1994  
A:Title: cDNA cloning of the rat IGF I receptor: Structural analysis of rat and human  
A:Reference number: JC2461; MUID:94324926  
A:Accession: JC2461  
A:Molecule type: mRNA  
A:Residues: 1-1371 <PED>  
R:Werner, H.; Woloschak, M.; Adamo, M.; Shen-Ort, Z.; Roberts Jr., C.T.; LeRoith, D.  
Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989  
A:Title: Developmental regulation of the rat insulin-like growth factor I receptor ge  
A:Reference number: A33837; MUID:90017496  
A:Accession: A33837  
A:Molecule type: mRNA  
A:Residues: 1-364 <WER>  
A:CROSS-references: GB:M27293  
R:Kurachi, H.; Jobo, K.; Ohta, M.; Kawasaki, T.; Itoh, N.  
Biochem. Biophys. Res. Commun. 187, 934-939, 1992  
A:Title: A new member of the insulin receptor family, insulin receptor-related recept  
A:Reference number: PC1130; MUID:92412145  
A:Accession: PC1131  
A:Molecule type: mRNA  
A:Residues: 913-984, 'PY', 987-1017 <KUR>  
A:CROSS-references: GB:D12679; NID:g220918; PIDN:BAA20983.1; PID:g4433359  
C:Superfamily: insulin receptor; protein kinase homology  
C:Keywords: ATP; growth factor receptor; kinase-related transforming protein; transme  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-741/Product: insulin-like growth factor I alpha chain #status predicted <IGA>  
F:742-1371/Product: insulin-like growth factor I beta chain #status predicted <IGB>  
F:937-959/Domain: transmembrane #status predicted <TM>  
F:971-974/Region: GPV motif  
F:978-981/Region: NPXY motif  
F:998-1275/Domain: protein kinase homology <KIN>  
F:1006-1014/Region: protein kinase ATP-binding motif

Query Match 11.9%; Score 115.5; DB 2; Length 1371;  
Best Local Similarity 27.1%; Pred. No. 0.085;  
Matches 57; Conservative 22; Mismatches 52; Indels 79; Gaps 20;

Qy 8 GAFRA-----LCGLA-----LLCALSD----LGQRPTGGPGCG-----PGRLL-----L 40  
|||  
Db 139 GAIRLEKNADLCYLSTLIDAVSNYYIVGNKPP--KEGDLCPGTLKPKMCEKTT 196  
|||  
Qy 41 LGTGTDCRCRVHTTRC---CRDYPGEECCSEWDCMCVQPEPHCGDPC-----CTTC 89  
|||

C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <Sig>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TMM>

Query Match 15.6%; Score 151; DB 2; Length 271;  
Best Local Similarity 28.5%; Pred. No. 5.1e-05;  
Matches 47; Conservative 12; Mismatches 62; Indels 44; Gaps 8;  
Qy 26 ORPTGCGCGPRLLLG--TGTDAKRCRRVHTT-----RCRD-YPEEECCSEWD----- 71  
Db 6 QOPT-----AFLLLGLSLGVTVKLVKVDYPSGHKCCRCQPEHGMVSRCDHTRDTV 58  
Qy 72 CMVQPEFHCG----DPC--CTTCRRH-----PCPPQGGVQSQGKFSF 108  
Db 59 CHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTPTEDIVCQCRPTQPRQDSSHKL 118  
Qy 109 GFQCIDCASGTFSGGHEGHCKPWTCTQGFVTVPGNKNHNAV 153  
Db 119 GVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 6  
JC5559  
lectin-B - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: JC5559  
R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)  
A:Reference number: JC5559; MUID:97290889  
A:Accession: JC5559  
A:Molecule type: protein  
A:Residues: 1-295 <YAM>  
A:Experimental source: root  
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharide  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant lectin  
C:Keywords: glycoprotein  
F:96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 139; DB 2; Length 295;  
Best Local Similarity 28.8%; Pred. No. 0.00046;  
Matches 36; Conservative 18; Mismatches 41; Indels 30; Gaps 8;  
Qy 20 CALSLGQRPTGCP-----GCGPRLLLGTGTDARCCRVHTTRCCRDYPG-----EECC 67  
Db 133 CGVDFGNRTCPNDLCCSEWGMCGITEGYCGECQSQC---NHQRCGKDFAGRTLNDLCC 189  
Qy 68 SEWDCMCVQPEPHCGDPCTTCRRHPCPPGQGVQSQGKFSFGQ-C---IDCASGTFSGG 123  
Db 190 SEWGW-WCSSEAHCGGCGQSNYNRC-----GR-NFGFRTCPNELCCSSGGWCGS 238  
Qy 124 HEGHC 128  
Db 239 NDAHC 243

RESULT 7  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C:Accession: A46476; A46515  
R:Torres, R.M.; Clark, E.A.  
J. Immunol. 146, 620-626, 1992  
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40  
A:Reference number: A46476; MUID:92105763  
A:Accession: A46476  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-305 <TOR>  
A:Cross-references: GB:M83312; NID:gl553058  
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:75207)  
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay  
J. Immunol. 149, 3921-3926, 1992  
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A:Reference number: A46515; MUID:93094586  
A:Accession: A46515  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-287, LV, <GRI>  
A:Cross-references: GB:M83312; NID:gl553058; PIDN:AAB08705.1; PID:gl553059; GB:M94126  
A:Experimental source: BALB/C, liver  
A:Note: sequence extracted from NCBI backbone (NCBI:120357)  
C:Comment: For an alternative splice form, see PIR:A46515.  
C:Comment: For an alternative splice form, see PIR:A46476.  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: alternative splicing; transmembrane protein  
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 14.0%; Score 135.5; DB 2; Length 305;  
Best Local Similarity 26.1%; Pred. No. 0.00089;  
Matches 49; Conservative 10; Mismatches 74; Indels 55; Gaps 8;  
Qy 13 LCGL--ALLCALSLGSRPTGPGCGPGRLLLTGCTDARCC----- 50  
Db 7 LCALWGCLLTAVHLGQCVT----CSDKQYL-----HDGQCCLDLCQPGSRLTSHCTALEKTQ 58  
Qy 51 -----RVHTTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCCTT 88  
Db 59 CHPDCSGEFAQNNREIRCHQHRCPEPQGLRVKKEGTASDVTCTCKEGOHCSTKCEA 118  
Qy 89 C-RHHPCCPGGQVQSQGKFSFGQICDASGTFSGGHE--GHCKPWTCTQGFGLTVFP 145  
Db 119 CAQHTPCIPGFGVEMATETTDVCHPCVPVFFSNQSLFEKCYPMWTSCEKDNLEVLQKG 178  
Qy 146 NKTHNAV 153  
Db 179 TSQTNVIC 186

RESULT 8  
MMRTS  
laminin beta-2 chain precursor - rat  
N:Alternate names: laminin chain B3; S-laminin  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C:Accession: S03539  
R:Hunter, D.D.; Shah, V.; Merille, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neocortex  
A:Reference number: S03539; MUID:89159410  
A:Accession: S03539  
A:Molecule type: mRNA  
A:Residues: 1-1801 <HUN>  
A:Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: interact with cells and with other basement membrane proteins to promote cell adhesion  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular matrix  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F:36-285/Domain: VI <DOM6>  
F:286-555/Domain: V <DOM5>  
F:286-347/Domain: laminin-type EGF-like homology <LE01>  
F:350-410/Domain: laminin-type EGF-like homology <LE02>  
F:413-470/Domain: laminin-type EGF-like homology <LE03>  
F:473-522/Domain: laminin-type EGF-like homology <LE04>  
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:556-784/Domain: IV <DOM4>

F:786-831/Domain: laminin-type EGF-like homology <LE06>  
F:788-1196/Domain: III <DOM3>  
F:834-877/Domain: laminin-type EGF-like homology <LE07>  
F:880-927/Domain: laminin-type EGF-like homology <LE08>  
F:930-986/Domain: laminin-type EGF-like homology <LE09>  
F:989-1038/Domain: laminin-type EGF-like homology <LE10>  
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>  
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>  
F:1197-1412/Domain: II <DOM2>  
F:1197-1412/Region: heptad repeats  
F:1413-1445/Domain: alpha <ALP>  
F:1446-1801/Region: heptad repeats  
F:1446-1801/Domain: I <DOM1>  
F:145-50/Disulfide bonds: #status predicted  
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p  
F:1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 13.9%; Score 134.5; DB 1; Length 1801;  
Best Local Similarity 26.9%; Pred. No. 0.0034;  
Matches 63; Conservative 6; Mismatches 60; Indels 105; Gaps 15;

QY 8 GAFAALC-GLALLCALSLG-----QRTGG-PCGCP-----GRLLGTGTDAACRV 52  
DB 840 GALSALCEGTSGQCLCRTGAFGLRCDHCQRGWGFPCNRCVCVNGR-----ADEEDA 891

QY 53 HTTRC--CRDYPGECCSEWDCMCVQPEFHCGDPCCT---TCRHHPGPPGQVQSGQKFS 107  
DB 892 HTGACLCGRDVTGGEHCEH-----CI-AGFH-GDPLPYGGQCRPCPCPEGG--SORHFA 943

QY 108 -----FGQCIDCASGTF----- 120

DB 944 TSCHRDYSSQIVCHCRAGYTLGLRCEACAPGHGDPKPGRCCLCECSGNIDPTDPGAC 1003

QY 121 -----SGHEGHCXPTWDTCTQFGFLTPVPGNKNHNAV-VPGSP 159

DB 1004 DPHTGQCLRLHHTEGPHCAHCKP-----GFHQAAAROSCHRCCTCNLLGTDP 1050

RESULT 9  
I48854  
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
C:Accession: I48854  
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
Mamm. Genome 5, 726-727, 1994  
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
A:Reference number: I48854; MUID:95178848  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-459 <RES>  
A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 12.4%; Score 120.5; DB 2; Length 459;  
Best Local Similarity 30.3%; Pred. No. 0.017;  
Matches 37; Conservative 11; Mismatches 57; Indels 17; Gaps 6;

QY 48 RCRRVHTTCRRDYPGECCSEWDCMCVQPEF-----HCGDPCCTTC-RHHPCPPGQ 98  
DB 77 RTCLSCSSSSTQVETRACTKQNRVCAACEAGRYCALKTHSGS--CRQCMRLSKCGPGF 134

QY 99 GVSQCKFSFGQCIDCASGTFSG--GHEGHCXPTWDTCTQFGFLTPVPGNKNHNAVCPVG 156  
DB 135 GVASSRAPNGVNLKACAPCTFSDTTSSTVDCRPHRCS-----ILAIPGNASTDAVCAPE 190

QY 157 SP 158  
II

Query Match 12.3%; Score 119.5; DB 2; Length 1798;  
Best Local Similarity 23.9%; Pred. No. 0.05;  
Matches 57; Conservative 10; Mismatches 62; Indels 109; Gaps 14;

QY 8 GAFAALC-GLALLCALSLGQ-----PTGGPGCGPGRLLLTGTCTDARC----- 49  
DB 837 GALSALCEKTSQCLCRTGAFGLRCDRCQRGWGFPCSCP-----CVCNGHAD 884

QY 50 -CRVHTTRC--CRDYPGECCSEWDCMCVQPEFHCGDPCCT---TCRHHPGPPGQVQ--- 101

DB 885 ECNPTHTGACLCGRDVTGGEHCEH-----CI-AGFH-GDPLPYGGQCRPCPCPEGSGQRH 938

QY 102 -----SOGKFS-----FGQCIDCASGTF----- 120

DB 939 PATSCHODEYSQQIVCHCRAGYTLGLRCEACAPGHGDPSPRGRCCLCECSGNIDPMDPD 998

QY 121 -----SGHEGHCXPTWDTCTQFGFLTPVPGNKNHNAV-VPGSPPAE 161  
II

DB 999 ACDPHTGQCLRLHHTEGPHCAHCKP-----GFHQAAAROSCHRCCTCNLLGTNPQQ 1049

RESULT 11  
A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A35356; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular A:Reference number: A35356; MUID:90260639  
A:Accession: A35356

Db 191 SP 192

RESULT 10  
S53869  
laminin beta-2 chain precursor (version 2) - human  
N:Alternate names: s-laminin  
C:Species: Homo sapiens (man)  
C:Date: 27-Oct-1995 #sequence\_revision 23-Feb-1996 #text\_change 24-Sep-1998  
C:Accession: S53869  
R:Ilvainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tr Matrix Biol. 14, 489-497, 1994  
A:Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal t  
A:Reference number: S53869  
A:Accession: S53869  
A:Molecule type: mRNA  
A:Residues: 1-1798 <IIV>  
C:Genetics:  
A:Gene: GDB:LAMB2  
A:Cross-references: GDB:132363; OMIM:150325  
A:Map position: 3p21.3-3p21.2  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:33-1798/Product: laminin beta-2 chain #status predicted <MAT>  
F:283-344/Domain: laminin-type EGF-like homology <LE01>  
F:347-407/Domain: laminin-type EGF-like homology <LE02>  
F:410-467/Domain: laminin-type EGF-like homology <LE03>  
F:470-519/Domain: laminin-type EGF-like homology <LE04>  
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:783-828/Domain: laminin-type EGF-like homology <LE06>  
F:831-874/Domain: laminin-type EGF-like homology <LE07>  
F:877-924/Domain: laminin-type EGF-like homology <LE08>  
F:927-983/Domain: laminin-type EGF-like homology <LE09>  
F:986-1035/Domain: laminin-type EGF-like homology <LE10>  
F:1038-1092/Domain: laminin-type EGF-like homology <LE11>  
F:1095-1140/Domain: laminin-type EGF-like homology <LE12>  
F:1143-1187/Domain: laminin-type EGF-like homology <LE13>

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:10 ; Search time 80.15 Seconds  
(without alignments)  
153.965 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_162

Perfect score: 969  
Sequence: 1 MAQHGAAGAFRALCGLALC.....FPGKTHNAVCPGSPPAEP 162

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68.\*

1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	16.7	272	I48700	gene ox40 protein
2	162	16.7	277	I37552	OX40 homolog - hum
3	160.5	16.6	255	I38426	lymphocyte activat
4	153	15.8	256	B32393	T-cell antigen 4-1
5	151	15.6	271	S12783	OX40 antigen precu
6	139	14.3	295	JC5559	lectin-B - Virgini
7	135.5	14.0	305	A46476	B cell-associated
8	134.5	13.9	1801	1 MWRTS	laminin beta-2 cha
9	120.5	12.4	459	I48854	gene murine tumour
10	119.5	12.3	1798	S33869	laminin beta-2 cha
11	119	12.3	461	A35356	tumor necrosis fac
12	119	12.3	474	B38634	tumor necrosis fac
13	118.5	12.2	277	A60771	B-cell activation
14	117	12.1	435	I34182	tumor necrosis fac
15	115.5	11.9	1371	I34837	insulin-like growt
16	114.5	11.8	329	A48805	insulin-like growt
17	112.5	11.6	1797	A55677	laminin beta-2 cha
18	112	11.6	152	T18975	hypothetical prote
19	111	11.5	1111	I276972	hypothetical prote
20	110.5	11.4	1687	I30176	EGF repeat transme
21	110.5	11.4	2907	A57278	fibriillin-2 precu
22	109.5	11.3	164	T24272	hypothetical prote
23	109.5	11.3	2531	A46019	Notch-1 protein -
24	109	11.2	1574	I213954	MEGF6 protein - ra
25	109	11.2	3635	I210053	laminin alpha 5 ch
26	106.5	11.0	2918	A34105	fibriillin-2 precu
27	105	10.8	188	T15651	hypothetical prote
28	105	10.8	1172	1 TSHUP2	thrombospondin 2 p
29	102.5	10.6	956	1 A46016	thrombospondin 3 -

30	101.5	10.5	1367	1 IGHUR1	insulin-like growt
31	101.5	10.5	2318	2 S45306	notch 3 protein -
32	101	10.4	4543	1 A53102	alpha-2-macroglobu
33	100.5	10.4	1737	2 T00209	MEGF8 protein - hu
34	100.5	10.4	2531	2 S18188	notch protein homo
35	100	10.3	186	2 A28401	agglutinin isolect
36	100	10.3	540	2 B47417	insulin receptor-f
37	100	10.3	996	2 JE0237	apolipoprotein E r
38	100	10.3	1106	2 T13938	gene shuttle craft
39	99.5	10.3	169	1 S18946	ultra high-sulfur
40	99.5	10.3	227	1 LNR2	lectin precursor -
41	99	10.2	213	1 AEW72	agglutinin isolect
42	99	10.2	1820	2 A54494	latent transformin
43	99	10.2	4544	1 S02392	alpha-2-macroglobu
44	98.5	10.2	755	2 A44315	cartilage oligomer
45	98.5	10.2	2139	2 A35672	crumbs protein - f

#### ALIGNMENTS

RESULT 1

I48700

gene ox40 protein - mouse

N:Alternate names: OX40 antigen

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000

C:Accession: I48700; I48334; S34377

R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J

J. Immunol. 151, 5261-5271, 1993

A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell

A:Reference number: I48700; MUID:94044750

A:Accession: I48700

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-272 <RE2>

A:Cross-references: EMBL:421674; NID:g312827; PIDN:CAA79772.1; PID:g312828

R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.

Eur. J. Immunol. 25, 926-930, 1995

A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX

A:Reference number: I48334; MUID:95255413

A:Accession: I48334

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-14,'G',16-272 <RE2>

A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819

C:Genetics:

A:Gene: ox40

A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 16.7%; Score 162; DB 2; Length 272;  
Best Local Similarity 28.3%; Pred. No. 7.2e-06;  
Matches 45; Conservative 11; Mismatches 51; Indels 52; Gaps 7;

QY 39 LLIGTGTGAR--CCRVHT-----TRCCRD-YPG-----EECCSEWDCMCVQPEFHGCDPC-- 85

DB 14 LALTGLVTARRLNCVKVTPSGHKCCRCQPGHGWSCDHTDTLC-----HPCET 65

QY 86 -----CPTCRHP-----CPPGGVQSQGKFSFGFQCID 114

DB 66 GFYNEAVNYDTCKQTCNHRSSSELKQNTPTQDTVCRCPGTPQKDSGKYLKGVDCVP 125

QY 115 CASCTSGSGGHEGHCWPWTDCTQFGFLTVPFGNKTHNAV 153

DB 126 CPPGHSPGNQACKPWNTCTLSKQTRHRPASDSDAVC 164

RESULT 2

I37552

OX40 homolog - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, O.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat  
Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A:Reference number: I37552; MUID:941170844  
A:Accession: I37552  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 16.7%; Score 162; DB 2; Length 277;  
Best Local Similarity 29.7%; Pred. No. 7.2e-06;  
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAGAFRALCGLALLCALSLG-----QRTGGPGGPGRLLLGTGTDAACRVRHT 54  
DB 4 GARRLRGPCAALLLLGLGLSTVTLGHCVDYTPSNDRCCHECR--PCNGMVSRCSRQN 61  
QY 55 TRCRDYPG--EECCSBWDCM-CVQPEFHGCD---PCTTCRHHPCPPGQGVQSGQKFSF 108  
DB 62 TVCRPCPGFYNDVSSKPKCPCTWNLRSRERKQLCTATQDTVCRCRAGTQPLDSYKP 121  
QY 109 GFQICDCASTGFSGGHGCKPMTDCTQFGFLTPFPNGKTHNAVCPGSPPA 160  
DB 122 GVDCAPCPPGHFSPGDNQACKPWNTNCTLAGKHTLQPASNSSDAICEDRDPPA 173

RESULT 3  
I38426  
Lymphocyte activation-induced receptor ILA precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C:Accession: I38426; J10752  
R:Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R  
Eur. J. Immunol. 24, 2219-2227, 1994  
A:Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A:Reference number: I38426; MUID:94374434  
A:Accession: I38426  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-255 <RES>  
A:Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321  
R:Schwarz, H.; Tuckwell, J.; Lotz, M.  
Gene 134, 295-298, 1993  
A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne  
A:Reference number: J10752; MUID:94085794  
A:Accession: J10752  
A:Molecule type: mRNA  
A:Residues: 1-106, 'R', 108-255 <SCH>  
C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neuro  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>  
F:187-213/Domain: transmembrane status predicted <TM>  
F:138,149/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict  
F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 16.6%; Score 160.5; DB 2; Length 255;  
Best Local Similarity 30.9%; Pred. No. 9e-06;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLGCTDARCRVHTTRCCRDYPG-----EECCS-----EWDCMCVQPEFHCGDP 84  
DB 48 CPPNSFSSAGG--QRTCDI-----CROCKGVFRTRKESSTNSAECDC---TPGFHCLGA 97

QY 85 CCTTCRHHPCPPGQGVQSGQKFSFGFCIDCASGTFSGGHEGCKPWTCTQFGFLTVFP 144  
DB 98 GCSMC-EQDCQGGELTKKK-----CKDCFCGFNDKRGICRPWTNCSLDGKSVLVN 149  
QY 145 GNKTHNAVCPG-----SPPA---EP 162  
DB 150 GTERDVCVCGSPADLSPGASSVTPPPAPAREP 181

RESULT 4  
B32393  
T-cell antigen 4-1BB precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R:Kwon, B.S.; Weissman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A:Title: cDNA sequence of two inducible T-cell genes.  
A:Reference number: A32393; MUID:89184547  
A:Accession: B32393  
A:Molecule type: mRNA  
A:Residues: 1-256 <KWO>  
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994  
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B  
A:Reference number: I48879; MUID:94179805  
A:Accession: I48879  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-256 <RES>  
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178  
C:Genetics:  
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 15.8%; Score 153; DB 2; Length 256;  
Best Local Similarity 31.5%; Pred. No. 3.4e-05;  
Matches 40; Conservative 17; Mismatches 52; Indels 18; Gaps 7;

QY 34 CGPGRLLGCTDARCRVHTTRCCRDYPGECCSEW---DCMCVQPEFHCGDCCTTC 89  
DB 47 CPPSTESSIGQPCNICRV---CAGYFRKKFKCSSTHNAECECIE-GFHCGLGQCCTRC 101  
QY 90 RHPCPPGQGVQSGQKFSFGFCIDCASGTFSGGH-EGHCKPWTCTQFGFLTVFPNGKT 148  
DB 102 -EKDCRPQELTKQG-----CKTCSLGTFTNDQNGTGVCRPWTNCSLDGSRVLKTGTE 153  
QY 149 HNAVCP 155  
DB 154 KDVCVCP 160

RESULT 5  
S12783  
OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: S12783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc  
A:Reference number: S12783; MUID:90214614  
A:Accession: S12783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology





```
FT DOMAIN 831 876 LAMININ EGF-LIKE 7.
FT DOMAIN 877 926 LAMININ EGF-LIKE 8.
FT DOMAIN 927 985 LAMININ EGF-LIKE 9.
FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.
FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.
FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.
FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.
FT DOMAIN 1190 1409 DOMAIN 11.
FT DOMAIN 1410 1442 DOMAIN ALPHA.
FT DOMAIN 1443 1798 COILED COIL (POTENTIAL).
FT DOMAIN 1799 1839 COILED COIL (POTENTIAL).
FT DISULFID 283 292 BY SIMILARITY.
FT DISULFID 285 310 BY SIMILARITY.
FT DISULFID 312 321 BY SIMILARITY.
FT DISULFID 324 344 BY SIMILARITY.
FT DISULFID 347 356 BY SIMILARITY.
FT DISULFID 349 374 BY SIMILARITY.
FT DISULFID 377 386 BY SIMILARITY.
FT DISULFID 389 407 BY SIMILARITY.
FT DISULFID 410 423 BY SIMILARITY.
FT DISULFID 412 438 BY SIMILARITY.
FT DISULFID 440 449 BY SIMILARITY.
FT DISULFID 452 467 BY SIMILARITY.
FT DISULFID 470 484 BY SIMILARITY.
FT DISULFID 472 491 BY SIMILARITY.
FT DISULFID 493 502 BY SIMILARITY.
FT DISULFID 505 519 BY SIMILARITY.
FT DISULFID 783 795 BY SIMILARITY.
FT DISULFID 785 802 BY SIMILARITY.
FT DISULFID 804 813 BY SIMILARITY.
FT DISULFID 816 828 BY SIMILARITY.
FT DISULFID 831 843 BY SIMILARITY.
FT DISULFID 833 850 BY SIMILARITY.
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FT DISULFID 896 905 BY SIMILARITY.
FT DISULFID 908 924 BY SIMILARITY.
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FT DISULFID 956 965 BY SIMILARITY.
FT DISULFID 968 983 BY SIMILARITY.
FT DISULFID 986 1000 BY SIMILARITY.
FT DISULFID 988 1007 BY SIMILARITY.
FT DISULFID 1010 1019 BY SIMILARITY.
FT DISULFID 1022 1035 BY SIMILARITY.
FT DISULFID 1095 1107 BY SIMILARITY.
FT DISULFID 1097 1114 BY SIMILARITY.
FT DISULFID 1116 1125 BY SIMILARITY.
FT DISULFID 1128 1140 BY SIMILARITY.
FT DISULFID 1143 1155 BY SIMILARITY.
FT DISULFID 1145 1162 BY SIMILARITY.
FT DISULFID 1164 1173 BY SIMILARITY.
FT DISULFID 1176 1187 BY SIMILARITY.
FT DISULFID 1190 1190 INTERCHAIN (PROBABLE).
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
FT DISULFID 1797 1797 INTERCHAIN (PROBABLE).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1348 1348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 914 914 R -> G (IN REF. 2).
FT CONFLICT 1179 1179 G -> A (IN REF. 2).
SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;
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Query Match

11.5%; Score 111.5; DB 1; Length 1798;

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Best Local Similarity 23.2%; Pred. No. 0.017;
Matches 55; Conservative 10; Mismatches 65; Indels 107; Gaps 13;
QY 8 GAFRALC---GLALLCALSLGOR-----PTGGPCGPGRLLLGTGTDCAR----- 49
Db 837 GALSSICEKTSQGLCRTGAFGLRCDCRCQRGQGFPPSCR-----CVCNGHAD 884
QY 50 -CRVHTTRC--CRDYPGEECCSEWDCMCVQEPHFHCGD--PCCTTCRHHPCPPGGQGVQ--- 101
Db 885 ECNTHTGACILGCRDHTTGEHCEH---CI-AGPHRDRPLPYGGQCRPCPCPEGSGRHF 939
QY 102 -----SOGKFS-----FGQCIDCASGTF----- 120
Db 940 ATSCHQDEYSQIIVCHCRAGYTLGRCEACAPGHFGDPSPRPGRCQLCECSGNIDPMDPDA 999
QY 121 -----SGGHEGHCKPWTDCDCTQFGFLTVFPGNKTHNAV---VPGSPPAE 161
Db 1000 CDPHTGQCLRLHHTTEGPHCAHCKP-----GFHQAARQSCHRCTNLLGTNPQQ 1049
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Search completed: September 4, 2001, 16:15:21  
Job time: 1133 sec



KW Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 741 INSULIN-LIKE GROWTH FACTOR I RECEPTOR,  
FT ALPHA-CHAIN.  
FT CHAIN 742 1370 INSULIN-LIKE GROWTH FACTOR I RECEPTOR,  
FT BETA-CHAIN.  
FT DOMAIN 742 936 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 937 960 POTENTIAL.  
FT DOMAIN 961 1370 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 608 829 FIBRONECTIN TYPE-III.  
FT DOMAIN 830 929 FIBRONECTIN TYPE-III.  
FT DOMAIN 1000 1275 PROTEIN KINASE.  
FT NP\_BIND 1006 1014 ATP (BY SIMILARITY).  
FT BINDING 1034 1034 ATP (BY SIMILARITY).  
FT ACT\_SITE 1136 1136 BY SIMILARITY.  
FT MOD\_RES 1166 1166 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 314 314 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 418 418 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 535 535 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 641 641 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 748 748 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 757 757 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 765 765 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 901 901 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 914 914 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 985 986 AD -> PY (IN REF. 3).  
SQ SEQUENCE 1370 AA; 155395 MW; A5946897A41CB145 CRC64;

Query Match 11.9%; Score 115.5; DB 1; Length 1370;  
Best Local Similarity 27.1%; Pred. No. 0.0064;  
Matches 57; Conservative 22; Mismatches 52; Indels 79; Gaps 20;

QY 8 GAFA-----LCGLA-----LICALS-----LQRPRTGGPGCG--PGRL-----L 40  
DB 139 GAIRIENADLCYLSTIDWLSILDVSNNTVGNKPP--KEGDLCPGTLEKPMCKRTT 196  
QY 41 LGTGTDAKRCVHTTRC---CRDYPGECCSEWDMCVQPEFHCGDPC-----CTTC 89  
DB 197 INNEYNYRCWT--TNRCQKWCPSVCGKRACTE--NNECCHPE--CLGSCHTPDDNTTCVAC 251  
QY 90 RH-----PCPPGGVQVSGKFSP-GFQCID--CAS-----GTFSGG--HEGHCK 129  
DB 252 RHYHYKGVCPVCPACPP-----GTYREGWRVDRDFCANIPNAESDSGDFVHDGEC- 303  
QY 130 PWTDCQTFGLTFPPGNKTNVAVCPGSP 159  
DB 304 -MECPSP-GFIR-----NSTOSMYCIPCEGP 327

RESULT 15  
LMB2\_HUMAN STANDARD; PRT; 1798 AA.  
ID LMB2\_HUMAN  
AC P55268; Q16321;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).  
GN LAMB2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-95213013; PubMed-7698745;

RA Wever U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,  
RA Champlaud M.F., Burgeson R.E., Albrechtsen R.;  
RT "Human beta 2 chain of laminin (formerly S chain): cDNA cloning,  
RT chromosomal localization, and expression in carcinomas.";  
RL Genomics 24:243-252(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-95316263; PubMed-7795887;  
RA Iivainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,  
RA Sariola H., Tryggvason K.;  
RT "The human laminin beta 2 chain (S-laminin): structure, expression in  
RT fetal tissues and chromosomal assignment of the LAMB2 gene.";  
RL Matrix Biol. 14:489-497(1995).  
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC  
CC CLEFT OF THE NEUROMUSCULAR JUNCTION.  
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
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CC -----  
CC EMBL; Z68155; CA92279.1; -;  
CC EMBL; Z68156; CA92279.1; JOINED.  
CC EMBL; X79683; CA56130.1; -;  
CC EMBL; S77512; AAB34682.2; -;  
CC HSSP; P02468; 1KLO.  
CC MIM; 150325; -;  
CC InterPro; IPR000561; -;  
CC InterPro; IPR001886; -;  
CC InterPro; IPR002049; -;  
CC Pfam; PF00053; laminin\_EGF; 13.  
CC Pfam; PF00055; laminin\_Nterm; 1.  
CC PRINTS; PR00011; EGF\_LAMININ.  
CC PROSITE; PS00022; EGF\_1; 10.  
CC PROSITE; PS01186; EGF\_2; 2.  
CC PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
CC KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 32 POTENTIAL  
FT CHAIN 33 1798 LAMININ BETA-2 CHAIN.  
FT DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 281 552 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN  
FT V).  
FT DOMAIN 283 346 LAMININ EGF-LIKE 1.  
FT DOMAIN 347 409 LAMININ EGF-LIKE 2.  
FT DOMAIN 410 469 LAMININ EGF-LIKE 3.  
FT DOMAIN 470 521 LAMININ EGF-LIKE 4.  
FT DOMAIN 522 552 LAMININ EGF-LIKE 5 (INCOMPLETE).  
FT DOMAIN 553 781 LAMININ DOMAIN IV.  
FT DOMAIN 782 1190 8 X LAMININ EGF-LIKE REPEATS (DOMAIN  
FT III).  
FT DOMAIN 783 830 LAMININ EGF-LIKE 6.

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DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.
DR EMBL; U52163; AAC50622.1; JOINED.
DR EMBL; U52164; AAC50622.1; JOINED.
DR EMBL; M55994; AAA36755.1; -.
DR PIR; A35356; A35356.
DR PIR; A36007; A36007.
DR PIR; A36475; A36475.
DR PIR; B35010; B35010.
DR PIR; A23666; A23666.
DR PDB; 1CA9; 12-APR-99.
DR MIN; 191191; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 4.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW Phosphorylation; Pharmaceutical; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 258 287 POTENTIAL.
FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 201 4 X TNFR-CYS.
FT REPEAT 39 76 TNFR-CYS 1.
FT REPEAT 77 118 TNFR-CYS 2.
FT REPEAT 119 162 TNFR-CYS 3.
FT REPEAT 163 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 193 193 R -> P (IN REF. 4).
FT CONFLICT 141 141 R -> M (IN REF. 1 AND 3).
FT CONFLICT 196 196 A -> T (IN REF. 4).
FT CONFLICT 363 363
SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

Query Match 12.5%; Score 121; DB 1; Length 461;
Best Local Similarity 26.3%; Pred. No. 0.00096;
Matches 41; Conservative 14; Mismatches 63; Indels 38; Gaps 8;

QY 34 CGPG---RLLGTTGTDCR-----GDPCCTTCHRHPPGQVSGQKFSFGFCIDCASGTFSG-- 71
Db 57 CSPGQAKVFTKTSDDTVCDSCEDSTYTLQNNWPECLSCGRSCSDQVETQACTREQNR 116
QY 72 -CMCVQPEFHC-----GDPCTTCHRHPPGQVSGQKFSFGFCIDCASGTFSG-- 122
Db 117 ICTC-RPGWYCALSKQECRCICAPLR--KCRPGFGVARGPTETSDVCKPCAPGIFSNTT 173
QY 123 GHEGHCKPWTDTQFGFTVFPFGKNKTHNACVPGSP 158
Db 174 SSTDICRPHQICN----VVAIPGNASRDVACTSTSP 205

RESULT 11
TNR2_MOUSE
ID TNR2_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91197885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RT Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Kissenerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL; M60459; AAA39752.1; -.
CC EMBL; M59378; AAA40463.1; -.
CC EMBL; U39488; AAA85021.1; -.
CC EMBL; X87128; CAA60618.1; -.
CC PIR; B38634; B38634.
CC HSP; P19438; INCF.
CC MGD; MGI:1314883; Tnfrsf1b.
CC InterPro; IPR001368; -.
CC Pfam; PF00020; TNFR_C6; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.

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FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 12.3%; Score 119; DB 1; Length 474;
Best Local Similarity 31.0%; Pred. No. 0.0015;
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;

QY 46 DARCCRVHTRCCRDYGECCSWDCMCVQPEPHCGDPCCTTC-RHPCPPGGVQSOG 104
DB 107 EIRACTKQQRVACAGRYCAL-----KTHSGS--CRQCMRLSKGPGGEVASSR 155
QY 105 KFGSGFCIDCASGTFSG--GHEGHCRTWTDCTQFGELTVFPGKNTNNAVCVPGSP 158
DB 156 APNGVNLKACAPCTFSDTTSSTDVCRPHRCS-----ILAIPGNASTDAVCAPESP 207

RESULT 12
CD40_HUMAN
ID CD40_HUMAN STANDARD; PRT; 277 AA.
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
RN [3]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC -----
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CC -----
DR EMBL; X60592; CAA43045.1;
DR PIR; S04460; S04460.
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DR PDB; 1CDF; 01-APR-97.
DR MIM; 109535;
DR InterPro; IPR001368;
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 277 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 153 153
FT CARBOHYD 180 180
SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 12.2%; Score 118.5; DB 1; Length 277;
Best Local Similarity 27.7%; Pred. No. 0.0011;
Matches 36; Conservative 10; Mismatches 73; Indels 11; Gaps 5;

QY 34 CGPGRLLLTGTGDARCCRVHTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 88
DB 62 CGSEFLDTWNRETHC---HQHKYCDPNLGLRVQKQGTSETDTICTEGWHCTSEACES 118
QY 89 C-RHPCPPGGVQSOGKFSFGFCIDCASGTFSGHEG--HCKPWTCTQFGELTVFPG 145
DB 119 CVLHRSCTSPGFGVKQIATGVSDTICEPCPVGFFSNVSAFEKCHPWTSCETKDLVVQAG 178
QY 146 NKTHNAVCVP 155
DB 179 TNKTDVVCVP 188

RESULT 13
TNRC_HUMAN
ID TNRC_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTBR OR TNFR OR TNFRSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human 12p
RT transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
```

FT	SIGNAL	1	35	POTENTIAL.	FT	DISULFID	1798	1798	INTERCHAIN (PROBABLE).
FT	CHAIN	36	1799	LAMININ BETA-2 CHAIN.	FT	CARBOHYD	251	251	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	36	283	LAMININ N-TERMINAL (DOMAIN VI).	FT	CARBOHYD	371	371	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	284	555	4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN V).	FT	CARBOHYD	1086	1086	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	286	349	LAMININ EGF-LIKE 1.	FT	CARBOHYD	1250	1250	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	350	412	LAMININ EGF-LIKE 2.	FT	CARBOHYD	1309	1309	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	413	472	LAMININ EGF-LIKE 3.	FT	CARBOHYD	1349	1349	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	473	524	LAMININ EGF-LIKE 4.	FT	CARBOHYD	1500	1500	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	525	555	LAMININ EGF-LIKE 5 (INCOMPLETE).	SQ	SEQUENCE	1799	AA; 196352 MW; 1f28967a67aede33 CRC64;	
FT	DOMAIN	556	782	LAMININ DOMAIN IV.					
FT	DOMAIN	783	1191	8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).					
FT	DOMAIN	784	831	LAMININ EGF-LIKE 6.					
FT	DOMAIN	832	877	LAMININ EGF-LIKE 7.					
FT	DOMAIN	878	927	LAMININ EGF-LIKE 8.	QY	5	GANGAFRALC----	GLALLCALSLGSRPT-----	GGPGCGP---GRL 39
FT	DOMAIN	928	986	LAMININ EGF-LIKE 9.	Db	825	GPAGCQCQSPGALSGTSGCPCRGAFGLRCDHCQRCQWGFPPNCRPCVNGR-	883	
FT	DOMAIN	987	1038	LAMININ EGF-LIKE 10.					
FT	DOMAIN	1039	1095	LAMININ EGF-LIKE 11.					
FT	DOMAIN	1096	1143	LAMININ EGF-LIKE 12.	QY	40	LLGTGTDAARCCRVHTTRC--	CRDYPGEECCSEWDCMCVQPEFHGCGDPCT---	TCRIHPC 94
FT	DOMAIN	1144	1190	LAMININ EGF-LIKE 13.	Db	884	-----	ADECDTHTGACLCGRDYGGEHCE	-----CI-AGFH-GDPLRYPGGQCRPC 930
FT	DOMAIN	1191	1410	DOMAIN II.					
FT	DOMAIN	1411	1443	DOMAIN ALPHA.	QY	95	PGGQVQSQGKFS-----	FGQCIDCASGTF-----	120
FT	DOMAIN	1444	1799	DOMAIN I.	Db	931	PEGPG--	SQRHFATSHRDGYSQIVCHCRAGYTLRCEACAPGFGDPSKPGRCOLCE	988
FT	DOMAIN	1257	1304	COILED COIL (POTENTIAL).	QY	121	-----	SGGHEGHCCKPWTCTQGFPLTVFGNKNTHNAV	153
FT	DOMAIN	1473	1527	COILED COIL (POTENTIAL).	Db	989	CSGNIDPMDPADCPHTGQCLRLHNTGPHGCKP-----	GFHQGAARQSCIRCTC	1041
FT	DISULFID	1577	1791	BY SIMILARITY.					
FT	DISULFID	286	295	BY SIMILARITY.					
FT	DISULFID	288	313	BY SIMILARITY.					
FT	DISULFID	315	324	BY SIMILARITY.					
FT	DISULFID	327	347	BY SIMILARITY.					
FT	DISULFID	350	359	BY SIMILARITY.					
FT	DISULFID	352	377	BY SIMILARITY.					
FT	DISULFID	380	389	BY SIMILARITY.					
FT	DISULFID	392	410	BY SIMILARITY.					
FT	DISULFID	413	426	BY SIMILARITY.					
FT	DISULFID	415	441	BY SIMILARITY.					
FT	DISULFID	443	452	BY SIMILARITY.					
FT	DISULFID	455	470	BY SIMILARITY.					
FT	DISULFID	473	487	BY SIMILARITY.					
FT	DISULFID	475	494	BY SIMILARITY.					
FT	DISULFID	496	505	BY SIMILARITY.					
FT	DISULFID	508	522	BY SIMILARITY.					
FT	DISULFID	784	796	BY SIMILARITY.					
FT	DISULFID	786	803	BY SIMILARITY.					
FT	DISULFID	805	814	BY SIMILARITY.					
FT	DISULFID	817	829	BY SIMILARITY.					
FT	DISULFID	832	844	BY SIMILARITY.					
FT	DISULFID	834	851	BY SIMILARITY.					
FT	DISULFID	853	862	BY SIMILARITY.					
FT	DISULFID	865	875	BY SIMILARITY.					
FT	DISULFID	878	887	BY SIMILARITY.					
FT	DISULFID	880	894	BY SIMILARITY.					
FT	DISULFID	897	906	BY SIMILARITY.					
FT	DISULFID	909	925	BY SIMILARITY.					
FT	DISULFID	928	944	BY SIMILARITY.					
FT	DISULFID	930	955	BY SIMILARITY.					
FT	DISULFID	957	966	BY SIMILARITY.					
FT	DISULFID	969	984	BY SIMILARITY.					
FT	DISULFID	987	1001	BY SIMILARITY.					
FT	DISULFID	989	1008	BY SIMILARITY.					
FT	DISULFID	1011	1020	BY SIMILARITY.					
FT	DISULFID	1023	1036	BY SIMILARITY.					
FT	DISULFID	1096	1108	BY SIMILARITY.					
FT	DISULFID	1098	1115	BY SIMILARITY.					
FT	DISULFID	1117	1126	BY SIMILARITY.					
FT	DISULFID	1129	1141	BY SIMILARITY.					
FT	DISULFID	1144	1156	BY SIMILARITY.					
FT	DISULFID	1146	1163	BY SIMILARITY.					
FT	DISULFID	1165	1174	BY SIMILARITY.					
FT	DISULFID	1177	1188	BY SIMILARITY.					
FT	DISULFID	1191	1191	INTERCHAIN (PROBABLE).					
FT	DISULFID	1194	1194	INTERCHAIN (PROBABLE).					

DR PFAST: PF00020; TNFR\_C6; 4;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1;  
 DR KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 >269 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 269  
 SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

Query Match 12.6%; Score 122.5; DB 1; Length 269;  
 Best Local Similarity 28.7%; Pred. No. 0.00048;  
 Matches 37; Conservative 9; Mismatches 70; Indels 13; Gaps 5;

QY 34 CGPGRLLGTGDARCCRVHTTCRDYPGEECCSEWD-----CMCVQPEFHCGDPCCT 87  
 DB 62 CGRGEFLTNWREKIC---HEHRYCNPLNLRIQSEGLTNTDTICVCGEQ-HCTSHTC 117  
 QY 88 TCRHHP-CPGQGVOSGKSFQPCIDCASGTFSGGHEG--HCKPTDCTQFGFLVFP 144  
 DB 118 SCTPHSLCLPFGVKQIATGLLDVCEPCLGFFSNVSSAFKCHRTWTCERKGLVEQHV 177  
 QY 145 GNKTHNAVC 153  
 DB 178 GTNKTDDVC 186

RESULT 10  
 TNFR2\_HUMAN  
 ID TNFR2\_HUMAN STANDARD; PRT; 461 AA.  
 AC P20333;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
 DE BINDING PROTEIN 2) (TPPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; PubMed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins";  
 RL Science 248:1019-1023(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91045991; PubMed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96299745; PubMed=8661109;  
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,  
 RA Brodeur G.M.;

"Physical mapping and genomic structure of the human TNFR2 gene."; Genomics 35:94-100(1996).  
 [4]  
 RN SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=90349572; PubMed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor."; Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
 [5]  
 RN SEQUENCE OF 27-31.  
 RX MEDLINE=90110215; PubMed=2153136;  
 RA Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors."; J. Biol. Chem. 265:1531-1536(1990).  
 [6]  
 RN SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE=91056048; PubMed=2173696;  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W., Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).  
 [7]  
 RN CHARACTERIZATION.  
 RX MEDLINE=93016040; PubMed=1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor phosphorylation."; J. Biol. Chem. 267:21172-21178(1992).  
 [8]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 RX MEDLINE=99221490; PubMed=10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of human TRAF2"; Nature 398:533-538(1999).  
 CC -|- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -|- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.  
 CC -|- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WYETH-AVERST); USED TO TREAT MODERATE TO SEVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -|- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".  
 CC -|- DATABASE: NAME=Enbrel; NOTE=Clinical information On Enbrel; WWW="http://www.enbrelinfo.com/".  
 CC -----  
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 CC -----  
 CC EMBL; M32315; AAA59929.1; -;  
 CC EMBL; M35857; AAA63262.1; -;  
 CC EMBL; U52165; AAC50622.1; -;  
 CC EMBL; U52156; AAC50622.1; JOINED.  
 CC EMBL; U52157; AAC50622.1; JOINED.  
 CC EMBL; U52158; AAC50622.1; JOINED.  
 CC EMBL; U52159; AAC50622.1; JOINED.

DR Pfam: PF00020; TNFR\_c6; 4.  
 DR PROSITE: PS00852; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS00850; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 289 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

Query Match 14.0%; Score 135.5; DB 1; Length 289;  
 Best Local Similarity 26.1%; Pred. No. 3.8e-05;  
 Matches 49; Conservative 10; Mismatches 74; Indels 55; Gaps 8;

QY 13 LCGL--ALLCALSLGPRGPGCGPGRLLGLGTARCC----- 50  
 Db 7 LCALLMGCLLTAVHLGQCVT-----CDKQYL----HDGQCDDLQCPGSRLTSHCTALEKTQ 58  
 QY 51 -----RVHTTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 88  
 Db 59 CHPCDSGEFSAQNRIRCHQHCEPNOGLRVKKEGTADSVCKEKGCHTSDCEA 118  
 QY 89 C-RHHPCPQGVQSGKFSFGQCIDCASGTFSGGHE--GHCKPWTCTCFQGLAVFP 145  
 Db 119 CAQHTPCIPGFGVMEMATETDTVCHPCVPVGFPSNOSSLFEKCYPWTSCEDKNLEVLOKG 178  
 QY 146 NKTHNAVC 153  
 Db 179 TSQTNVIC 186

RESULT 7  
 LMB2\_RAT  
 ID LMB2\_RAT STANDARD; PRT: 1801 AA.  
 AC P15800;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).  
 GN LMB2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89159410; PubMed=2922051;  
 RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;  
 RT "A laminin-like adhesive protein concentrated in the synaptic cleft  
 of the neuromuscular junction.";  
 RL Nature 338:229-234(1989).  
 CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
 IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
 CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
 WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
 CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
 DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
 TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
 COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
 COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC

CC CLEFT OF THE NEUROMUSCULAR JUNCTION.  
 CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
 WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
 CC -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
 CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
 CC -!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: X16563; CAA34561.1; -  
 DR PIR: S03539; MMRTS.  
 DR HSSP: P02468; IKLO.  
 DR InterPro: IPR000561; -  
 DR InterPro: IPR001886; -  
 DR InterPro: IPR002049; -  
 DR Pfam: PF00053; laminin\_EGF; 13.  
 DR Pfam: PF00055; laminin\_Nterm; 1.  
 DR PRINTS: PR00011; EGF\_LAMININ.  
 DR PROSITE: PS00022; EGF\_1; 10.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01248; LAMININ\_TYPE\_EGF; 12.  
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 FT SIGNAL 1 35  
 FT CHAIN 36 1801 LAMININ BETA-2 CHAIN.  
 FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).  
 FT DOMAIN 286 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 V).  
 FT DOMAIN 286 349  
 FT DOMAIN 350 412 LAMININ EGF-LIKE 1.  
 FT DOMAIN 413 472 LAMININ EGF-LIKE 2.  
 FT DOMAIN 473 524 LAMININ EGF-LIKE 3.  
 FT DOMAIN 525 555 LAMININ EGF-LIKE 4.  
 FT DOMAIN 556 785 LAMININ EGF-LIKE 5 (INCOMPLETE).  
 FT DOMAIN 786 1192 8 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 III).  
 FT DOMAIN 786 833 LAMININ EGF-LIKE 6.  
 FT DOMAIN 834 879 LAMININ EGF-LIKE 7.  
 FT DOMAIN 880 929 LAMININ EGF-LIKE 8.  
 FT DOMAIN 930 988 LAMININ EGF-LIKE 9.  
 FT DOMAIN 989 1040 LAMININ EGF-LIKE 10.  
 FT DOMAIN 1041 1097 LAMININ EGF-LIKE 11.  
 FT DOMAIN 1098 1145 LAMININ EGF-LIKE 12.  
 FT DOMAIN 1146 1192 LAMININ EGF-LIKE 13.  
 FT DOMAIN 1193 1412 DOMAIN II.  
 FT DOMAIN 1413 1445 DOMAIN ALPHA.  
 FT DOMAIN 1446 1801 DOMAIN I.  
 FT DOMAIN 1259 1306 COILED COIL (POTENTIAL).  
 FT DOMAIN 1475 1529 COILED COIL (POTENTIAL).  
 FT DOMAIN 1576 1793 COILED COIL (POTENTIAL).  
 FT DISULFID 286 295 BY SIMILARITY.  
 FT DISULFID 288 313 BY SIMILARITY.  
 FT DISULFID 315 324 BY SIMILARITY.  
 FT DISULFID 327 347 BY SIMILARITY.  
 FT DISULFID 350 359 BY SIMILARITY.  
 FT DISULFID 352 377 BY SIMILARITY.  
 FT DISULFID 380 389 BY SIMILARITY.  
 FT DISULFID 392 410 BY SIMILARITY.  
 FT DISULFID 413 426 BY SIMILARITY.  
 FT DISULFID 415 441 BY SIMILARITY.  
 FT DISULFID 443 452 BY SIMILARITY.  
 FT DISULFID 455 470 BY SIMILARITY.  
 FT DISULFID 473 487 BY SIMILARITY.  
 FT DISULFID 475 494 BY SIMILARITY.  
 FT DISULFID 496 505 BY SIMILARITY.  
 FT DISULFID 508 522 BY SIMILARITY.



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FT DISULFID 786 798 BY SIMILARITY.
FT DISULFID 788 805 BY SIMILARITY.
FT DISULFID 807 816 BY SIMILARITY.
FT DISULFID 819 831 BY SIMILARITY.
FT DISULFID 834 846 BY SIMILARITY.
FT DISULFID 836 853 BY SIMILARITY.
FT DISULFID 855 864 BY SIMILARITY.
FT DISULFID 867 877 BY SIMILARITY.
FT DISULFID 880 889 BY SIMILARITY.
FT DISULFID 882 896 BY SIMILARITY.
FT DISULFID 899 908 BY SIMILARITY.
FT DISULFID 911 927 BY SIMILARITY.
FT DISULFID 930 946 BY SIMILARITY.
FT DISULFID 932 957 BY SIMILARITY.
FT DISULFID 959 968 BY SIMILARITY.
FT DISULFID 971 986 BY SIMILARITY.
FT DISULFID 989 1003 BY SIMILARITY.
FT DISULFID 991 1010 BY SIMILARITY.
FT DISULFID 1013 1022 BY SIMILARITY.
FT DISULFID 1025 1038 BY SIMILARITY.
FT DISULFID 1098 1110 BY SIMILARITY.
FT DISULFID 1100 1117 BY SIMILARITY.
FT DISULFID 1119 1128 BY SIMILARITY.
FT DISULFID 1131 1143 BY SIMILARITY.
FT DISULFID 1146 1158 BY SIMILARITY.
FT DISULFID 1148 1165 BY SIMILARITY.
FT DISULFID 1167 1176 BY SIMILARITY.
FT DISULFID 1179 1190 BY SIMILARITY.
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
FT DISULFID 1196 1196 INTERCHAIN (PROBABLE).
FT DISULFID 1800 1800 INTERCHAIN (PROBABLE).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1088 1088 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1252 1252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1311 1311 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1351 1351 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1502 1502 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1801 AA: 196473 MW; 97AEF32F8F31FA75 CRC64;

Query Match 13.9%; Score 134.5; DB 1; Length 1801;
Best Local Similarity 26.9%; Pred. No. 0.00018;
Matches 63; Conservative 6; Mismatches 60; Indels 105; Gaps 15;

QY 8 GAFRALC-GLALLCALSIG-----QRTGG-PCGCP-----GRLLGTGTDAICRV 52
Db 840 GALSALCEGTSQCCLRTGAFGLRCDHCQRCQGWGFPCRCVCNGR-----ADECA 891

QY 53 HTRTC--CRDYPGEECCSEWDCMCVPEFHCGDPCCT---TCRHHPCPPGQVSGQKFS 107
Db 892 HTGACLCGRDYGTEGHCER----CI-AGFH-GDRLPYGGQCRPCPCPEGPG--SQRHFA 943

QY 108 -----FGFCIDCASCTF----- 120
Db 944 TSHRDGYSQQIVCHCRAGYTGFLRCEACAPHFHGDPSKPGRCOLCRCSGNIDPTDFGAC 1003

QY 121 -----SGGHEGHCKPWTCTQFGFLTVFPGNKTHNAV-VPGSPP 159
Db 1004 DPHGTQCLRLHHTGPHGCHKP-----GFHQARQSCHRCTCNLLGTDP 1050

RESULT 8
LMB2_MOUSE STANDARD; PRT; 1799 AA.
AC Q61252; Q62182;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR.
GN LAMB2 OR S-LAM OR LAMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=129/J;
RX MEDLINE=96278760; PubMed=8662701;
RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
RT "Structural organization of the human and mouse laminin beta2 chain
RT genes, and alternative splicing at the 5' end of the human
RT transcript.";
RL J. Biol. Chem. 271:13407-13416(1996).
RN [2]
RP SEQUENCE OF 348-428 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94319092; PubMed=8043959;
RA Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;
RT "S-laminin gene (Lams) maps to F1 band of mouse chromosome 9.";
RL Mamm. Genome 5:393-394(1994).
RN [3]
RP FUNCTION.
RX STRAIN=129/J;
RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
RT "Aberrant differentiation of neuromuscular junctions in mice lacking
RT s-laminin/laminin beta 2.";
RL Nature 374:258-262(1995).
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -1- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR
CC NERVE TERMINALS.
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -1- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAINS IV AND V ARE GLOBULAR.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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CC -----
CC EMBL; U43541; AAC53535.1; -.
CC EMBL; U42624; AAC53535.1; JOINED.
CC EMBL; X75928; CAA53532.1; -.
CC HSSP; P02468; IKLO.
CC MGD; MGI:999116; Lamb2.
CC InterPro; IPR001886; -.
CC InterPro; IPR002049; -.
CC Pfam; PF00053; laminin_EGF; 13.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGF_LAMININ.
CC PROSITE; PS00022; EGF_1; 10.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

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RN [3]
RA REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RT Kwon B.S.;
RL "Characterization of human homologue of 4-lbB and its ligand.";
RL Immunol. Lett. 45:67-73(1995).
CC -|- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-LBB. POSSIBLY
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -|- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
CC CELLS.
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -|- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
CC -----
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CC -----
DR EMBL; U03397; AAA53133.1; -
DR EMBL; L12964; AAA62478.2; -
DR HSSP; P19438; 1EXT.
DR MIM; 602250; -
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17
FT CHAIN 18 255
FT DOMAIN 18 186
FT TRANSMEM 187 213
FT DOMAIN 214 255
FT REPEAT 47 159
FT REPEAT 87 86
FT REPEAT 119 159
FT REPEAT 138 138
FT CARBOHYD 149 149
FT CARBOHYD 149 149
SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;

Query Match 16.6%; Score 160.5; DB 1; Length 255;
Best Local Similarity 30.9%; Pred. No. 2.3e-07;
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTGDARCCVHTTRCCRDYGP-----EECCS-----EWDCMCVQPEFHCGDP 84
DB 48 CPNFSFSSAGG--QRTCDI-----CRQKGVTRFKESCTSNACDC---TPGFHCLGA 97
QY 85 CQTCRRHHPCPGQVQSGKFSFGFCQIDCASGTFSGGHEGCKPWTDTCTQFGFLTVFP 144
DB 98 GCSMC-EQDCKQKQELTKKG-----CKDCCFGTFNDQKRGICRWTNCSLDGKSVLNV 149
QY 145 GNKTHNAVCPG-----SPPA----EP 162
DB 150 GTRKDVVCGPSPADLSPGASSVTPAPAREP 181

RESULT 4
ID 4LBB_MOUSE STANDARD; PRT; 256 AA.
AC P20334;
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Query Match 15.8%; Score 153; DB 1; Length 256;  
 Best Local Similarity 31.5%; Pred. No. 1e-06;  
 Matches 40; Conservative 17; Mismatches 52; Indels 18; Gaps 7;

QY 34 CGPRL-LLGTTGTCARCRVHTTCCRDYPCGECSEW---DCMCVQPEFHCGDPCCCTTC 89  
 DB 47 CPPTFSSIGQPCNCRV---CAGYFRKFKCSSTHNAECIE-GFCHLGPQCTRC 101  
 QY 90 RHHPCPGQGVQSGKFSFGQCIDCASGTFSGGH-EGHCKPWTCTQFGFLTVPFGNKT 148  
 DB 102 -EKDCRFQQLTKG-----CKTCSLGTENDQGTGVCRPWTNCSLDGRSVLKTGTE 153  
 QY 149 HNAVCVP 155  
 DB 154 KDVCVCP 160

RESULT 5  
 OX40\_RAT STANDARD; PRT; 271 AA.

AC P15725;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).  
 GN TNFRSF4 OR TXGPIL OR OX40.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-T-cell;  
 RX MEDLINE=90214614; PubMed=2157591;  
 RA Mallett S., Fossum S., Barclay A.N.;  
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";  
 RL EMBO J. 9:1063-1068(1990).  
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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 CC -----  
 DR EMBL: X17037; CAA34897.1; -  
 DR PIR: S08036; S08036.  
 DR PIR: S12783; S12783.  
 DR HSP: P25942; ICDF.  
 DR InterPro: IPR001368; -  
 DR Pfam: PF00020; TNFR\_C6; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 271 OX40L RECEPTOR.  
 FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 211 235 POTENTIAL.  
 FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 164 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 102 TNFR-CYS 2.  
 FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 124 164 TNFR-CYS 4.  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 15.6%; Score 151; DB 1; Length 271;  
 Best Local Similarity 28.5%; Pred. No. 1.6e-06;  
 Matches 47; Conservative 12; Mismatches 62; Indels 44; Gaps 8;

QY 26 QRPCTGPGCGRLLLG--TGTDARCCRVHTT-----RCCRD-YGEECCSEWD----- 71  
 DB 6 QQPT-----AFLLLGLSLGVTVKLNCVKDTPYSGHKCCRCQFQGHGMVSRCDHTRDTV 58  
 QY 72 CMCVQPEFHCG---DPC-CYTCRHH-----PCPPGQGVQSGQKFSF 108  
 DB 59 CHPCEPGFYNEAVYDTCKQCTQCNHRSGSELKQNTPTEDTVCCQRPQTQPRQDSSHL 118  
 QY 109 GFQCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTNAV 153  
 DB 119 GVDVCVCPGHPGSPGNSQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 6  
 CD40\_MOUSE STANDARD; PRT; 289 AA.

AC P27512;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).  
 GN TNFRSF5 OR CD40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92105763; PubMed=1370315;  
 RA Torres R.M., Clark E.A.;  
 RT "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";  
 RL J. Immunol. 148:620-626(1992).  
 CC [2]  
 CC REVISIONS.  
 CC STRAIN=BALB/C;  
 CC Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=BALB/C; TISSUE=Liver;  
 CC MEDLINE=93094586; PubMed=1281194;  
 CC Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,  
 CC Howard M., Cockayne D.A.;  
 CC "Genomic structure and chromosomal mapping of the murine CD40 gene.";  
 CC J. Immunol. 149:3921-3926(1992).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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 CC -----  
 DR EMBL: M83312; AAB08705.1; -  
 DR EMBL: M94126; AAA37404.1; -  
 DR EMBL: M94129; AAA37404.1; JOINED.  
 DR EMBL: M94128; AAA37404.1; JOINED.  
 DR EMBL: M94127; AAA37404.1; JOINED.  
 DR PIR: A46476; A46476.  
 DR HSP: P25942; ICDF.  
 DR MGI: MGI:88336; Tnfrsf5.  
 DR InterPro: IPR001368; -.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:20 ; Search time 43.78 Seconds  
(without alignments)  
126.756 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_162  
Perfect score: 969  
Sequence: 1 MAQHGANGAFRALCGLALC.....FPGNKTHNAVCPGSPPAEP 162

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	162	16.7	272	1	OX40_MOUSE	P47741 mus musculus
2	162	16.7	277	1	OX40_HUMAN	P43489 homo sapien
3	160.5	16.6	255	1	41BB_HUMAN	Q07011 homo sapien
4	153	15.8	256	1	41BB_MOUSE	P20334 mus musculus
5	151	15.6	271	1	OX40_RAT	P15725 rattus norv
6	135.5	14.0	289	1	OX40_MOUSE	P27512 mus musculus
7	134.5	13.9	1801	1	LMB2_RAT	P15800 rattus norv
8	127.5	13.2	1799	1	LMB2_MOUSE	Q61292 mus musculus
9	122.5	12.6	269	1	CD40_BOVIN	Q28203 bos taurus
10	121	12.5	461	1	TNR2_HUMAN	P20333 homo sapien
11	119	12.3	474	1	TNR2_MOUSE	P25119 mus musculus
12	118.5	12.2	277	1	CD40_HUMAN	P25942 homo sapien
13	117	12.1	435	1	TNRC_HUMAN	P36941 homo sapien
14	115.5	11.9	1370	1	IG1R_RAT	P24062 rattus norv
15	111.5	11.5	1798	1	LMB2_HUMAN	P55268 homo sapien
16	110.5	11.4	2907	1	FN2_MOUSE	Q61555 mus musculus
17	109.5	11.3	2531	1	NTC1_MOUSE	Q01705 mus musculus
18	109	11.2	3635	1	LMA5_MOUSE	Q61001 mus musculus
19	108.5	11.2	1373	1	IG1R_MOUSE	Q60751 mus musculus
20	106.5	11.0	2911	1	FN2_HUMAN	P35556 homo sapien
21	105	10.8	1172	1	TSP2_HUMAN	P35442 homo sapien
22	104.5	10.8	684	1	FBL1_CHICK	Q73775 gallus gall
23	102.5	10.6	956	1	TSP3_MOUSE	Q05895 mus musculus
24	101.5	10.5	1367	1	IG1R_HUMAN	P08069 homo sapien
25	101.5	10.5	2318	1	NTC3_MOUSE	Q61982 mus musculus
26	101	10.4	4543	1	LRP1_CHICK	P98157 gallus gall
27	100.5	10.4	2531	1	NTC1_RAT	Q07008 rattus norv
28	100	10.3	186	1	AG13_WHEAT	P10969 triticum ae
29	100	10.3	581	1	IRR_RAT	Q64716 rattus norv
30	100	10.3	1106	1	STC_DROME	P40798 drosophila
31	99.5	10.3	169	1	KRUA_HUMAN	P26371 homo sapien
32	99.5	10.3	227	1	AG1_ORYSA	P11219 oryza sativ
33	99.5	10.3	2569	1	LMA3_MOUSE	Q61789 mus musculus

ALIGNMENTS

RESULT 1	OX40_MOUSE	STANDARD;	PRT;	272 AA.
ID	OX40_MOUSE			
AC	P47741;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).			
GN	TNFRSF4 OR TXGP1 OR OX40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RX	MEDLINE=94044750; PubMed=8228223;			
RA	Calderhead D.M., Buhmann J.E., van den Eertwegh A.J.,			
RA	Claassen E., Noelle R.J., Fell H.;			
RT	"Cloning of mouse OX40: a T cell activation marker that may mediate			
RT	T-B cell interactions."			
RL	J. Immunol. 151:5261-5271(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95255413; PubMed=7737295;			
RA	Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,			
RA	Barclay A.N.;			
RT	"Gene structure and chromosomal localization of the mouse homologue			
RT	of rat OX40 protein."			
RL	Eur. J. Immunol. 25:926-930(1995).			
CC	-1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
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CC	-----			
CC	EMBL; Z21674; CAA79772.1; -			
DR	EMBL; X85214; CAA59476.1; -			
DR	HSSP; P25942; ICDF.			
DR	MGD; MGI:104512; Tnfrsf4.			
DR	InterPro; IPR001368; -			
DR	Pfam; PF00020; TNFR_c6; 3.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.			
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;			
KW	Signal.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	272	OX40L RECEPTOR.
FT	DOMAIN	20	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	212	236	POTENTIAL.

P02876 triticum ae  
Q07934 homo sapien  
P35444 rattus norv  
P10040 drosophila  
P18519 gallus gall  
Q16787 homo sapien  
P98133 bos taurus  
P10968 triticum ae  
P21532 homo sapien  
P22105 homo sapien  
P50284 mus musculus  
Q01279 mus musculus

```
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT REPEAT 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 15 15 A > G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 16.7%; Score 162; DB 1; Length 272;
Best Local Similarity 28.3%; Pred. No. 1.8e-07;
Matches 45; Conservative 11; Mismatches 51; Indels 52; Gaps 7;

QY 39 LLTGTDAR--CCRVT---TPCRD-YPG-----ECCSEWDCMCVQPEFHGDPD-- 85
DB 14 LALTGLVTARLNLCKVITYPSGHKKRCQCPGHGMSRCDHTRDLTLC-----HPCET 65
QY 86 -----CTTCRHHP-----CPPGQGVQSGKFSFGFCID 114
DB 66 GFYNEAVNYDTCQCTOCNHRSGSELQNCPTPTQDTCRCRPGTQPRQDSGYKLGVDVCP 125
QY 115 CASGTFSGHGHGCKPWTCTQFGFLTVFPGNKTHNAV 153
DB 126 CPPGHFSPGNQACKPWTNCTLTKGQTRHPASDLDVAVC 164

RESULT 2
OX40_HUMAN STANDARD; PRT; 277 AA.
ID OX40_HUMAN
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
GN TNFRSF4 OR TXGPIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94170844; PubMed=7510240;
RA Latza U., Duerkop H., Schnitzger S., Ringeling J., Eitelbach F.,
RA Hummel M., Fonatsch C., Stein H.;
RT "The human OX40 homologue: cDNA structure, expression and chromosomal
RT assignment of the ACT35 antigen."
RL Eur. J. Immunol. 24:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95219871; PubMed=7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of
RT its activities on OX40 receptor."
RL Circ. Shock 44:30-34(1994).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".
CC -----
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CC -----
EMBL; X75962; CAA53576.1; -
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DR EMBL; S76792; AAB33944.1; ALT_INIT.
DR HSP; P25942; ICDF.
DR MIM; 600315; -
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_C6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 277 OX40L RECEPTOR.
FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 235 POTENTIAL.
FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 30 169 4 X TNFR-CYS.
FT REPEAT 30 65 TNFR-CYS 1.
FT REPEAT 66 107 TNFR-CYS 2.
FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 127 167 TNFR-CYS 4.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 16.7%; Score 162; DB 1; Length 277;
Best Local Similarity 29.7%; Pred. No. 1.8e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGALICALSLG-----QRPFGGCGGPRLLLTGTGTARCRVHT 54
DB 4 GARRLGRGPCAALLLLGLGLSTVTLGCVGDTPTNSDRCCHECR--PGNGMYSRCRSQN 61
QY 55 TRCCRDYPG--ECCSEWDCM-CVQPEFHGCD---PCCTTCRRHPCPGCGVQSGKFSF 108
DB 62 TVCRPGGPFYNDVVSFKPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPC 121
QY 109 GFQCIDCASGTFSGHGHGCKPWTCTQFGFLTVFPGNKTHNAVCPVSPPA 160
DB 122 GVDCAPCPPGHFSPCDNQACKPWTNCTLAKGHTLQPASNSSDAICEDRDPPA 173

RESULT 3
41BB_HUMAN STANDARD; PRT; 255 AA.
ID 41BB_HUMAN
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
GN TNFRSF9 OR ILA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand."
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor
RT family."
RL Gene 134:295-298(1993).
```



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Db      107 EIRACTQQRNVKACAGRYCAL-----KTHSGS--CROCRLSLKCGPGEGVASSR 155
QY      80 KFSFGFOCIDCASGTFSG--GHEGHCKPWTDCDTQFGFLTVFPNGKHTNAVCPGPS 133
       :   ||| |||| |. | | : | | : ||| | | |
Db     156 APGNVLKCACTFSDTTSSTDVCRPHICS----ILAIPGNASTDAVCAPESP 207

RESULT 12
A60771
B-cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen bp50
C:Species: Homo sapiens (man)
C>Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A:Reference number: S04460; MUID:89356608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BKA>
A:Experimental source: Burkitt lymphoma cell line Raj1
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TMW>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          14.1%; Score 118.5; DB 2; Length 277;
Best Local Similarity 27.7%; Pred. No. 0.01;
Matches 36; Conservative 10; Mismatches 73; Indels 11; Gaps 5;

QY      9 CGPGRLLGTGDARCCRVHTRCCRDPYG-----EECCSEWDCMCVQPE-FHCGRPCCITT 63
       || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     62 CGESEFLDWNRETHC---HQHKYCDPNLGRVQOKTSETDTICTCEGWCHTSEACES 118

QY      64 C-RHIPCPCGGVOSQSKFEFGQCICASGTFSSQGHEG--HCKPWTDCTQFGFLTVPFG 120
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    119 CVLHRSCPGFGVKIATGVSDTICEPCPVGFSSNSAFEKCHPMTSCETKDLVVQQAG 178

QY      121 NKTHNAVCP 130
       : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     179 TNKTDDVVGCP 188

RESULT 13
I54182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chalfanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq
A:Reference number: I54182; MUID:93252381
A:Accession: I54182
A>Status: preliminary; translated from GB/EMBL/DDBB

```

A:Molecule type: mRNA  
A:Residues: 1-435 <RES>  
A:Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762  
C:Genetics:  
A:Gene: GDB:LTBR  
A:Cross-references: GDB:l230195; OMIM:600979  
A:Map position: l2p13.3-l2p13.1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 13.9%; Score 117; DB 2; Length 435;  
Best Local Similarity 25.8%; Pred. NO. 0.018;  
Matches 42; Conservative 12; Mismatches 66; Indels 44; Gaps 10;

QY 9 CGPGRLLLGTTGDARCRVHTTRC-----CRDYPGEE----C 41  
||| ||| : | : |  
Db 62 CPP-----GYVSAKCSRIKDTVCATCAENSNEHNWLVITICQLRCPCDPVMGLEETAPC 116  
  
QY 42 CS--EWDNCMCVPBEHCGDCPC--CTTCR-HHPCCPPGGVGQSOGKFSEF-PQCIDCASGTFF 95  
||| ||| : | : |  
Db 117 TSRRKTQCR-QPGMFCAAWALECHCELLSDCPPPTGAELKDVEKGNNHCVPCKAGHF 175  
  
QY 96 --SGHGEGHKPWTDCTQFGFLTVFPGNKNTHNAVCPGPSPAEP 137  
:||| ||| : | : |  
Db 176 QNTSSPSARCOPHTRCENQGLVEAAPGTAOSDTTC-----KNPLEP 216

RESULT 14  
S53869  
laminin beta-2 chain precursor (version 2) - human  
N:Alternate names: s-laminin  
C:Species: Homo sapiens (man)  
C>Date: 27-Oct-1995 #sequence\_revision 23-Feb-1996 #text\_change 24-Sep-1998  
C:Accession: S53869  
R:Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tryggvason, J.  
Matrix Biol. 14, 489-497, 1994  
A:Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tissues  
A:Reference number: S53869  
A:Accession: S53869  
A:Molecule type: mRNA  
A:Residues: 1-1798 <LI>  
C:Genetics:  
A:Gene: GDB:LAMB2  
A:Cross-references: GDB:l32363; OMIM:150325  
A:Map position: 3p21.3-3p21.2  
C:Superfamily: laminin-beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:33-1798/Product: laminin beta-2 chain #status predicted <MAT>  
F:283-344/Domain: laminin-type EGF-like homology <LEO1>  
F:347-407/Domain: laminin-type EGF-like homology <LEO2>  
F:410-467/Domain: laminin-type EGF-like homology <LEO3>  
F:470-519/Domain: laminin-type EGF-like homology <LEO4>  
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LEO5>  
F:583-628/Domain: laminin-type EGF-like homology <LEO6>  
F:783-828/Domain: laminin-type EGF-like homology <LEO7>  
F:831-874/Domain: laminin-type EGF-like homology <LEO8>  
F:877-924/Domain: laminin-type EGF-like homology <LEO9>  
F:927-983/Domain: laminin-type EGF-like homology <LEO10>  
F:986-1033/Domain: laminin-type EGF-like homology <LEO11>  
F:1038-1092/Domain: laminin-type EGF-like homology <LEI1>  
F:1095-1140/Domain: laminin-type EGF-like homology <LEI2>  
F:1143-1187/Domain: laminin-type EGF-like homology <LEI3>

Query Match 13.7%; Score 115; DB 2; Length 1798;  
Best Local Similarity 23.9%; Pred. No. 0.067;  
Matches 49; Conservative 8; Mismatches 50; Indels 98; Gaps 12;

QY 5 GPCCGPRLLLTGTGTDAAC-----CRVHTTRC--CRDYPGECCSCSWCMCVQPEF 54  
||| ||| : | : |  
Db 870 GFPCR-----CVCNGHADECNTHTGALIGCDRTDGHEHCE-----CI-AGF 912  
  
QY 55 HCGDPDCT--TCRHHPCCPPGQGVQ-----SQGKFS-----FGFOCIDCASG 93



F:1146-1190/Domain: laminin-type EGF-like homology <LE13>

F:1197-1412/Domain: II <DOM2>

F:1197-1412/Region: heptad repeats

F:1413-1445/Domain: alpha <ALP>

F:1446-1801/Region: heptad repeats

F:1446-1801/Domain: I <DOM1>

F:45-50/Disulfide bonds: #status predicted

F:251.371.1088.1252.1311.1351.1502/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:1193.1196.1800/Disulfide bonds: interchain #status predicted

Query Match 14.9%; Score 125; DB 1; Length 1801;  
Best Local Similarity 26.4%; Pred. No. 0.011;  
Matches 53; Conservative 5; Mismatches 49; Indels 94; Gaps 12;

QY 5 GPGCGP-----GRLLGTGTDAKCRVHTTRC--CRDYPGECCSDWCMCVQPFHCGD 58

DB 873 GFPCRCPCVNGR-----ADECDATGACGLCRDYGGEHCEK---CI-AGPH-GD 918

QY 59 PCCT--TCRHHCPCPGQGVQSQKFS-----FGQCIDCAGTGF 95

DB 919 PRLPYGQCRCPCPEPGP--SORHEATSHRDYGSQIVCHCRAGVTGLRCEACAPGHE 976

QY 96 -----SGHEGCHCKPWTDCITQGF 114

DB 977 GDSKPGRCQCECGNIDPTDPCADPHYGQCLRLHTEGPHGCHCRP-----GF 1029

QY 115 LTVFPGNKTHNVC-VPGSP 134

DB 1030 HGQAARQSRCHRCTNLLGTDP 1050

#### RESULT 9

I48854  
gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999

C:Accession: I48854

R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.

Mamm. Genome 5, 726-727, 1994

A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A:Reference number: I48854; MUID:95178848

A:Accession: I48854

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-459 <RES>

A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831

C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 14.3%; Score 120.5; DB 2; Length 459;  
Best Local Similarity 30.3%; Pred. No. 0.0099;  
Matches 37; Conservative 11; Mismatches 57; Indels 17; Gaps 6;

QY 23 RCRVHTRCRDYPGECCSEND--CMCVQPEF-----HCGDPCCTTC-RHHPCPPGQ 73

DB 77 RTCLSSSSSSQDQVETRACTQKQNRVCAEAGRYCALKTHSGS--CRQCMRLSKCQPGF 134

QY 74 GVOSQKFSFGFQIDCAGTFSG--GHEGCHCKPWTDCITQGFELVPPGNKTHNVCVPG 131

DB 135 GVASSRAPNGVILKACAPGTFSDTSSDVCVRPHRCS-----ILAIPGNASTDAVCAPE 190

QY 132 SP 133

DB 191 SP 192

#### RESULT 10

A35356

tumor necrosis factor receptor 2 precursor [validated] - human

N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2

C:Species: Homo sapiens (man)

F:1-22/Domain: signal sequence #status predicted <SIG>

F:1-22/Domain: signal sequence #status predicted <SIG>

F:1-22/Domain: signal sequence #status predicted <SIG>

F:1-22/Domain: signal sequence #status predicted <SIG>

F:1-22/Domain: signal sequence #status predicted <SIG>

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a  
A:Reference number: A35356; MUID:90260639  
A:Accession: A35356  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649  
A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden  
A:Reference number: A35010; MUID:90110215  
A:Accession: B35010  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kuhnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region  
A:Reference number: I38094; MUID:95121934  
A:Accession: I38094  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:Cross-references: GDB:I25914; OMIM:191191  
A:Map position: lp36.2-1p36.2  
A:Introns: 26/3  
A:Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>

C;Keywords: growth factor receptor; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-271/Product: OX40 antigen #status predicted <SIG>  
F;211-235/Domain: transmembrane #status predicted <TM>

Query Match 18.0%; Score 151; DB 2; Length 271;  
Best Local Similarity 28.5%; Pred. No. 2.6e-05;  
Matches 47; Conservative 12; Mismatches 62; Indels 44; Gaps 8;

QY 1 QRPYGGCGGRLLLG--TGFDAKCCRVHTT-----RCCRD-YGEECCSEWD----- 46  
Db 6 QQPT-----AFLLLGLSLGVTVKLVCKDTPYSGHKKCCQGHGVMVSRCDHTRDTPV 58  
QY 47 CMVQPEFHCG----DPC--CTTCRHH-----PCPPQGGVQSQGKFSF 83  
Db 59 CHPCEGFYNEAVNYDTCKQCTQCNHRSGSELKQNCITETDVTVCQCRGTPQRODSSHL 118

QY 84 GFQCIDASGTFSGHGHCXKPTWDTQFGFLTVFPGNKTNAV 128  
Db 119 GVDCVPCPGHFGSPGNOACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 6  
JC5559  
Lectin-B - Virginian pokeweed  
C;Species: Phytolacca americana (Virginian pokeweed)  
C;Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C;Accession: JC5559  
R;Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A;Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)  
A;Reference number: JC5559; MUID:97290889  
A;Accession: JC5559  
A;Molecule type: protein  
A;Residues: 1-295 <YAM>  
A;Experimental source: root  
C;Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharides  
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p  
C;Keywords: glycoprotein  
F;96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.5%; Score 138.5; DB 2; Length 295;  
Best Local Similarity 31.7%; Pred. No. 0.00027;  
Matches 33; Conservative 17; Mismatches 31; Indels 23; Gaps 7;

QY 9 CGPGRLLGTGDARCCRVHTTRCCRDYPG-----EECCSEWDCMCVQPEFHCGDPCCTT 63  
Db 154 CGITEGYGEGCQSQC---NHQRCGKDFAGRTCLNDLCCSEWG-WCGSSEAHCGGCGQSN 209

QY 64 CRHHPCPPGQGVQSGKFSFGQ-C---IDCASGTFSGHGHC 103  
Db 210 CNYNRC-----GR-NFGRTCPNELCCSSGCGWGSNDAAHC 243

RESULT 7  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C;Accession: A46476; A46515  
R;Torres, R.M.; Clark, E.A.  
J. Immunol. 148, 620-626, 1992  
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40  
A;Reference number: A46476; MUID:92105763  
A;Accession: A46476  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-305 <TOR>  
A;Cross-references: GB:M83312; NID:g1553058  
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)  
A;Note: this translation is not annotated in GenBank entry MUSCDA0A, release 113.0

R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay  
J. Immunol. 149, 3921-3926, 1992  
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A;Reference number: A46515; MUID:93094586  
A;Accession: A46515

A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-287, 'LV' <GR>  
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126  
A;Experimental source: BALB/c, liver  
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)  
C;Comment: For an alternative splice form, see PIR:A46515.  
C;Comment: For an alternative splice form, see PIR:A46476.  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: alternative splicing; transmembrane protein  
F;105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 15.2%; Score 127.5; DB 2; Length 305;  
Best Local Similarity 28.9%; Pred. No. 0.0021;  
Matches 37; Conservative 8; Mismatches 72; Indels 11; Gaps 5;

QY 9 CGPGRLLGTGDARCCRVHTTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 63  
Db 62 CDSGEFSAQWNRIRCI---QHRRHCEPNQGLRVYKKEGTAESDVTCTCKEQGHCTSKDCEA 118

QY 64 C-RHHPCPPGQGVQSGKFSFGFCQICDCASGTFSGGHE--GHCKPWTDCQFGFLTVFPG 120  
Db 119 CAQHTPCIPGFGVMEMATETDTVCHPCVPGVFFSNSSOLFERYCPWTSCBCKNLEVLQKG 178

QY 121 NKTHNAV 128  
Db 179 TSQTNVIC 186

RESULT 8  
NMRTS  
Laminin beta-2 chain precursor - rat  
N;Alternate names: laminin chain B3; S-laminin  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C;Accession: S03539  
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neocortex  
A;Reference number: S03539; MUID:89159410  
A;Accession: S03539  
A;Molecule type: mRNA  
A;Residues: 1-1801 <HUN>  
A;Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251  
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C;Function: interact with cells and with other basement membrane proteins to promote cell adhesion  
A;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular matrix  
F;1-35/Domain: signal sequence #status predicted <SIG>  
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F;36-285/Domain: VI <DOM6>  
F;286-555/Domain: V <DOM5>  
F;286-347/Domain: laminin-type EGF-like homology <LE01>  
F;350-410/Domain: laminin-type EGF-like homology <LE02>  
F;413-470/Domain: laminin-type EGF-like homology <LE03>  
F;473-522/Domain: laminin-type EGF-like homology <LE04>  
F;525-555/Domain: laminin-type EGF-like homology <LE05>  
F;556-784/Domain: IV <DOM4>  
F;786-831/Domain: laminin-type EGF-like homology <LE06>  
F;788-1196/Domain: III <DOM3>  
F;834-877/Domain: laminin-type EGF-like homology <LE07>  
F;880-927/Domain: laminin-type EGF-like homology <LE08>  
F;930-986/Domain: laminin-type EGF-like homology <LE09>  
F;989-1038/Domain: laminin-type EGF-like homology <LE10>  
F;1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:11 ; Search time 80.15 Seconds  
(without alignments)  
130.205 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162  
Perfect score: 841  
Sequence: 1 QRPTEGPGCGRLLLGTT.....FPGKTHNAVCPGSPPAEP 137  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	19.3	272	2 148700	gene ox40 protein
2	160.5	19.1	255	2 138426	lymphocyte activat
3	158.5	18.8	277	2 137552	OX40 homolog - hum
4	153	18.2	256	2 B32393	T-cell antigen 4-1
5	151	18.0	271	2 S12783	OX40 antigen precu
6	138.5	16.5	295	2 JC5559	lectin-B - Virgini
7	127.5	15.2	305	2 A46476	B cell-associated
8	125	14.9	1801	1 MWRTS	laminin beta-2 cha
9	120.5	14.3	459	2 148854	gene murine tumour
10	119	14.1	461	1 A35356	tumor necrosis fac
11	119	14.1	474	2 B38634	tumor necrosis fac
12	118.5	14.1	277	2 A60771	B-cell activation
13	117	13.9	435	2 154182	tumor necrosis fac
14	115	13.7	1798	2 S53859	laminin beta-2 cha
15	112	13.3	152	2 T18975	hypothetical prote
16	111	13.2	1371	2 A34837	insulin-like growt
17	110	13.1	329	2 A48805	insulin-like growt
18	109	13.0	1574	2 T13954	MEGF6 protein - ra
19	109	13.0	3635	2 T10053	laminin alpha 5 ch
20	108	12.8	2907	2 A57278	fibrillin-2 precu
21	107	12.7	164	2 T24272	hypothetical prote
22	106	12.6	1797	2 A55677	laminin beta-2 cha
23	104	12.4	2918	2 A54105	fibrillin-2 precu
24	102.5	12.2	188	2 T15651	hypothetical prote
25	102.5	12.2	955	1 A46016	thrombospondin 3 -
26	101	12.0	1367	1 IGHURI	insulin-like growt
27	100	11.9	540	2 B47417	insulin receptor-r
28	100	11.9	1106	2 T13938	gene shuttle craft
29	99	11.8	1820	2 A55494	latent transformin

30	98	11.7	1111	2 T26972	hypothetical prote
31	97.5	11.6	1713	2 A55347	adhesive ligand ep
32	97	11.5	1106	2 T44598	hypothetical prote
33	97	11.5	1251	2 A57293	latent transformin
34	96.5	11.5	3623	2 T08618	intrinsic factor-B
35	96	11.4	416	1 JN0006	nerve growth facto
36	96	11.4	1364	2 T00250	MEGF2 protein - hu
37	95.5	11.4	1172	1 TSHUP2	thrombospondin 2 p
38	95.5	11.4	1786	1 MMHUB1	laminin beta-1 cha
39	95	11.3	1268	2 B36502	insulin receptor-r
40	95	11.3	2825	2 T14271	doc4 protein, stre
41	94.5	11.2	956	2 A57121	thrombospondin 3 p
42	94.5	11.2	1408	2 S16148	gene serrate prote
43	94	11.2	1203	2 A49175	Notch B protein -
44	94	11.2	1737	2 T00209	MEGF8 protein - hu
45	94	11.2	2871	2 A55567	fibrillin I - bovi

ALIGNMENTS

RESULT 1  
I48700  
gene ox40 protein - mouse  
N:Alternate names: OX40 antigen  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
C:Accession: I48700; I48334; S34377  
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J  
J. Immunol. 151, 5261-5271, 1993  
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell  
A:Reference number: I48700; MUID:94044750  
A:Accession: I48700  
A>Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-272 <RES>  
A:Cross-references: EMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828  
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.  
Eur. J. Immunol. 25, 926-930, 1995  
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX  
A:Reference number: I48334; MUID:95255413  
A:Accession: I48334  
A>Status: translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-14, 'G', 16-272 <RE2>  
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819  
C:Genetics:  
A:Gene: ox40  
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match	19.3%	Score	162;	DB	2;	Length	272;
Best Local Similarity	28.3%	Pred. No.	3.5e-06;				
Matches	45;	Conservative	11;	Mismatches	51;	Indels	52;
Gaps	7;						
QY	14	LLLTGCTDAR--CCRVHT-----TRCCRD-YPG-----ECCSEWDCMCVQPEFHCGDFC--	60				
DB	14	LALTGLVTARLLNCVAKHTYPSGHKKCCRECQPGHGMVSRCDTRDTLC-----HPCET	65				
QY	61	-----CUTCRRHP-----CPPGGVQSQGKESFGFOCID	89				
DB	66	GFYNEAVNYDTCKQCQCNHRSSSEKLNCTPTQDTVCRCPGTPQRQDSGYKLGVDVCP	125				
QY	90	CASGTGSGGHEGCKEPTDCTQFGFLTVPFNKTHNAV	128				
DB	126	CPPGHSPGNNQACKPTWNTCTLSGKQTRHPASDSDAVC	164				

\* RESULT 2  
I38426  
Lymphocyte activation-induced receptor ILA precursor - human  
C:Species: Homo sapiens (man)





```
DOMAIN 1749 1781 LAMININ EGF-LIKE 16 (C-TERMINAL).
FT DOMAIN 1782 1831 LAMININ EGF-LIKE 17.
FT DOMAIN 1832 1887 LAMININ EGF-LIKE 18.
FT DOMAIN 1888 1941 LAMININ EGF-LIKE 19.
FT DOMAIN 1942 1988 LAMININ EGF-LIKE 20.
FT DOMAIN 1989 2035 LAMININ EGF-LIKE 21.
FT DOMAIN 2036 2085 LAMININ EGF-LIKE 22.
FT DOMAIN 2086 2678 DOMAIN II AND I.
FT DOMAIN 2679 3635 5 X LAMININ G-LIKE REPEATS (DOMAIN G).
FT DOMAIN 3636 3679 LAMININ G-LIKE 1.
FT DOMAIN 3680 3849 LAMININ G-LIKE 2.
FT DOMAIN 3850 4035 LAMININ G-LIKE 3.
FT DOMAIN 4036 4241 LAMININ G-LIKE 4.
FT DOMAIN 4242 4426 LAMININ G-LIKE 5.
FT DOMAIN 4427 4611 COILED COIL (POTENTIAL).
FT DOMAIN 4612 4800 COILED COIL (POTENTIAL).
FT DOMAIN 4801 5000 COILED COIL (POTENTIAL).
FT DOMAIN 5001 5200 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1640 1642 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1756 1758 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 222 231 BY SIMILARITY.
FT DISULFID 224 244 BY SIMILARITY.
FT DISULFID 246 255 BY SIMILARITY.
FT DISULFID 258 278 BY SIMILARITY.
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FT DISULFID 452 461 BY SIMILARITY.
FT DISULFID 464 476 BY SIMILARITY.
FT DISULFID 466 483 BY SIMILARITY.
FT DISULFID 485 494 BY SIMILARITY.
FT DISULFID 497 507 BY SIMILARITY.
FT DISULFID 510 522 BY SIMILARITY.
FT DISULFID 512 528 BY SIMILARITY.
FT DISULFID 530 539 BY SIMILARITY.
FT DISULFID 542 552 BY SIMILARITY.
FT DISULFID 555 567 BY SIMILARITY.
FT DISULFID 557 573 BY SIMILARITY.
FT DISULFID 575 584 BY SIMILARITY.
FT DISULFID 587 597 BY SIMILARITY.
FT DISULFID 600 612 BY SIMILARITY.
FT DISULFID 602 619 BY SIMILARITY.
FT DISULFID 621 630 BY SIMILARITY.
FT DISULFID 633 643 BY SIMILARITY.
FT DISULFID 1360 1372 BY SIMILARITY.
FT DISULFID 1362 1379 BY SIMILARITY.
FT DISULFID 1381 1390 BY SIMILARITY.
FT DISULFID 1393 1403 BY SIMILARITY.
FT DISULFID 1450 1465 BY SIMILARITY.
FT DISULFID 1452 1472 BY SIMILARITY.
FT DISULFID 1474 1483 BY SIMILARITY.
FT DISULFID 1486 1496 BY SIMILARITY.
FT DISULFID 1499 1511 BY SIMILARITY.
FT DISULFID 1501 1518 BY SIMILARITY.
FT DISULFID 1520 1529 BY SIMILARITY.
FT DISULFID 1532 1547 BY SIMILARITY.
FT DISULFID 1782 1791 BY SIMILARITY.
FT DISULFID 1784 1798 BY SIMILARITY.
FT DISULFID 1801 1810 BY SIMILARITY.
FT DISULFID 1813 1829 BY SIMILARITY.
FT DISULFID 1832 1847 BY SIMILARITY.
FT DISULFID 1834 1856 BY SIMILARITY.
FT DISULFID 1858 1867 BY SIMILARITY.
FT DISULFID 1870 1885 BY SIMILARITY.
FT DISULFID 1888 1903 BY SIMILARITY.

FT DISULFID 1890 1910 BY SIMILARITY.
FT DISULFID 1913 1922 BY SIMILARITY.
FT DISULFID 1925 1939 BY SIMILARITY.
FT DISULFID 1989 2000 BY SIMILARITY.
FT DISULFID 1991 2007 BY SIMILARITY.
FT DISULFID 2009 2018 BY SIMILARITY.
FT DISULFID 2021 2033 BY SIMILARITY.
FT DISULFID 2036 2043 BY SIMILARITY.
FT DISULFID 2038 2050 BY SIMILARITY.
FT DISULFID 2052 2061 BY SIMILARITY.
FT DISULFID 2064 2083 BY SIMILARITY.
FT DISULFID 2086 2096 INTERCHAIN (PROBABLE).
FT DISULFID 2089 2099 INTERCHAIN (PROBABLE).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 822 822 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 843 843 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 881 881 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1252 1252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1451 1451 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1938 1938 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2115 2115 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2128 2128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2282 2282 N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 13.0%; Score 109; DB 1; Length 3635;
Best Local Similarity 27.8%; Pred. No. 0.032;
Matches 44; Conservative 9; Mismatches 51; Indels 54; Gaps 10;

QY 3 PTGGPGCGP--GRLLLTGTDAKCRVHTRCRDYPG--EECCSEWDCMCVQPFHCGDP 59
Db 1946 PGGTETCDPQSGRCCLCKAGVTGQRC---DRCLEGYFGFQCQGRPCAC-----GP 1993
QY 60 CCTTCRHHP-----CPPGGVQSCKFSFGFOCIDCASGTFSGGHE-----GHCK 104
Db 1994 AAKGSECHPQSGOCHCQPG-----TTGPQCLCAPGYWGLPEKGCRRRCQPRGHCD 2044
QY 105 PWTDCCTQFGFLVFPG-----NKTNAVCPVGPSP 133
Db 2045 PHT-----GHCTCPGLSGERCDCSCQHQ--VPVPCKP 2076

Search completed: September 4, 2001, 16:15:22
Job time: 1134 sec
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-----
CC EMBL; L04270; AAA36757.1; -.
CC DR HSSP; P25942; 1CDF.
CC DR MIN; 600979; -.
CC DR InterPro; IPR001368; -.
CC DR Pfam; PF00020; TNFR_C6; 4.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE; PS50050; TNFR_NGFR_2; 3.
CC KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
CC FT SIGNAL 1 30
CC FT CHAIN 31 435
CC FT DOMAIN 31 227
CC FT TRANSMEM 228 248
CC FT DOMAIN 249 435
CC FT DOMAIN 42 211
CC FT REPEAT 42 81
CC FT REPEAT 82 124
CC FT REPEAT 125 168
CC FT REPEAT 169 211
CC FT DISULFID 43 58
CC FT DISULFID 59 72
CC FT DISULFID 62 80
CC FT DISULFID 83 98
CC FT DISULFID 101 116
CC FT DISULFID 104 124
CC FT DISULFID 126 132
CC FT DISULFID 139 148
CC FT DISULFID 142 167
CC FT DISULFID 170 185
CC FT CARBOHYD 40 40
CC FT CARBOHYD 177 177
CC SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;
Query Match 13.9%; Score 117; DB 1; Length 435;
Best Local Similarity 25.6%; Pred. NO. 0.0013;
Matches 42; Conservative 12; Mismatches 66; Indels 44; Gaps 10;
Qy 9 CGPGLLLGTGTDARCRVHTRC-----CDYDPEE-----C 41
Db 62 CPP-----GTYSAKRSIRDVTCATCAENSYNEHNYLTICQLCRPCDPVNGLEEIAPC 116
Qy 42 CS--EWDGCMQVPEPHCGDPC--CTTCR-HHPCPPGQVSGQKFSFG-FQCIDCASGTF 95
Db 117 TSKRKTQRC-OPGMFCANALECTHCELLSDCPPTGTEAELKDEVGKGNHNCVPCRKAGHF 175
Qy 96 --SGGHEGCRPWTCTDQFGFLTVPPGNKTHNAVCPGSPPAEP 137
Db 176 QNTSSPSARCQPTFCENQGLVEAPAGTAQSDTTC--KNPLEP 216
RESULT 14
IGIR_RAT
ID IGIR_RAT STANDARD; PRO; 1370 AA.
AC P24062.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
GN IGfR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=95277910; PubMed=7758167;
RA Du J., Delafontaine P.;
RT "Inhibition of vascular smooth muscle cell growth through antisense
transcription of a rat insulin-like growth factor I receptor cDNA.";
RL Circ. Res. 76:963-972(1995).
RN [2]
RP SEQUENCE OF 1-364 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=90017496; PubMed=2477843;
RA Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
RA Leroith D.;
RT "Developmental regulation of the rat insulin-like growth factor I
receptor gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).
RN [3]
RP SEQUENCE OF 913-1017 FROM N.A.
RX MEDLINE=92412145; PubMed=1530648;
RA Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
RT "A new member of the insulin receptor family, insulin
receptor-related receptor, is expressed preferentially in the
kidney.";
RL Biochem. Biophys. Res. Commun. 187:934-939(1992).
CC CC -!- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
CC CC TYROSINE-PROTEIN KINASE ACTIVITY.
CC CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
CC CC -!- SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide
bonds. The alpha chains contribute to the formation of the ligand-
binding domain, while the beta chain carries the kinase domain.
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- SIMILARITY: Belongs to the insulin receptor family of tyrosine-
protein kinases.
CC CC -!- SIMILARITY: Contains 2 fibronectin type III-like domains.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC EMBL; L29232; AAA1392.1; -.
CC DR EMBL; M27293; AAA1384.1; -.
CC DR PIR; A33837; A33837.
CC DR HSSP; P06213; IIRK.
CC DR InterPro; IPR000494; -.
CC DR InterPro; IPR000719; -.
CC DR InterPro; IPR001245; -.
CC DR InterPro; IPR001777; -.
CC DR InterPro; IPR002011; -.
CC DR InterPro; IPR002174; -.
CC DR Pfam; PF00757; Furin-like; 1.
CC DR Pfam; PF01030; Recep_L_domain; 2.
CC DR Pfam; PF00041; fn3; 2.
CC DR Pfam; PF00069; pkinase; 1.
CC DR PRINTS; PR00109; TYRKINASE.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC KW Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
CC FT SIGNAL 1 30
CC FT CHAIN 31 741
CC FT CHAIN 742 1370
CC FT DOMAIN 742 936
CC FT TRANSMEM 937 960

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FT DOMAIN 961 1370 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 608 829 FIBRONECTIN TYPE-III.
FT DOMAIN 830 929 FIBRONECTIN TYPE-III.
FT DOMAIN 1000 1275 PROTEIN KINASE.
FT NP_BIND 1006 1014 ATP (BY SIMILARITY).
FT BINDING 1034 1034 ATP (BY SIMILARITY).
FT ACT_SITE 1136 1136 BY SIMILARITY.
FT MOD_RES 1166 1166 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 535 535 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 641 641 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 757 757 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 765 765 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 901 901 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 914 914 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 985 986 AD -> PY (IN REF. 3).
SQ SEQUENCE 1370 AA; 155395 MW; A5946897A41CB145 CRC64;

Query Match 13.2%; Score 111; DB 1; Length 1370;
Best Local Similarity 27.2%; Pred. No. 0.01; Indels 62; Gaps 16;
Matches 46; Conservative 17; Mismatches 44;

QY 9 CG----PGLR-----LLGTGTDARCCRVHTTRC---CRDYPGECSCSEWDCMCVQPE 53
   || || | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 178 CGDLCPTGLEKPMCKETTTINNEYRCWT--TNRCKMCPSCVGRKACTE--NNECCHP 234

QY 54 FHCGDPC-----CTTCRRH-----PCPPGQGVQSGKFSEF-GFOCID---CAS- 92
   || || | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 235 --CLGSCHTPDNTTTCVACRHHYKYGCVCPACPP-----GTYRFGRCVDRDFCANI 285

QY 93 ----GTFSGG---HEGCKPWTCTQFGFLTVPGNKNTHNACVPGSP 134
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 286 PNAESSDSGFIHGDGC--MQECPG--GFIR-----NSTQSMYCIPEGP 327

RESULT 15
LMA5_MOUSE STANDARD; PRT; 3635 AA.
AC Q61001;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LAMININ ALPHA-5 CHAIN (FRAGMENT).
GN LMA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;
RX MEDLINE=96081906; PubMed=7499364;
RA Miner J.H., Lewis R.M., Sanes J.R.;
RT "Molecular cloning of a novel laminin chain, alpha 5, and widespread
expression in adult mouse tissues";
RL J. Biol. Chem. 270:28523-28526(1995).
RN [2]
RP REVISIONS.
RA Miner J.H., Lewis R.M., Sanes J.R.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING

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CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -1- FUNCTION: ALPHA-5 CHAIN MAY BE THE MAJOR LAMININ ALPHA CHAIN OF
CC ADULT EPITHELIAL AND/OR ENDOTHELIAL BASAL LAMINAE.
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -1- TISSUE SPECIFICITY: IN ADULT, HIGH LEVELS IN HEART, LUNG, AND
CC KIDNEY; LOWER IN BRAIN, MUSCLE AND TESTIS; VERY LOW IN LIVER, GUT
CC AND SKIN. EXPRESSED IN MANY TISSUES IN EMBRYONIC DAY 11.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 21-5 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: ALPHA-5 CHAIN IS MORE RELATED TO DROSOPHILA ALPHA
CC CHAIN THAN TO MAMMALIAN ALPHA CHAINS 1-4.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U37501; AAC53430.1; -.
CC HSSP; P02468; ITLE.
CC MGD; MGI:105382; Lama5.
CC InterPro; IPR000034; -.
CC InterPro; IPR000561; -.
CC InterPro; IPR001791; -.
CC InterPro; IPR001886; -.
CC InterPro; IPR002049; -.
CC Pfam; PF00052; laminin_B; 1.
CC Pfam; PF00053; laminin_EGF; 19.
CC Pfam; PF00054; laminin_G; 2.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PROSITE; PS00022; EGF_1; 19.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat.
FT NON_TER 1 1
FT DOMAIN <1 221 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 222 772 10.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
V).
FT DOMAIN 222 280 LAMININ EGF-LIKE 1.
FT DOMAIN 281 350 LAMININ EGF-LIKE 2.
FT DOMAIN 351 396 LAMININ EGF-LIKE 3.
FT DOMAIN 417 463 LAMININ EGF-LIKE 4.
FT DOMAIN 464 509 LAMININ EGF-LIKE 5.
FT DOMAIN 510 554 LAMININ EGF-LIKE 6.
FT DOMAIN 555 599 LAMININ EGF-LIKE 7.
FT DOMAIN 600 645 LAMININ EGF-LIKE 8.
FT DOMAIN 646 698 LAMININ EGF-LIKE 9.
FT DOMAIN 699 750 LAMININ EGF-LIKE 10.
FT DOMAIN 751 772 LAMININ EGF-LIKE 11 (INCOMPLETE).
FT DOMAIN 773 1359 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 1360 1559 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
III B).
FT DOMAIN 1360 1405 LAMININ EGF-LIKE 12.
FT DOMAIN 1406 1449 LAMININ EGF-LIKE 13.
FT DOMAIN 1450 1498 LAMININ EGF-LIKE 14.
FT DOMAIN 1499 1549 LAMININ EGF-LIKE 15.
FT DOMAIN 1550 1559 LAMININ EGF-LIKE 16 (N-TERMINAL).
FT DOMAIN 1560 1748 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1749 2085 6.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
III A).
FT

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FT DISULFID 853 862 BY SIMILARITY.
FT DISULFID 865 875 BY SIMILARITY.
FT DISULFID 878 887 BY SIMILARITY.
FT DISULFID 880 894 BY SIMILARITY.
FT DISULFID 897 906 BY SIMILARITY.
FT DISULFID 909 925 BY SIMILARITY.
FT DISULFID 928 944 BY SIMILARITY.
FT DISULFID 930 955 BY SIMILARITY.
FT DISULFID 957 966 BY SIMILARITY.
FT DISULFID 969 984 BY SIMILARITY.
FT DISULFID 987 1001 BY SIMILARITY.
FT DISULFID 989 1008 BY SIMILARITY.
FT DISULFID 1011 1020 BY SIMILARITY.
FT DISULFID 1023 1036 BY SIMILARITY.
FT DISULFID 1036 1108 BY SIMILARITY.
FT DISULFID 1098 1115 BY SIMILARITY.
FT DISULFID 1117 1126 BY SIMILARITY.
FT DISULFID 1129 1141 BY SIMILARITY.
FT DISULFID 1144 1156 BY SIMILARITY.
FT DISULFID 1165 1174 BY SIMILARITY.
FT DISULFID 1177 1188 BY SIMILARITY.
FT DISULFID 1191 1191 INTERCHAIN (PROBABLE).
FT DISULFID 1194 1194 INTERCHAIN (PROBABLE).
FT DISULFID 1798 1798 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1086 1086 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1250 1250 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1309 1309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1349 1349 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1500 1500 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1799 AA; 196352 MW; 1F28967A67AEDE33 CRC64;

Query Match 14.3%; Score 120; DB 1; Length 1799;
Best Local Similarity 25.9%; Pred. No. 0.0021;
Matches 52; Conservative 6; Mismatches 49; Indels 94; Gaps 12;

Qy 5 GPGGCGP---GRLLTGTDARCCRVHTTRC--CRDYPGECCESEWDCMCVQPEFHCD 58
Db 871 GPNCRPCVNGR-----ADECDTHTGACLGCRDVTGGHCHER----CI-AGFH-GD 916

Qy 59 PCCT---TCRHHPCPPPGVQSGQKFS-----FGFCQICDCASTGF 95
Db 917 PRLPYGGQCRPCPEGPG--SQRFHFSCHRDGYSQIVCHCRAGYTGLCREACAPGPF 974

Qy 96 -----SGGHEGHCKPWTDCTQFGF 114
Db 975 GDSKPGRCQCECSGNIDPMDPCDPHTGQCLRLHNTGPHGVCYK-----GF 1027

Qy 115 LTVPGNKTHNVC--VPGSPP 134
Db 1028 HQAARQSCHRCTCNLLGTD 1048

RESULT 11
TNR2_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (p75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
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RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Kissoneghis M., Fellowes R., Feldmann M., Chernaiovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC -----
DR EMBL; M60469; AAA39752.1; -
DR EMBL; M59378; AAA40463.1; -
DR EMBL; U39488; AAA85021.1; -
DR EMBL; X87128; CAA60618.1; -
DR PIR; B38634; B38634.
DR HSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462AE398C4D6563 CRC64;

Query Match 14.1%; Score 119; DB 1; Length 474;
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Best Local Similarity   31.0%;   Pred. No. 0.00093;
Matches 36; Conservative      8; Mismatches 54; Indels 18; Gaps 5;

QY    21 DARCRCVHTTRCCRDYPGECCSEWDCMCVQPEFHGDPDCTTC-RHHPCPPGGGVQSOG 79
Db          : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
107 EIRACTKQONRVACAEAGRYCAL-----KTHSSS--CRQCWRLSKCQGGFGVASR 155
           : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY    80 KFSFGFCIDCASGTFFSG--GHEGHCKPWTDTQFGLTFVPFGNKHNAVCPGSP 133
           : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db     156 APNGNVLCACAPGTESDTSSTDVCRPHRTCS---ILAIPGNASTDAVCAPESP 207
           : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
CD40L_HUMAN CD40L_HUMAN STANDARD; PRT; 277 AA.
ID ID CD40L_HUMAN STANDARD; PRT; 277 AA.
AC AC P25942;
DT DT 01-MAY-1992 (Rel. 22, Created)
DT DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
DE DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
DE DE TNFRSF5 OR CD40.
OS OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_NCBITaxID=9606;
RN RN [1]
RP RP MEDLINE=89356608; PubMed=2475341;
RX RX Stamenkovic I., Clark E.A., Seed B.;
RT RT "A B-lymphocyte activation molecule related to the nerve growth
RT RT factor receptor and induced by cytokines in carcinomas.";
RL RL EMBO J. 8:1403-1410(1989).
RN RN [2]
RP RP 3D-STRUCTURE MODELING OF 24-144.
RX RX MEDLINE=97189482; PubMed=9037712;
RA RA Bajorath J., Aruffo A.;
RT RT "Construction and analysis of a detailed three-dimensional model of
RT RT the ligand binding domain of the human B cell receptor CD40.";
RL RL Proteins 27:59-70(1997).
RN RN [3]
RP RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX RX MEDLINE=98266353; PubMed=9605317;
RA RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RT RT Zheng Z., Naismith J.H., Thomas D.;
RL RL "The role of polar interactions in the molecular recognition of CD40L
RT RT with its receptor CD40.";
RL RL Protein Sci. 7:1124-1135(1998).
CC CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -I- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC CC -I- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC CC WWW=:http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC CC -----
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CC CC -----
DR DR EMBL; X60592; CAA43045.1; -.
DR DR PIR; S04460;.S04460.
DR DR PDB; 1CDF; 01-APR-97.
DR DR MIM; 109535; -.
DR DR InterPro; IPR001368; -.
DR DR Pfam; PF00020; TNFR_C6; 4.
DR DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR DR PROSITE; PSS0050; TNFR_NGFR_2; 4.
DR DR Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW KW 3D-structure.

```



QY	9	CGGP----RLLLGTGT	DARC-----CRVHTTRCCRDYPGECCSEWD--	46
Db	57	CSPQHAQVFKT	KTSITVCDSTYTQLWNVPCLSCGSRCSDDQVETQACTRQNR	116
QY	47	-CMCQVQEFHC-----	GDPCCTTCRHHCPCPGQGVQSGKSFQGCIDCASGTFSG--	97
Db	117	ICTC-RFGWCYCALSKQGCRC	LCAPLR--KCRPGFGVARFCTETSDVVVCKPCAGTFSNT	173
QY	98	GHEGCHKPTWDC	TQFGFLTVFPCNKTHNAVCPGSP	133
Db	174	SSTDICRPHQICN----	VVAIPGNASRDVACTISTP	205
RESULT	10			
LMB2_MOUSE				
ID	LMB2_MOUSE	STANDARD;	PRT; 1799 AA.	
AC	Q61292; Q62182;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	LAMININ BETA-2 CHAIN PRECURSOR.			
GN	LAMB2 OR S-LAM OR LAMS.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/J;			
RX	MEDLINE=96278760; PubMed=8662701;			
RA	Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,			
RA	Albrechtsen R., Wewer U.M.;			
RT	"Structural organization of the human and mouse laminin beta2 chain			
RT	genes, and alternative splicing at the 5' end of the human			
RT	transcript.";			
RN	J. Biol. Chem. 271:13407-13416(1996).			
RN	[2]			
RP	SEQUENCE OF 348-428 FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=94319092; PubMed=8043959;			
RA	Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;			
RA	"s-laminin gene (Lams) maps to F1 band of mouse chromosome 9.";			
RN	Mamm. Genome 5:393-394(1994).			
RN	[3]			
RP	FUNCTION.			
RC	STRAIN=129/J;			
RX	MEDLINE=95191650; PubMed=7885444;			
RA	Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;			
RA	"Aberrant differentiation of neuromuscular junctions in mice lacking			
RT	s-laminin/laminin beta 2.";			
RT	Nature 374:258-262(1995).			
CC	-1-	FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ ON		
CC	IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF	CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING		
CC	WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.			
CC	-1-	FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR		
CC	NERVE TERMINALS.			
CC	-1-	SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE		
CC	DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND	TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE		
CC	COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.			
CC	THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4			
CC	(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).			
CC	-1-	SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT		
CC	MEMBRANES (MAJOR COMPONENT).			
CC	-1-	TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.		
CC	-1-	DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT		
CC	WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.			
CC	-1-	DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.		
CC	-1-	SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).		
CC	-1-	SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.		
CC	-1-	SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.		

DR Pfam: PF00020; TNFR\_C6: 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS0050; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 289 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 194 215 POTENTIAL.  
 FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

Query Match 15.2%; Score 127.5; DB 1; Length 289;  
 Best Local Similarity 28.9%; Pred. No. 0.00011;  
 Matches 37; Conservative 8; Mismatches 72; Indels 11; Gaps 5;

Qy 9 CGPGRLLGTGDARCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-RHCGDPCCCTT 63  
 Db 62 CDSGEFSQWNRIRC---HQRHCEPNQGLRVKRGTAESTVCTCKEGQCHTKDCEA 118  
 Qy 64 C-RHHPCCPGGVQSGQSFSGFQICDASGTFSGGHE--GHCKPWTDCQFGFLTVFPG 120  
 Db 119 CAQHTPCIPGVGMEMATETDTTVCPCPVGVFFSQSSILFEKCYPTWSCDKNLEVLQKG 178  
 Qy 121 NKTHNAV 128  
 Db 179 TSQTNVIC 186

RESULT 7  
 LMB2\_RAT ID LMB2\_RAT STANDARD: PRT; 1801 AA.  
 AC P15800;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 39, Last annotation update)  
 DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).  
 GN LAMB2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89159410; PubMed=2922051;  
 RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;  
 RT "A laminin-like adhesive protein concentrated in the synaptic cleft  
 of the neuromuscular junction.";  
 RL Nature 338:229-234(1989).  
 CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
 IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
 CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
 WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
 CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
 DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
 TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
 COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
 COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC  
 CLEFT OF THE NEUROMUSCULAR JUNCTION.  
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
 WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
 CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.

CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
 CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
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 CC EMBL: X16563; CAA34561.1; -.  
 DR PIR: S03539; MWRTS.  
 DR HSSP: P02468; 1KLO.  
 DR InterPro: IPR000561; -.  
 DR InterPro: IPR001886; -.  
 DR InterPro: IPR002049; -.  
 DR Pfam: PF00053; laminin\_EGF; 13.  
 DR Pfam: PF00055; laminin\_Nterm; 1.  
 DR PRINTS: PR00011; EGFLAMININ.  
 DR PROSITE: PS00022; EGF\_1; 10.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01248; LAMININ\_TYPE\_EGF; 12.  
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 FT SIGNAL 1 35  
 FT CHAIN 36 1801  
 FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI). (DOMAIN  
 FT DOMAIN 286 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 FT DOMAIN 286 349 V).  
 FT DOMAIN 350 412 LAMININ EGF-LIKE 1.  
 FT DOMAIN 413 472 LAMININ EGF-LIKE 2.  
 FT DOMAIN 473 524 LAMININ EGF-LIKE 3.  
 FT DOMAIN 525 555 LAMININ EGF-LIKE 4.  
 FT DOMAIN 556 785 LAMININ EGF-LIKE 5 (INCOMPLETE).  
 FT DOMAIN 786 1192 8 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 FT DOMAIN 786 833 III).  
 FT DOMAIN 834 879 LAMININ EGF-LIKE 6.  
 FT DOMAIN 880 929 LAMININ EGF-LIKE 7.  
 FT DOMAIN 930 988 LAMININ EGF-LIKE 8.  
 FT DOMAIN 989 1040 LAMININ EGF-LIKE 9.  
 FT DOMAIN 1041 1097 LAMININ EGF-LIKE 10.  
 FT DOMAIN 1098 1145 LAMININ EGF-LIKE 11.  
 FT DOMAIN 1146 1192 LAMININ EGF-LIKE 12.  
 FT DOMAIN 1193 1412 LAMININ EGF-LIKE 13.  
 FT DOMAIN 1413 1445 DOMAIN II.  
 FT DOMAIN 1446 1801 DOMAIN ALPHA.  
 FT DOMAIN 1259 1306 COILED COIL (POTENTIAL).  
 FT DOMAIN 1475 1529 COILED COIL (POTENTIAL).  
 FT DOMAIN 1576 1793 COILED COIL (POTENTIAL).  
 FT DISULFID 286 295 BY SIMILARITY.  
 FT DISULFID 288 313 BY SIMILARITY.  
 FT DISULFID 315 324 BY SIMILARITY.  
 FT DISULFID 327 347 BY SIMILARITY.  
 FT DISULFID 350 359 BY SIMILARITY.  
 FT DISULFID 352 377 BY SIMILARITY.  
 FT DISULFID 380 389 BY SIMILARITY.  
 FT DISULFID 392 410 BY SIMILARITY.  
 FT DISULFID 413 426 BY SIMILARITY.  
 FT DISULFID 415 441 BY SIMILARITY.  
 FT DISULFID 443 452 BY SIMILARITY.  
 FT DISULFID 455 470 BY SIMILARITY.  
 FT DISULFID 473 487 BY SIMILARITY.  
 FT DISULFID 495 494 BY SIMILARITY.  
 FT DISULFID 496 505 BY SIMILARITY.  
 FT DISULFID 508 522 BY SIMILARITY.  
 FT DISULFID 786 798 BY SIMILARITY.  
 FT DISULFID 788 805 BY SIMILARITY.  
 FT DISULFID 807 816 BY SIMILARITY.  
 FT DISULFID 819 831 BY SIMILARITY.

FT DISULFID 834 846 BY SIMILARITY.  
 FT DISULFID 836 853 BY SIMILARITY.  
 FT DISULFID 855 864 BY SIMILARITY.  
 FT DISULFID 867 877 BY SIMILARITY.  
 FT DISULFID 880 889 BY SIMILARITY.  
 FT DISULFID 882 896 BY SIMILARITY.  
 FT DISULFID 889 908 BY SIMILARITY.  
 FT DISULFID 911 927 BY SIMILARITY.  
 FT DISULFID 930 946 BY SIMILARITY.  
 FT DISULFID 932 957 BY SIMILARITY.  
 FT DISULFID 959 968 BY SIMILARITY.  
 FT DISULFID 971 986 BY SIMILARITY.  
 FT DISULFID 989 1003 BY SIMILARITY.  
 FT DISULFID 991 1010 BY SIMILARITY.  
 FT DISULFID 1013 1022 BY SIMILARITY.  
 FT DISULFID 1025 1038 BY SIMILARITY.  
 FT DISULFID 1098 1110 BY SIMILARITY.  
 FT DISULFID 1100 1117 BY SIMILARITY.  
 FT DISULFID 1119 1128 BY SIMILARITY.  
 FT DISULFID 1131 1143 BY SIMILARITY.  
 FT DISULFID 1146 1158 BY SIMILARITY.  
 FT DISULFID 1148 1165 BY SIMILARITY.  
 FT DISULFID 1167 1176 BY SIMILARITY.  
 FT DISULFID 1179 1190 BY SIMILARITY.  
 FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).  
 FT DISULFID 1196 1196 INTERCHAIN (PROBABLE).  
 FT DISULFID 1800 1800 INTERCHAIN (PROBABLE).  
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1088 1088 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1252 1252 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1311 1311 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1351 1351 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1502 1502 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1801 AA; 196473 MW; 97AEF32F8F31FA75 CRC64;

Query Match 14.9%; Score 125; DB 1; Length 1801;  
 Best Local Similarity 26.4%; Pred. No. 0.00075;  
 Matches 53; Conservative 5; Mismatches 49; Indels 94; Gaps 12;

QY 5 GPGGCGP-----GRLLGTGTDCRCRVHTRC---CRDYPGEECCSEWDCMCVQPEFHCGD 58  
 DB 873 GFPCNRCPCVNGR-----ADECDHAHTGACLGCRDYGTEGHCER-----CI-AGFH-GD 918  
 QY 59 PCCT---TCRHHPCPPGQVQSOGKES-----FGQCIDCASGTF 95  
 DB 919 PRLPYGGQCRPCPCPGPG--SORHFATSCHRDGYSOQIVCHCRAGYTGURCACPAGHF 976  
 QY 96 -----SGGHEGHCCKPWTDCDTQFGF 114  
 DB 977 GDSKPGRCQJCECSGNIDPTDPGACDHPHTGQCLRLHHTEGPHGCHKP-----GF 1029  
 QY 115 LVVFPNGKTHNAV-C-VPGSP 134  
 DB 1030 HGQAARQSCHRCTCNLLGTDP 1050

RESULT 8  
 CD40\_BOVIN  
 ID CD40\_BOVIN STANDARD; PRT; 269 AA.  
 AC Q28203;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).  
 GN TNFRSF5 OR CD40.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97281252; PubMed=9135560;  
 RA Hirano A., Brown W.C., Estes D.M.;  
 RT "Cloning" expression and biological function of the bovine CD40  
 RT homologue: role in B-lymphocyte growth and differentiation in  
 RT cattle.";  
 RL Immunology 90:294-300(1997).  
 CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 DR EMBL; U57745; AAC48710.1; .  
 DR HSSP; P25942; ICDF.  
 DR InterPro; IPR001368; .  
 DR Pfam; PF00020; TNFR\_c6; 4  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 1.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 >269 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 269 269  
 SQ SEQUENCE 269 AA; 25983 MW; 746903F30F95F387 CRC64;

Query Match 14.6%; Score 122.5; DB 1; Length 269;  
 Best Local Similarity 28.7%; Pred. No. 0.0003;  
 Matches 37; Conservative 9; Mismatches 70; Indels 13; Gaps 5;

QY 9 CGPGRLLGTGTDCRCRVHTRC---CRDYPGEECCSEWD-----CMCVQPEFHCGDPCCT 62  
 DB 62 CGKGEFLSTWNRKYC---HEHRYCNPNLGRISQEGTLNTDTICVCVEGQ-HCTSHTC 117  
 QY 63 TCRHHP-CPPGQVQSOGKESFGQCIDCASGTFSGGHEG--HCKPWTDCDTQFGFLTVP 119  
 DB 118 SCFPHSLCLPFGVQKQATGLLDTVCEPLGFFSNVSSAFEKCHRWTSCKERGLVEQHV 177  
 QY 120 GNKTHNAV 128  
 DB 178 GTNKTDVVC 186

RESULT 9  
 TNFR2\_HUMAN  
 ID TNFR2\_HUMAN STANDARD; PRT; 461 AA.  
 AC P20333;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
 DE BINDING PROTEIN 2) (TNF-R2) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;

RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,  
RA Hummel M., Fonatsch C., Stein H.;  
RT "The human OX40 homolog: cDNA structure, expression and chromosomal  
RT assignment of the ACT35 antigen.";  
RL Eur. J. Immunol. 24:677-683(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95219871; PubMed=7704935;  
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,  
RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;  
RT "Identification of OX40 ligand and preliminary characterization of  
RT its activities on OX40 receptor.";  
RL Circ. Shock 44:30-34(1994).  
CC -|- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -|- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".  
CC -----  
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CC -----  
DR EMBL; X75962; CAA53576.1; -;  
DR EMBL; S76792; AAB33944.1; ALT\_INIT.  
DR HSSP; P25942; ICDF.  
DR MIM; 600315; -;  
DR InterPro; IPR001368; -;  
DR Pfam; PF00020; TNFR\_C6; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
KW Signal.  
FT SIGNAL 1 28  
FT CHAIN 29 277  
FT DOMAIN 29 214  
FT TRANSMEM 215 235  
FT DOMAIN 236 277  
FT DOMAIN 30 169  
FT REPEAT 30 65  
FT REPEAT 66 107  
FT REPEAT 108 126  
FT REPEAT 127 167  
FT CARBOHYD 146 146  
FT CARBOHYD 160 160  
FT CARBOHYD 160 160  
SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 18.8%; Score 158.5; DB 1; Length 277;  
Best Local Similarity 31.6%; Pred. No. 2.1e-07;  
Matches 42; Conservative 10; Mismatches 70; Indels 11; Gaps 4;  
QY 9 CGPGRLLGTGDACRCRVRHTTCRDRYFG--EECCSEWDCM-CVQPEFHCGD---PCCT 62  
Db 46 CRP-----GNGMYVSCRSQNTVCRPCGFGFYNDVVVSSKPCPCTWCNLRSGSERKQLCT 100  
QY 63 TCRHHPCPPGQVQSGKPSFGFCOICDASGTFSGHGHCCKPWTDTCTQFGFLTVPFGNK 122  
Db 101 ATQDITVCRACRAGTQPLDSYKPGVDCAPCPGPHFSPGDNQACRPWTNCTLAGKHTLQPASN 160  
QY 123 THNAVCPGSPPA 135  
Db 161 SSDAICEDRDPPA 173  
RESULT 4  
ID 41BB\_MOUSE STANDARD; PRT; 256 AA.  
AC P20334;

DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).  
GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89184547; PubMed=2784565;  
RA Kwon B.S., Weissman S.M.;  
RT "cDNA sequences of two inducible T-cell genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RX MEDLINE=94179805; PubMed=8133039;  
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;  
RT "Genomic organization and chromosomal localization of the T-cell  
RT antigen 4-1BB.";  
RL J. Immunol. 152:2256-2262(1994).  
RN [3]  
RP CHARACTERIZATION, AND SEQUENCE OF 25-29.  
RX MEDLINE=93139510; PubMed=7678621;  
RA Pollock K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,  
RA Kwon B.S.;  
RT "Inducible T cell antigen 4-1BB. Analysis of expression and  
RT function.";  
RL J. Immunol. 150:771-781(1993).  
CC -|- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY  
CC ACTIVE DURING T CELL ACTIVATION.  
CC -|- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.  
CC ASSOCIATES WITH PS6-LCK.  
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -|- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.  
CC -|- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.  
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -----  
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CC -----  
DR EMBL; J04492; AAA40167.1; -;  
DR EMBL; U02567; AAA93113.1; -;  
DR PIR; B32393; B32393.  
DR HSSP; P25942; ICDF.  
DR MGD; MGI:1101059; Tnfrsf9.  
DR InterPro; IPR001368; -;  
DR Pfam; PF00020; TNFR\_C6; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE\_NEG.  
DR Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 24  
FT CHAIN 25 256  
FT DOMAIN 25 187  
FT TRANSMEM 188 208  
FT DOMAIN 209 256  
FT DOMAIN 17 159  
FT REPEAT 17 45  
FT REPEAT 46 85  
FT REPEAT 86 117  
FT REPEAT 118 159  
FT CARBOHYD 128 128  
FT CARBOHYD 138 138  
FT CARBOHYD 138 138  
SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;



Query Match 18.2%; Score 153; DB 1; Length 256;  
 Best Local Similarity 31.5%; Pred. No. 6e-07;  
 Matches 40; Conservative 17; Mismatches 52; Indels 18; Gaps 7;

QY 9 CGGRL-LLGTGTDARCRVHTTRCCRDYDGECCSEW---DCMVOPFHCDDPCCTTC 64  
 DB 47 CPSTSSIGQGNICRV-----CAGYFRFKFCSTHNAECIE-GFHCGLPQCITC 101  
 QY 65 RHHPCCPPGQVGSQGRFSGFGQCIDCASGTFSGGH-BGHCKPWTDCQFGLTVFPNGKT 123  
 DB 102 -ERDCRPGQLTKQ-----CKTCSLGTFDQNGTGVCRPWTNCSLDGRSVLKTCTTE 153  
 QY 124 HNAVCP 130  
 DB 154 KDVCVP 160

RESULT 5  
 OX40\_RAT  
 ID OX40\_RAT STANDARD; PRT; 271 AA.  
 AC P15725;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).  
 GN TNFRSF4 OR TXGPIL OR OX40.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RX MEDLINE=90214614; PubMed=2157591;  
 RA Mallett S., Fossum S., Barclay A.N.;  
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";  
 RL EMBO J. 9:1063-1068(1990).  
 CC 1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC 1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
 CC 1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC EMBL; X17037; CAA34897.1; -  
 CC PIR; S08036; S08036.  
 CC PIR; S12783; S12783.  
 CC HSP; P25942; ICDF.  
 CC InterPro; IPR001368; -  
 CC Pfam; PF00020; TNFR\_C6; 3.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 CC PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
 CC Receptor; t-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 271 OX40L RECEPTOR.  
 FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 211 235 POTENTIAL.  
 FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 164 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 102 TNFR-CYS 2.  
 FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 124 164 TNFR-CYS 4.  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64; -

Query Match 18.0%; Score 151; DB 1; Length 271;  
 Best Local Similarity 28.5%; Pred. No. 9.4e-07;  
 Matches 47; Conservative 12; Mismatches 62; Indels 44; Gaps 8;

QY 1 QRPFGGCGGGRLLG--TCTDARCCRVHTT-----RCCRD-YDGECCSEWD----- 46  
 DB 6 QQPT-----AFLLLGLSLGTVTKLNCVKDTPYSGHKCCRECQPGHGMVSRCDTRDTV 58  
 QY 47 CMCVQPFHCG---DPC--CTTCRHH-----PCPPGQGVGSQGRKFSF 83  
 DB 59 CHPCEGFYNEAVNYDTCKQCTQCNHRSGSELKQNCCTPTEDTVCCRCGTQPRDSSHL 118  
 QY 84 GFQCIDCASGTFSGGHEGCHKPWTDCQFGLTVFPNGKTHNAV 128  
 DB 119 GVDVCPGPGHFGSPGNSQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 6  
 CD40\_MOUSE  
 ID CD40\_MOUSE STANDARD; PRT; 289 AA.  
 AC P27512;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).  
 GN TNFRSF5 OR CD40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92105763; PubMed=1370315;  
 RA Torres R.M., Clark E.A.;  
 RT "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";  
 RL J. Immunol. 148:620-626(1992).  
 CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC 1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
 CC 1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC EMBL; M83312; AAB08705.1; -  
 CC EMBL; M94126; AAA37404.1; -  
 CC EMBL; M94129; AAA37404.1; JOINED.  
 CC EMBL; M94128; AAA37404.1; JOINED.  
 CC EMBL; M94127; AAA37404.1; JOINED.  
 CC PIR; A46476; A46476.  
 CC HSP; P25942; ICDF.  
 CC MGD; MGI:88336; Tnfrsf5.  
 CC InterPro; IPR001368; -



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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:21 ; Search time 43.78 Seconds  
(without alignments)  
107.195 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162

Perfect score: 841

Sequence: 1 ORPTGGPGCGPGRLLLTGT.....FFGNKTHNAVCPGPPAP 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	162	19.3	272	1	OX40_MOUSE
2	160.5	19.1	255	1	41BB_HUMAN
3	158.5	18.8	277	1	OX40_HUMAN
4	153	18.2	256	1	41BB_MOUSE
5	151	18.0	271	1	OX40_RAT
6	127.5	15.2	289	1	CD40_MOUSE
7	125	14.9	1801	1	LMB2_MOUSE
8	122.5	14.6	269	1	CD40_BOVIN
9	121	14.4	461	1	TNR2_HUMAN
10	120	14.3	1799	1	LMB2_MOUSE
11	119	14.1	474	1	TNR2_MOUSE
12	118.5	14.1	277	1	CD40_HUMAN
13	117	13.9	435	1	TNR2_HUMAN
14	111	13.2	1370	1	IG1R_RAT
15	109	13.0	3635	1	LMA5_MOUSE
16	108	12.8	2907	1	FBN2_MOUSE
17	107	12.7	1798	1	LMB2_HUMAN
18	104	12.4	1373	1	IG1R_MOUSE
19	104	12.4	2911	1	FBN2_HUMAN
20	102.5	12.2	956	1	TSP3_MOUSE
21	101	12.0	1367	1	IG1R_HUMAN
22	100	11.9	581	1	IRR_RAT
23	100	11.9	1106	1	STC_DROME
24	99.5	11.8	2569	1	LMA3_MOUSE
25	97.5	11.6	1713	1	LMA3_HUMAN
26	96	11.4	416	1	NGFR_CHICK
27	95.5	11.4	415	1	TNR2_MOUSE
28	95.5	11.4	1172	1	TSP2_HUMAN
29	95.5	11.4	1786	1	LMB1_HUMAN
30	95	11.3	1297	1	IRR_HUMAN
31	94.5	11.2	956	1	TSP3_HUMAN
32	94.5	11.2	1408	1	SERR_DROME
33	94	11.2	2871	1	FBN1_BOVIN

34 94 11.2 2871 1 FBN1\_HUMAN  
35 93.5 11.1 212 1 AG1\_HORVU  
36 93.5 11.1 1786 1 LMB1\_MOUSE  
37 93.5 11.1 1964 1 NTC4\_MOUSE  
38 93 11.1 213 1 AG12\_WHEAT  
39 93 11.1 555 1 DP87\_DICDI  
40 93 11.1 2318 1 NTC3\_MOUSE  
41 92.5 11.0 169 1 KRUA\_HUMAN  
42 92.5 11.0 2139 1 CRB\_DROME  
43 92 10.9 2531 1 NTC1\_MOUSE  
44 92 10.9 4289 1 TENX\_HUMAN  
45 91.5 10.9 186 1 AG13\_WHEAT

#### ALIGNMENTS

RESULT 1  
OX40\_MOUSE  
ID OX40\_MOUSE STANDARD; PRT; 272 AA.  
AC P47741;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).  
GN TNFRSF4 OR TXGP1 OR OX40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C.  
RX MEDLINE=94044750; PubMed=8228223;  
RA Calderhead D.M., Buhlmann J.E., van den Bortwegh A.J.,  
Claassen E., Noelle R.J., Fell H.;  
RT Cloning of mouse OX40: a T cell activation marker that may mediate  
T-B cell interactions.;  
RL J. Immunol. 151:5261-5271(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95255413; PubMed=7737295;  
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
Barclay A.N.;  
RT "Gene structure and chromosomal localization of the mouse homologue  
of rat OX40 protein.";  
RL Eur. J. Immunol. 25:926-930(1995).  
CC -|- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; Z21674; CAA79772.1; -;  
DR EMBL; X85214; CAA59476.1; -;  
DR HSSP; P25942; 1CDF.  
DR MGD; MGI:104512; Tnfrsf4.  
DR InterPro; IPR001368; -;  
DR Pfam; PF00020; TNFR\_C6; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_2; 2.  
DR PROSITE; PS00650; TNFR\_NGFR\_2; 2.  
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
Signal.  
FT CHAIN 1 19 POTENTIAL.  
FT CHAIN 20 272 OX40L RECEPTOR.  
FT DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 212 236 POTENTIAL.

```
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 19.3%; Score 162; DB 1; Length 272;
Best Local Similarity 28.3%; Pred. No. 1e-07;
Matches 45; Conservative 11; Mismatches 51; Indels 52; Gaps 7;

QY 14 LLLGTGTGTDAR--CCRVHT-----TRCCRD-YPG-----EECCSEWDCMCVQPEFHCGDPC-- 60
Db 14 LALTGLVTARRLNCVHTVPSGHKKCRCPQGHGMVSRCDHTDTC-----HPCET 65
QY 61 -----CTTCRHPP-----CPTGGQVQSQKGFSGFQCID 89
Db 66 GFYNEAVNYDTCKQCQCNHRSSSELKQNCPTPTQDTVCRCRCPTQPRQDSGYKLGVDCVP 125
QY 90 CASGTFSGGHEGCKPWTCTQFGFLTVPGNKTHNAV 128
Db 126 CPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSDAVC 164

RESULT 2
41BB_HUMAN STANDARD; PRT; 255 AA.
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
GN TNFRSF9 OR ILA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand.";
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor
RT family.";
RL Gene 134:295-298(1993).
RN [3]
RP REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA Kwon B.S.;
RT "Characterization of human homologue of 4-1BB and its ligand.";
RL Immunol. Lett. 45:67-73(1995).
CC -!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
```

```
CC ACTIVE DURING T CELL ACTIVATION.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
CC CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U03397; AAA5133.1; -
CC EMBL: L12964; AAA62478.2; -
CC HSP: P19438; TEXT.
CC MIM: 602250; -
CC InterPro: IPR001368; -
CC Pfam: PF00020; TNFR_C6; 2.
CC PROSITE: PS00652; TNFR_NGFR_1; 1.
CC PROSITE: PS00500; TNFR_NGFR_2; 1.
CC KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 255 4-1BB LIGAND RECEPTOR.
FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 213 POTENTIAL.
FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).
FT REPEAT 47 159 3 X TNFR-CYS.
FT REPEAT 87 118 TNFR-CYS 1.
FT REPEAT 119 159 TNFR-CYS 2.
FT REPEAT 138 138 TNFR-CYS 3.
FT CARBOHYD 149 149 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;

Query Match 19.1%; Score 160.5; DB 1; Length 255;
Best Local Similarity 30.9%; Pred. No. 1.3e-07;
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 9 CGPGRLLLTGTDAACRCRVHTTCCRDYPG-----EECCS-----EWDCMCVQPEFHCGDPC 59
Db 48 CPPNSFSAGG--QRTCDI-----CROCKGVFTRKECSSTNAECDG---TPGPHCLGA 97
QY 60 CCTTCRHPPGPPGGVQSQKGFSGFCIDCASGTFSGGHEGCKPWTCTQFGFLTVFP 119
Db 98 GCSMC-EQDCKQGOELTKG-----CKDCFCFTNDQKRGICRPWTNCSLDGKSVLVN 149
QY 120 GNKTHNAVCPG-----SPPA---EP 137
Db 150 GTRERDVVCGPSPADLSFGASSVTPPAPAREP 181

RESULT 3
OX40_HUMAN STANDARD; PRT; 277 AA.
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
GN TNFRSF4 OR TXGP1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94170844; PubMed=7510240;
```



C:Genetics:  
A:Gene: MEGF6

Query Match 14.8%; Score 105; DB 2; Length 1574;  
Best Local Similarity 28.8%; Pred. No. 0.22;  
Matches 34; Conservative 8; Mismatches 36; Indels 40; Gaps 8;  
QY 6 GPGCGPGRLLGTGTIDARCCRVHTTRC-----CR-DYPGECCSEWD----- 46  
Db 651 GPGC-----SEDCLEQSHTRSCNFKDSCSKAGFGQGERCAECESGFFGPGCRH 701  
QY 47 -CMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFCIDCASGTFSGGHEGHC 103  
Db 702 RCTC-QPGVAC-DPVSGERCTQ-CPEGYQGEDCGQ-----ECPVGTFGVNCSCGSC 748

Search completed: September 4, 2001, 16:12:12  
Job time: 1109 sec

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Query Match      19.1%; Score 135.5; DB 2; Length 255;
Best Local Similarity 32.5%; Pred. No. 0.00022;
Matches 37; Conservative 9; Mismatches 41; Indels 27; Gaps 7;

QY 9 CGPGRLLLGTTDARCCRVHTTRCCRDYPG-----EECCS-----EWDCCMCVQPERFHCDDP 59
Db 48 CPPNSFSSAGG--QRTCDI-----CROCKGVFTRKESSTSNACDC--TPGFHCLGA 97

QY 60 CCTTCRHHPCCPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTFG 113
Db 98 GCSMC-EQDCKQGOELTKKG-----CKDCFCFTFNDQKRGICRPWTNCSLDG 143

RESULT 6
I37552
OX40 homolog - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C:Accession: I37552
R:Latza, U.; Durrkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment o
A:Reference number: I37552; MUID:94170844
A:Accession: I37552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match      17.4%; Score 123.5; DB 2; Length 277;
Best Local Similarity 31.5%; Pred. No. 0.0022;
Matches 35; Conservative 5; Mismatches 60; Indels 11; Gaps 4;

QY 9 CGPGRLLLGTTDARCCRVHTTRCCRDYPG--EECCSEWDCM-CVQPFHCGD---PCCT 62
Db 46 CRP-----GNGMVSRCSRSQNTVCRPCGPGFYNDVYSSKPCPKCTWCNLRSGSERKQLCT 100

QY 63 TCRHHPCPPGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTFG 113
Db 101 ATQDTCRCRAGTQPLDSYKFGVDCAPCPGPFSGDQNAQCKPWTNCTLAG 151

RESULT 7
MMRTS
Laminin beta-2 chain precursor - rat
N:Alternate names: laminin chain B3; S-laminin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C:Accession: S03539
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro
A:Reference number: S03539; MUID:89159410
A:Accession: S03539
A:Molecule type: mRNA
A:Residues: 1-1801 <HUN>
A:Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C:Function: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C:Description: Interact with cells and with other basement membrane proteins to promote
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F:36-285/Domain: VI <DOM4>
F:286-555/Domain: V <DOM5>
F:286-347/Domain: laminin-type EGF-like homology <LE01>
F:350-410/Domain: laminin-type EGF-like homology <LE02>
F:413-470/Domain: laminin-type EGF-like homology <LE03>
F:473-522/Domain: laminin-type EGF-like homology <LE04>
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>

```

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F:556-784/Domain: IV <DOM4>
F:786-831/Domain: laminin-type EGF-like homology <LE06>
F:788-1196/Domain: III <DOM3>
F:834-877/Domain: laminin-type EGF-like homology <LE07>
F:880-927/Domain: laminin-type EGF-like homology <LE08>
F:930-986/Domain: laminin-type EGF-like homology <LE09>
F:989-1038/Domain: laminin-type EGF-like homology <LE10>
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>
F:1197-1412/Domain: II <DOM2>
F:1197-1412/Region: heptad repeats
F:1413-1445/Domain: alpha <ALP>
F:1446-1801/Region: heptad repeats
F:1446-1801/Domain: I <DOM1>
F:45-50/Disulfide bonds: #status predicted
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #statu
F:1193,1196,1800/Disulfide bonds: Interchain #status predicted

Query Match      17.2%; Score 122; DB 1; Length 1801;
Best Local Similarity 27.5%; Pred. No. 0.01;
Matches 47; Conservative 3; Mismatches 35; Indels 86; Gaps 10;

QY 5 GGPGGCGP-----GRLLLGTTDARCCRVHTTRC--CRDYPGECCSEWDCMCVQPFHCGD 58
Db 873 GFPNCRPCVCNGR-----ADECDATGACLCGRDYGTCHECER---CI-AGPH-GD 918

QY 59 PCCT---TCRHPCPPGVQSGVKFS-----FGQCIDCASGTF 95
Db 919 PRLPYGGQCRPCPEPG--SQRHEATSCHRDYGYSQIVCHCRAGYTGURCEACAPGHF 976

QY 96 -----SGGHEGCHKP 105
Db 977 GDSRPGGRQCCECSGNDPTDTPGACDPHTGQCLRLHHTGPHGCHKP 1027

RESULT 8
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of mur
A:Reference number: A46476; MUID:92105763
A:Accession: A46476
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: GB:M83312; NID:91553058
A:Note: sequence extracted from NCBI backbone (NCBI:75206, NCBI:75207)
A:Note: this translation is not annotated in Genbank entry MUSCD40A, release 113.0
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay
J. Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:93094586
A:Accession: A46515
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287 'LV' <GRI>
A:Cross-references: GB:M83312; NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M941126
A:Experimental source: BALB/c, liver
A:Comment: For an alternative splice form, see PIR:A46515
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match      16.4%; Score 116.5; DB 2; Length 305;

```

RESULT 10

S53869 laminin beta-2 chain precursor (version 2) - human  
S53869 N;Alternate names: s-laminin  
C;Species: Homo sapiens (man)  
C;Date: 27-Oct-1995 #sequence\_revision 23-Feb-1996 #text\_change 24-Sep-1998  
R;Accession: S53869  
R;Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tryg-  
Matrix Biol. 14, 489-497, 1994  
A;Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tiss-  
A;Reference number: S53869  
A;Accession: S53869  
A;Molecule type: mRNA  
A;Residues: 1-1798 <IIV>  
C;Genetics:  
A;Gene: GDB:LAMB2  
A;Cross-references: GDB:132363; OMIM:150325  
A;Map position: 3p21.3-3p21.2  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F;1-32/Domain: signal sequence #status predicted <SIG>  
F;33-1798/Product: laminin beta-2 chain #status predicted <MAT>  
F;283-344/Domain: laminin-type EGF-like homology <LE01>  
F;347-407/Domain: laminin-type EGF-like homology <LE02>  
F;410-467/Domain: laminin-type EGF-like homology <LE03>  
F;470-519/Domain: laminin-type EGF-like homology <LE04>  
F;522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>

QY 64 C-RHHPCCPGQGVQSOGKFSGFGQCIDCASGTFSGGHEG--HCKPWTDC 109

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:11; Search time 80.15 Seconds  
(without alignments)  
108.346 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_139

Perfect score:

Sequence: 1 QRPTGGPGCGPRLLLGTGT.....FSGHEGCHKPWTDTCTQEGF 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Minimum	DB seq	length:	0
Maximum	DB seq	length:	2000000000

post-processing: Minimum Match 0%

Post-processing: Minimum Match 10

Maximum Match 100%  
Listing first 45 summaries

Database :

PIR 68:★

```
1: p1r1:
```

pir2:

3: pir3:

4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	143	20.1	272	2	I48700	gene ox40 protein
2	141	19.8	271	2	S12783	Ox40 antigen precu
3	140	19.7	256	2	B32393	T-cell antigen 4-1
4	138.5	19.5	295	2	JC3559	lectin-B - Virgini
5	135.5	19.1	255	2	I38426	lymphocyte activat
6	123.5	17.4	277	2	I37552	Ox40 homolog - hum
7	122	17.2	1801	1	MMRTS	laminin beta-2 cha
8	116.5	16.4	305	2	A6476	B cell-associated
9	112	15.8	152	2	T18975	hypothetical prote
10	112	15.8	1798	2	S53869	laminin beta-2 cha
11	108.5	15.3	277	2	A60771	B-cell activation
12	107	15.0	164	2	T24272	hypothetical prote
13	106	14.9	1797	2	A53677	laminin beta-2 cha
14	105.5	14.8	2907	2	A52728	fibrillin-2 precu
15	105	14.8	1574	2	T13954	MEGF6 protein - ra
16	103.5	14.6	2918	2	A54105	fibrillin-2 precu
17	102.5	14.4	188	2	T15651	hypothetical prote
18	98	13.8	3635	2	T10053	laminin alpha 5 ch
19	97.5	13.7	1713	2	A53347	adhesive ligand ep
20	96.5	13.6	540	2	B47417	insulin receptor-r
21	96.5	13.6	1820	2	A55494	latent transformin
22	95.5	13.4	1786	1	MMHUB1	laminin beta-1 cha
23	94.5	13.3	435	2	I54182	tumor necrosis fac
24	94.5	13.3	1268	2	B36502	insulin receptor-r
25	94	13.2	1203	2	A43175	Moctch B protein -
26	93.5	13.2	212	2	T05936	agglutinin isolact
27	93.5	13.2	644	2	T36325	epidermal growth f
28	93.5	13.2	1786	1	MMNSB1	laminin beta-1 cha
29	92.5	13.0	3229	2	A48805	insulin-like growt

## ALIGNMENTS

```

RESULT 1
I48700
gene ox40 protein - mouse
N:Alternate names: OX40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell
A:Reference number: I48700; MUID:94044750
A:Accession: I48700
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A:Reference number: I48334; MUID:95255413
A:Accession: I48334
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-14,'G',16-272 <RE2>
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C:Genetics:
A:Gene: OX40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match          20.1%; Score 143; DB 2; Length 272;
Best Local Similarity 27.8%; Pred. No. 5.7e-05;
Matches 40; Conservative 8; Mismatches 44; Indels 52; Gaps 7;

QY 14 LLLLTGTGDAR---CCRVHT---TRCCRD-VPG----EECCSEWDCMCVQPEFHCGDPC-- 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 14 LALLTGLVTARLNCVKHTYPSGHKCCRCQPGHGWVSRCDHTRDTLC-----HFCET 65
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 -----CTTCRRHP-----CPPGQVGVSQGFSGFQCID 89
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 66 GFYNEAVNYDFCKOCTQCNHRSGSELKQNCPTTQDTCVRCRPGTQPRQDSGYKLGVDVCP 125
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 90 CASCTFSGGHEGHGCKPWTDTQFG 113
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 126 CPPGHFSPGNQACKPWTNCTLSG 149
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
S12783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homology

```

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: S12783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte  
A:Reference number: S12783; MUID:90214614  
A:Accession: S12783

A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: EMBL:XL7037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 19.8%; Score 141; DB 2; Length 271;  
Best Local Similarity 29.3%; Pred. No. 8.3e-05;  
Matches 44; Conservative 9; Mismatches 53; Indels 44; Gaps 8;

QY 1 ORPTGGPGGPGRLG--TGTDARCRVHTT-----RCRD-YPGECCSEWD----- 46

DB 6 QOPT-----AFLILSLGVTVKLVNCRDTPVSGHKCCRCQPGHGMVSRCDHTRTDV 58

QY 47 CMCVQPEFHCG-----DPC--CTTCRHH-----PCPPGGVQVQSGKFSF 83

DB 59 CHPCPGFNEAVNYDTCKQTCNHRSGSELKQNCPTEDTVCCRCRGTQPRQDSSHLK 118

QY 84 GFQICDASGTFSGGHEGHCCKPWTDCQTQFG 113

DB 119 GVDVCPGPHFSPGNSQACKPWTNCTLSG 148

RESULT 3

B32393  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R:Kwon, B.S.; Weisman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A:Title: cDNA sequence of two inducible T-cell genes.  
A:Reference number: A32393; MUID:89184547  
A:Accession: B32393  
A:Molecule type: mRNA  
A:Residues: 1-256 <KWO>  
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994  
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.  
A:Reference number: I48879; MUID:94179805  
A:Accession: I48879  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-256 <RES>  
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178  
C:Genetics:

A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 19.7%; Score 140; DB 2; Length 256;  
Best Local Similarity 32.7%; Pred. No. 9.6e-05;  
Matches 36; Conservative 15; Mismatches 41; Indels 18; Gaps 7;

QY 9 CGPGRLLGTGTDARCRVHTTCCRDYPGECCSEW---DCMCVQPEFHCGDPCCTTC 64

DB 47 CPPSTSSIGQPNICRY----CAGYFRFKKCSSTHNAECEIE-GFHCILGPQCTRC 101

QY 65 RHHPCPPGQVQSGKFSFGQICDASGTFSGGH-BGHCKPWTDCQTQFG 113  
DB 102 -EKDCRPGQELTKQG-----CKTSLGTFNDQNGTGVCPRWNTNCSLDG 143

RESULT 4

JC5559  
lectin-B - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: JC5559  
R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Ph)  
A:Reference number: JC5559; MUID:97290889  
A:Accession: JC5559

A:Molecule type: protein  
A:Residues: 1-295 <YAM>  
A:Experimental source: root  
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccha  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;  
C:Keywords: glycoprotein  
F:56;139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.5%; Score 138.5; DB 2; Length 295;  
Best Local Similarity 31.7%; Pred. No. 0.00014;  
Matches 33; Conservative 17; Mismatches 31; Indels 23; Gaps 7;

QY 9 CGPGRLLLTGTGTDARCRVHTTCCRDYPG-----ECCSEWDCMCVQPEFHCGDPCCTT 63

DB 154 CGITEGYCGEGCSQC---NHQRCGKDFAGRTCLNLDCCSEWG-WCGSSEAHRCGQGQSN 209

QY 64 CRHPCPPGQVQSGKFSFGQ-C----IDCASGTFSGGHEGHC 103

DB 210 CNYNRC-----GR-NFGFRTCPNELCCSSGGWCGSNDHAC 243

RESULT 5

I38426  
lymphocyte activation-induced receptor ILA precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C:Accession: I38426; JT0752  
R:Allderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.  
Eur. J. Immunol. 24, 2219-2227, 1994  
A:Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A:Reference number: I38426; MUID:94374434  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-255 <RES>  
A:Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321  
R:Schwarz, H.; Tuckwell, J.; Lotz, M.  
Gene 134, 295-298, 1993  
A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human  
A:Reference number: JT0752; MUID:94085794  
A:Accession: JT0752  
A:Molecule type: mRNA  
A:Residues: 1-106,'R',108-255 <SCH>  
C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-ne  
C:Comment: This receptor recognizes soluble, cell-surface bound or extracellular mat  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>  
F:187-213/Domain: transmembrane #status predicted <TM>  
F:138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status pred  
F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted



FT	DOMAIN	3036	3241	LAMININ G-LIKE 3.	FT	DISULFID	2086	2086	INTERCHAIN (PROBABLE).
FT	DOMAIN	3428	3427	LAMININ G-LIKE 4.	FT	DISULFID	2089	2089	INTERCHAIN (PROBABLE).
FT	DOMAIN	3635	3635	LAMININ G-LIKE 5.	FT	CARBOHYD	17	17	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	2122	2174	COILED COIL (POTENTIAL).	FT	CARBOHYD	65	65	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	2247	2381	COILED COIL (POTENTIAL).	FT	CARBOHYD	165	165	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	2521	2538	COILED COIL (POTENTIAL).	FT	CARBOHYD	300	300	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	2556	2622	COILED COIL (POTENTIAL).	FT	CARBOHYD	374	374	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SITE	1640	1642	CELL ATTACHMENT SITE (POTENTIAL).	FT	CARBOHYD	402	402	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SITE	1756	1758	CELL ATTACHMENT SITE (POTENTIAL).	FT	CARBOHYD	822	822	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	222	231	BY SIMILARITY.	FT	CARBOHYD	843	843	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	224	244	BY SIMILARITY.	FT	CARBOHYD	881	881	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	246	255	BY SIMILARITY.	FT	CARBOHYD	1252	1252	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	258	278	BY SIMILARITY.	FT	CARBOHYD	1451	1451	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	281	290	BY SIMILARITY.	FT	CARBOHYD	1938	1938	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	283	315	BY SIMILARITY.	FT	CARBOHYD	2115	2115	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	318	327	BY SIMILARITY.	FT	CARBOHYD	2128	2128	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	330	348	BY SIMILARITY.	FT	CARBOHYD	2128	2128	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	351	362	BY SIMILARITY.	FT	CARBOHYD	2282	2282	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	353	369	BY SIMILARITY.	Query Match 13.8%; Score 98; DB 1; Length 3635;				
FT	DISULFID	371	380	BY SIMILARITY.	Best Local Similarity 28.3%; Pred. No. 0.15;				
FT	DISULFID	383	393	BY SIMILARITY.	Matches 36; Conservative 7; Mismatches 44; Indels 40; Gaps 8;				
FT	DISULFID	417	429	BY SIMILARITY.	Qy	3	PTGGGCGGP--GRLLLTGTDAKCCRVHTTRCCRDYPG--EECCSEWDCMCVQPEFHCGDP	59	
FT	DISULFID	419	438	BY SIMILARITY.	Db	1946	PGGTETCDPSGRCLCKAGVTGQRC----DRCLGYGFEGCQCQCRPCAC-----GP	1993	
FT	DISULFID	440	449	BY SIMILARITY.	Qy	60	CCTTCRHHP-----CPPGGGVQSQGKSFSGFQCIDCASTFSGGHE-----GHCK	104	
FT	DISULFID	452	461	BY SIMILARITY.	Db	1994	AAKGSECHPQSGQCHCQPG-----TTGPOCLECAPGYWGLPKRGCRRCQCPRGHCD	2044	
FT	DISULFID	466	483	BY SIMILARITY.	Qy	105	PWT-DCT	110	
FT	DISULFID	485	494	BY SIMILARITY.	Db	2045	PHTGHT	2051	
FT	DISULFID	497	507	BY SIMILARITY.	Search completed: September 4, 2001, 16:15:23				
FT	DISULFID	510	522	BY SIMILARITY.	Job time: 1135 sec				
FT	DISULFID	512	528	BY SIMILARITY.					
FT	DISULFID	530	539	BY SIMILARITY.					
FT	DISULFID	542	552	BY SIMILARITY.					
FT	DISULFID	555	567	BY SIMILARITY.					
FT	DISULFID	557	573	BY SIMILARITY.					
FT	DISULFID	575	584	BY SIMILARITY.					
FT	DISULFID	587	597	BY SIMILARITY.					
FT	DISULFID	600	612	BY SIMILARITY.					
FT	DISULFID	602	619	BY SIMILARITY.					
FT	DISULFID	621	630	BY SIMILARITY.					
FT	DISULFID	633	643	BY SIMILARITY.					
FT	DISULFID	1360	1372	BY SIMILARITY.					
FT	DISULFID	1362	1379	BY SIMILARITY.					
FT	DISULFID	1381	1390	BY SIMILARITY.					
FT	DISULFID	1393	1403	BY SIMILARITY.					
FT	DISULFID	1450	1465	BY SIMILARITY.					
FT	DISULFID	1452	1472	BY SIMILARITY.					
FT	DISULFID	1474	1483	BY SIMILARITY.					
FT	DISULFID	1486	1496	BY SIMILARITY.					
FT	DISULFID	1499	1511	BY SIMILARITY.					
FT	DISULFID	1501	1518	BY SIMILARITY.					
FT	DISULFID	1520	1529	BY SIMILARITY.					
FT	DISULFID	1532	1547	BY SIMILARITY.					
FT	DISULFID	1782	1791	BY SIMILARITY.					
FT	DISULFID	1784	1798	BY SIMILARITY.					
FT	DISULFID	1801	1810	BY SIMILARITY.					
FT	DISULFID	1813	1829	BY SIMILARITY.					
FT	DISULFID	1832	1847	BY SIMILARITY.					
FT	DISULFID	1834	1856	BY SIMILARITY.					
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FT	DISULFID	1870	1885	BY SIMILARITY.					
FT	DISULFID	1888	1903	BY SIMILARITY.					
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FT	DISULFID	1913	1922	BY SIMILARITY.					
FT	DISULFID	1925	1939	BY SIMILARITY.					
FT	DISULFID	1989	2000	BY SIMILARITY.					
FT	DISULFID	1991	2007	BY SIMILARITY.					
FT	DISULFID	2009	2018	BY SIMILARITY.					
FT	DISULFID	2021	2033	BY SIMILARITY.					
FT	DISULFID	2036	2043	BY SIMILARITY.					
FT	DISULFID	2038	2050	BY SIMILARITY.					
FT	DISULFID	2052	2061	BY SIMILARITY.					
FT	DISULFID	2064	2083	BY SIMILARITY.					







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FT DISULFID 804 813 BY SIMILARITY.
FT DISULFID 816 828 BY SIMILARITY.
FT DISULFID 831 843 BY SIMILARITY.
FT DISULFID 833 850 BY SIMILARITY.
FT DISULFID 852 861 BY SIMILARITY.
FT DISULFID 864 874 BY SIMILARITY.
FT DISULFID 877 886 BY SIMILARITY.
FT DISULFID 879 893 BY SIMILARITY.
FT DISULFID 896 905 BY SIMILARITY.
FT DISULFID 908 924 BY SIMILARITY.
FT DISULFID 927 943 BY SIMILARITY.
FT DISULFID 929 954 BY SIMILARITY.
FT DISULFID 956 965 BY SIMILARITY.
FT DISULFID 968 983 BY SIMILARITY.
FT DISULFID 986 1000 BY SIMILARITY.
FT DISULFID 988 1007 BY SIMILARITY.
FT DISULFID 1010 1019 BY SIMILARITY.
FT DISULFID 1022 1035 BY SIMILARITY.
FT DISULFID 1095 1107 BY SIMILARITY.
FT DISULFID 1097 1114 BY SIMILARITY.
FT DISULFID 1116 1125 BY SIMILARITY.
FT DISULFID 1128 1140 BY SIMILARITY.
FT DISULFID 1143 1155 BY SIMILARITY.
FT DISULFID 1145 1162 BY SIMILARITY.
FT DISULFID 1164 1173 BY SIMILARITY.
FT DISULFID 1176 1187 BY SIMILARITY.
FT DISULFID 1190 1190 INTERCHAIN (PROBABLE).
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
FT DISULFID 1797 1797 INTERCHAIN (PROBABLE).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1348 1348 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 914 914 R -> G (IN REF. 2).
FT CONFLICT 1179 1179 G -> A (IN REF. 2).
SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;

Query Match 14.68; Score 104; DB 1; Length 1798;
Best Local Similarity 23.8%; Pred. No. 0.026;
Matches 41; Conservative 5; Mismatches 38; Indels 88; Gaps 9;

QY 5 GPGCGRLLGGTDARC-----CRVHTTRC--CRDYPGECSEWDCMCVQPEF 54
Db 870 GFPSCR-----CVCNGHADECNTHTGACLCGRDHTGGEHCE-----CI-AGF 912
QY 55 HCGD--PCCTTCRHHPPGGGVQ-----SOGKFS-----FGFCIDCAGST 94
Db 913 HRDPRLYGGCRPCPCPEGPGSQRHFATSCQDEYSQOIVCHCRAGYTGRLCEACAPGH 972
QY 95 F-----SGHEGHCKP 105
Db 973 FGDPSPGRCQLCECSGNIDPMDPDACDPTGQCLRLHHTGEPHCAHCKP 1024

RESULT 13
ID FBN2_HUMAN STANDARD; PRT; 2911 AA.
AC P35556;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FIBRILLIN 2 PRECURSOR.
GN FBN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE-94165150; PubMed-8120105;
RA Zhang H., Apfeiroth S.D., Hu W., Davis E.C., Sanguineti C.,
RA Bonadio J., Mecham R.P., Ramirez F.;
RT "Structure and expression of fibrillin-2, a novel microfibrillar
RT component preferentially located in elastic matrices.";
RL J. Cell Biol. 124:855-863(1994).
RN [2]
RP SEQUENCE OF 752-1505 FROM N.A.
RX MEDLINE-91304567; PubMed-1852206;
RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
RA Tsipouras P., Ramirez F., Hollister D.;
RT "Linkage of Marfan syndrome and a phenotypically related disorder to
RT two different fibrillin genes.";
RL Nature 352:330-334(1991).
RN [3]
RP VARIANT'S CCA TYR-1252 AND SER-1433, AND VARIANT ILE-964.
RX MEDLINE-96083599; PubMed-7493032;
RA Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.;
RT "Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder,
RT congenital contractural arachnodactyly.";
RL Nat. Genet. 11:456-458(1995).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
CC THAT BINDS CALCIUM. FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE
CC THE EARLY PROCESS OF ELASTIC FIBER ASSEMBLY.
CC -!- DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL
CC ARACHNOACTYLY (CCA) (ALSO KNOWN AS BEALS SYNDROME). CCA IS
CC PHENOTYPICALLY SIMILAR TO MARFAN SYNDROME, BUT DOES NOT EFFECT THE
CC AORTA AND THE EYES.
CC -!- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING
CC EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
CC
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CC
DR EMBL; U03272; AAA18950.1;
DR EMBL; X62009; -; NOT_ANNOTATED_CDS.
DR PIR; S17063; S17063.
DR PIR; S31101; S31101.
DR HSSP; P35555; 1EMO.
DR MIM; 121050; -;
DR InterPro; IPR000152; -;
DR InterPro; IPR000561; -;
DR InterPro; IPR001438; -;
DR InterPro; IPR001881; -;
DR InterPro; IPR002212; -;
DR Pfam; PF000008; EGF_46;
DR Pfam; PF00683; TB; 9;
DR PRINTS; PR00010; EGFBL00D.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 37.
DR PROSITE; PS01187; EGF_CA; 43.
KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
KW Repeat; Signal; Multigene family; Disease mutation; Polymorphism.
FT SIGNAL 1 28
FT CHAIN 29 2911 FIBRILLIN 2.
FT DOMAIN 111 142 EGF-LIKE 1, NON-CALCIUM BINDING.
FT DOMAIN 145 176 EGF-LIKE 2, NON-CALCIUM BINDING.
FT DOMAIN 176 207 EGF-LIKE 3, NON-CALCIUM BINDING.
FT DOMAIN 275 316 EGF-LIKE 4, CALCIUM-BINDING.
FT DOMAIN 317 358 EGF-LIKE 5, CALCIUM-BINDING.
FT REPEAT 359 425 TGFBP 1.
FT DOMAIN 493 533 EGF-LIKE 6, NON-CALCIUM BINDING.
FT DOMAIN 534 573 EGF-LIKE 7, CALCIUM-BINDING.
FT DOMAIN 574 615 EGF-LIKE 8, CALCIUM-BINDING.
FT DOMAIN 616 656 EGF-LIKE 9, CALCIUM-BINDING.
FT DOMAIN 657 697 EGF-LIKE 10, CALCIUM-BINDING.

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FT REPEAT 698 766 TGFBP 2. EGF-LIKE 11, CALCIUM-BINDING. 771 783 BY SIMILARITY.
FT DOMAIN 767 808 EGF-LIKE 12, CALCIUM-BINDING. 778 792 BY SIMILARITY.
FT DOMAIN 809 850 EGF-LIKE 13, CALCIUM-BINDING. 794 807 BY SIMILARITY.
FT DOMAIN 851 890 EGF-LIKE 14, CALCIUM-BINDING. 813 825 BY SIMILARITY.
FT DOMAIN 954 995 TGFBP 3. EGF-LIKE 15, CALCIUM-BINDING. 820 834 BY SIMILARITY.
FT REPEAT 996 1071 EGF-LIKE 16, CALCIUM-BINDING. 836 849 BY SIMILARITY.
FT DOMAIN 1072 1113 EGF-LIKE 17, CALCIUM-BINDING. 855 865 BY SIMILARITY.
FT DOMAIN 1114 1156 EGF-LIKE 18, CALCIUM-BINDING. 860 874 BY SIMILARITY.
FT DOMAIN 1157 1198 EGF-LIKE 19, CALCIUM-BINDING. 874 889 BY SIMILARITY.
FT DOMAIN 1199 1240 EGF-LIKE 20, CALCIUM-BINDING. 894 904 BY SIMILARITY.
FT DOMAIN 1241 1281 EGF-LIKE 21, CALCIUM-BINDING. 904 914 BY SIMILARITY.
FT DOMAIN 1282 1323 EGF-LIKE 22, CALCIUM-BINDING. 914 924 BY SIMILARITY.
FT DOMAIN 1324 1365 EGF-LIKE 23, CALCIUM-BINDING. 924 934 BY SIMILARITY.
FT DOMAIN 1366 1406 EGF-LIKE 24, CALCIUM-BINDING. 934 944 BY SIMILARITY.
FT DOMAIN 1407 1447 EGF-LIKE 25, CALCIUM-BINDING. 944 954 BY SIMILARITY.
FT DOMAIN 1448 1489 EGF-LIKE 26, CALCIUM-BINDING. 954 964 BY SIMILARITY.
FT DOMAIN 1490 1530 TGFBP 4. EGF-LIKE 27, CALCIUM-BINDING. 964 974 BY SIMILARITY.
FT DOMAIN 1531 1571 EGF-LIKE 28, CALCIUM-BINDING. 974 984 BY SIMILARITY.
FT REPEAT 1572 1648 EGF-LIKE 29, CALCIUM-BINDING. 984 994 BY SIMILARITY.
FT DOMAIN 1649 1690 EGF-LIKE 30, CALCIUM-BINDING. 994 1004 BY SIMILARITY.
FT DOMAIN 1691 1732 EGF-LIKE 31, CALCIUM-BINDING. 1004 1014 BY SIMILARITY.
FT REPEAT 1733 1806 EGF-LIKE 32, CALCIUM-BINDING. 1014 1024 BY SIMILARITY.
FT DOMAIN 1807 1848 EGF-LIKE 33, CALCIUM-BINDING. 1024 1034 BY SIMILARITY.
FT DOMAIN 1849 1890 EGF-LIKE 34, CALCIUM-BINDING. 1034 1044 BY SIMILARITY.
FT DOMAIN 1891 1932 EGF-LIKE 35, CALCIUM-BINDING. 1044 1054 BY SIMILARITY.
FT DOMAIN 1933 1971 EGF-LIKE 36, CALCIUM-BINDING. 1054 1064 BY SIMILARITY.
FT DOMAIN 1972 2014 EGF-LIKE 37, CALCIUM-BINDING. 1064 1074 BY SIMILARITY.
FT DOMAIN 2015 2054 EGF-LIKE 38, CALCIUM-BINDING. 1074 1084 BY SIMILARITY.
FT DOMAIN 2055 2096 EGF-LIKE 39, CALCIUM-BINDING. 1084 1094 BY SIMILARITY.
FT REPEAT 2097 2169 EGF-LIKE 40, CALCIUM-BINDING. 1094 1104 BY SIMILARITY.
FT DOMAIN 2170 2211 EGF-LIKE 41, CALCIUM-BINDING. 1104 1114 BY SIMILARITY.
FT DOMAIN 2212 2251 EGF-LIKE 42, CALCIUM-BINDING. 1114 1124 BY SIMILARITY.
FT DOMAIN 2252 2292 EGF-LIKE 43, CALCIUM-BINDING. 1124 1134 BY SIMILARITY.
FT DOMAIN 2293 2336 EGF-LIKE 44, CALCIUM-BINDING. 1134 1144 BY SIMILARITY.
FT DOMAIN 2337 2378 EGF-LIKE 45, CALCIUM-BINDING. 1144 1154 BY SIMILARITY.
FT REPEAT 2379 2447 EGF-LIKE 46, CALCIUM-BINDING. 1154 1164 BY SIMILARITY.
FT DOMAIN 2448 2489 EGF-LIKE 47, CALCIUM-BINDING. 1164 1174 BY SIMILARITY.
FT DOMAIN 2490 2530 EGF-LIKE 48, CALCIUM-BINDING. 1174 1184 BY SIMILARITY.
FT DOMAIN 2531 2569 EGF-LIKE 49, CALCIUM-BINDING. 1184 1194 BY SIMILARITY.
FT DOMAIN 2570 2612 EGF-LIKE 50, CALCIUM-BINDING. 1194 1204 BY SIMILARITY.
FT DOMAIN 2613 2652 EGF-LIKE 51, CALCIUM-BINDING. 1204 1214 BY SIMILARITY.
FT DOMAIN 2653 2693 EGF-LIKE 52, CALCIUM-BINDING. 1214 1224 BY SIMILARITY.
FT DOMAIN 2694 2733 EGF-LIKE 53, CALCIUM-BINDING. 1224 1234 BY SIMILARITY.
FT DISULFID 115 124 BY SIMILARITY. 1234 1244 BY SIMILARITY.
FT DISULFID 119 130 BY SIMILARITY. 1244 1254 BY SIMILARITY.
FT DISULFID 132 141 BY SIMILARITY. 1254 1264 BY SIMILARITY.
FT DISULFID 149 159 BY SIMILARITY. 1264 1274 BY SIMILARITY.
FT DISULFID 153 164 BY SIMILARITY. 1274 1284 BY SIMILARITY.
FT DISULFID 166 175 BY SIMILARITY. 1284 1294 BY SIMILARITY.
FT DISULFID 180 190 BY SIMILARITY. 1294 1304 BY SIMILARITY.
FT DISULFID 184 195 BY SIMILARITY. 1304 1314 BY SIMILARITY.
FT DISULFID 197 206 BY SIMILARITY. 1314 1324 BY SIMILARITY.
FT DISULFID 279 291 BY SIMILARITY. 1324 1334 BY SIMILARITY.
FT DISULFID 286 300 BY SIMILARITY. 1334 1344 BY SIMILARITY.
FT DISULFID 302 315 BY SIMILARITY. 1344 1354 BY SIMILARITY.
FT DISULFID 321 333 BY SIMILARITY. 1354 1364 BY SIMILARITY.
FT DISULFID 328 342 BY SIMILARITY. 1364 1374 BY SIMILARITY.
FT DISULFID 344 357 BY SIMILARITY. 1374 1384 BY SIMILARITY.
FT DISULFID 497 509 BY SIMILARITY. 1384 1394 BY SIMILARITY.
FT DISULFID 504 518 BY SIMILARITY. 1394 1404 BY SIMILARITY.
FT DISULFID 520 532 BY SIMILARITY. 1404 1414 BY SIMILARITY.
FT DISULFID 538 548 BY SIMILARITY. 1414 1424 BY SIMILARITY.
FT DISULFID 543 557 BY SIMILARITY. 1424 1434 BY SIMILARITY.
FT DISULFID 559 572 BY SIMILARITY. 1434 1444 BY SIMILARITY.
FT DISULFID 578 590 BY SIMILARITY. 1444 1454 BY SIMILARITY.
FT DISULFID 595 599 BY SIMILARITY. 1454 1464 BY SIMILARITY.
FT DISULFID 601 614 BY SIMILARITY. 1464 1474 BY SIMILARITY.
FT DISULFID 620 631 BY SIMILARITY. 1474 1484 BY SIMILARITY.
FT DISULFID 626 640 BY SIMILARITY. 1484 1494 BY SIMILARITY.
FT DISULFID 642 655 BY SIMILARITY. 1494 1504 BY SIMILARITY.
FT DISULFID 661 672 BY SIMILARITY. 1504 1514 BY SIMILARITY.
FT DISULFID 667 681 BY SIMILARITY. 1514 1524 BY SIMILARITY.
FT DISULFID 683 696 BY SIMILARITY. 1524 1534 BY SIMILARITY.

Query Match 14.6%; Score 103.5; DB 1; Length 2911;
Best Local Similarity 26.8%; Pred. No. 0.041;
Matches 33; Conservative 11; Mismatches 40; Indels 39; Gaps 8;

QY 9 CGPGRLLLTGTARCC-----RVHTTRCCRDYFGEECCSWDCMCVQPEHCG 57
DB 683 CPEG---LAVGMDGRVGVDMRSTCYGGIKKGVCPFPFGAVTKSE--CCANPDYGF 737
QY 58 DPCCTTCRHHPCPPGGVQSGKFSFGF-----QC-ID---CASG---TFSGGHE 100
DB 738 EPC-----QPCPAKNSAEFHGLCSSGVGTVGDRDINECALDPDICANGICENLRGSYR 791
QY 101 GHC 103
DB 792 CNC 794

RESULT 14
LMA3_MOUSE
ID LMA3_MOUSE STANDARD; PRT; 2569 AA.
AC Q61789; Q61788; Q61966;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ ALPHA-3 CHAIN PRECURSOR (FRAGMENT).
GN LAMA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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DR	InterPro; IPR000822; -	FT	DISULFID	153	164	BY SIMILARITY.
DR	InterPro; IPR001436; -	FT	DISULFID	166	175	BY SIMILARITY.
DR	InterPro; IPR001881; -	FT	DISULFID	180	190	BY SIMILARITY.
DR	InterPro; IPR002212; -	FT	DISULFID	184	196	BY SIMILARITY.
DR	Pfam; PF00008; EGF; 46.	FT	DISULFID	198	207	BY SIMILARITY.
DR	Pfam; PF00683; TB; 9.	FT	DISULFID	280	292	BY SIMILARITY.
DR	PRINTS; PR00010; EGFBLD.	FT	DISULFID	287	301	BY SIMILARITY.
DR	PROSITE; PS00010; ASX-HYDROXYL; 43.	FT	DISULFID	303	316	BY SIMILARITY.
DR	PROSITE; PS00022; EGF_1; 2.	FT	DISULFID	322	334	BY SIMILARITY.
DR	PROSITE; PS01186; EGF_2; 36.	FT	DISULFID	329	343	BY SIMILARITY.
DR	PROSITE; PS01187; EGF_CA; 43.	FT	DISULFID	345	358	BY SIMILARITY.
KW	Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;	FT	DISULFID	491	503	BY SIMILARITY.
KW	Repeat; Signal; Multigene family.	FT	DISULFID	498	512	BY SIMILARITY.
FT	SIGNAL	FT	DISULFID	514	526	BY SIMILARITY.
FT	CHAIN	FT	DISULFID	532	542	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	553	566	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	572	584	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	579	593	BY SIMILARITY.
FT	REPEAT	FT	DISULFID	614	625	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	620	634	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	636	649	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	655	666	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	661	675	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	677	690	BY SIMILARITY.
FT	REPEAT	FT	DISULFID	765	777	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	772	786	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	788	801	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	807	819	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	814	828	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	830	843	BY SIMILARITY.
FT	REPEAT	FT	DISULFID	849	859	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	854	868	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	870	883	BY SIMILARITY.
FT	REPEAT	FT	DISULFID	952	964	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	959	973	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	975	988	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1070	1082	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1077	1091	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1093	1106	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1112	1124	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1119	1133	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1135	1149	BY SIMILARITY.
FT	REPEAT	FT	DISULFID	1155	1167	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1162	1176	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1178	1191	BY SIMILARITY.
FT	REPEAT	FT	DISULFID	1197	1209	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1204	1218	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1220	1233	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1239	1250	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1246	1259	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1261	1274	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1280	1292	BY SIMILARITY.
FT	REPEAT	FT	DISULFID	1287	1301	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1303	1316	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1322	1334	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1329	1343	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1345	1358	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1364	1377	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1371	1386	BY SIMILARITY.
FT	REPEAT	FT	DISULFID	1388	1399	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1405	1418	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1412	1427	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1429	1440	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1446	1458	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1453	1467	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1469	1482	BY SIMILARITY.
FT	DOMAIN	FT	DISULFID	1488	1499	BY SIMILARITY.
FT	DISULFID	FT	DISULFID	1494	1508	BY SIMILARITY.
FT	DISULFID	FT	DISULFID	1510	1523	BY SIMILARITY.
FT	DISULFID	FT	DISULFID	1529	1540	BY SIMILARITY.
FT	DISULFID	FT	DISULFID	1535	1549	BY SIMILARITY.

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FT DISULFID 1551 1564 BY SIMILARITY.
FT DISULFID 1647 1659 BY SIMILARITY.
FT DISULFID 1654 1668 BY SIMILARITY.
FT DISULFID 1670 1683 BY SIMILARITY.
FT DISULFID 1689 1701 BY SIMILARITY.
FT DISULFID 1696 1710 BY SIMILARITY.
FT DISULFID 1712 1725 BY SIMILARITY.
FT DISULFID 1805 1817 BY SIMILARITY.

Query Match 14.8%; Score 105.5; DB 1; Length 2907;
Best Local Similarity 26.8%; Pred. No. 0.027;
Matches 33; Conservative 11; Mismatches 40; Indels 39; Gaps 8;

QY 9 CGPGRLLLTGTDAKCC-----RVHTTRCRDYPGECCSEWDCMVCQPEFHCG 57
Db 677 CPPG---LAVGDRGVCVTHMRSTCYGEIKGVCVRPFPAVTKSE--CCCANPDYGF 731
QY 58 DCCCTCRHPCPGGVQSGKFSFGF-----QC-ID---CAGS---TFSGGHE 100
Db 732 EPC-----QPCPAKNSAEFHGLCSSGIGITVDGRDINECALDPDICANGICENLRGTYR 785
QY 101 GHC 103
Db 786 CNC 788

RESULT 12
LMB2_HUMAN
ID LMB2_HUMAN STANDARD; PRT; 1798 AA.
AC P55268; Q16321;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).
GN LMB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95213013; PubMed=7698745;
RA Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,
RA Champlaud M.F., Burgess R.E., Albrechtsen R.;
RT "Human beta 2 chain of laminin (formerly S chain): cDNA cloning,
RT chromosomal localization, and expression in carcinomas.";
RL Genomics 24:243-252(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95316263; PubMed=7795887;
RA Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,
RA Sariola H., Tryggvason K.;
RT "The human laminin beta 2 chain (S-laminin): structure, expression in
RT fetal tissues and chromosomal assignment of the LMB2 gene.";
RL Matrix Biol. 14:489-497(1995).
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
CC CLEFT OF THE NEUROMUSCULAR JUNCTION.
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

```



GN TNFRSF5 OR CD40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=92105763; PubMed=1370315;  
 RA Torres R.M., Clark E.A.;  
 RA "Differential increase of an alternatively polyadenylated mRNA  
 RT species of murine CD40 upon B lymphocyte activation.";  
 RL J. Immunol. 148:620-626(1992).  
 RN [2]  
 RN REVISIONS.  
 RC STRAIN=BALB/C;  
 RA Torres R.M.;  
 RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Liver;  
 RX MEDLINE=93094586; PubMed=1281194;  
 RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,  
 RA Howard M., Cockayne D.A.;  
 RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";  
 RL J. Immunol. 149:3921-3926(1992).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC EMBL; M83312; AAB08705.1; -  
 DR EMBL; M94126; AAA37404.1; -  
 DR EMBL; M94129; AAA37404.1; JOINED.  
 DR EMBL; M94128; AAA37404.1; JOINED.  
 DR EMBL; M94127; AAA37404.1; JOINED.  
 DR PIR; A46476; A46476.  
 DR HSP; P25942; ICDF.  
 DR MGI; M83336; Tnfrsf5.  
 DR InterPro: IPR001368; -  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 289  
 FT DOMAIN 20 193  
 FT TRANSMEM 194 215  
 FT DOMAIN 216 289  
 FT DOMAIN 25 187  
 FT REPEAT 25 60  
 FT REPEAT 61 103  
 FT REPEAT 104 144  
 FT REPEAT 145 187  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180  
 FT NON\_TER 289  
 SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;  
 Query Match 16.4%; Score 116.5; DB 1; Length 289;  
 Best Local Similarity 31.2%; Pred. No. 0.00048;  
 Matches 34; Conservative 6; Mismatches 58; Indels 11; Gaps 5;  
 QY 9 CGPGRLLLTGTARCCRVHTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 63  
 Db 62 CDSGEFSQAWNREINCR---HQHRCPEPQGLRVKKEGTAVCTVCKREGHCTSKDCEA 118  
 QY 64 C-RHHPCPPGQGVQSGKFSFGFCQICDASGTFSGGHE--GHCKPWTDC 109

Db 119 CAQHTPCIFGFGVMEATETDTVCHPCVPVGFSSNQSSLFKEKCPWTSC 167  
 RESULT 9  
 CD40\_BOVIN STANDARD; PRT; 269 AA.  
 ID CD40\_BOVIN  
 AC Q28203;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).  
 GN TNFRSF5 OR CD40.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=97281252; PubMed=91355560;  
 RA Hirano A., Brown W.C., Estes D.M.;  
 RT "Cloning, expression and biological function of the bovine CD40  
 RT homologue: role in B-lymphocyte growth and differentiation in  
 RT cattle.";  
 RL Immunology 90:294-300(1997).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U57745; AAC48710.1; -  
 DR HSP; P25942; ICDF.  
 DR InterPro: IPR001368; -  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 1.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 >269  
 FT DOMAIN 20 193  
 FT TRANSMEM 194 215  
 FT DOMAIN 216 >269  
 FT DOMAIN 25 187  
 FT REPEAT 25 60  
 FT REPEAT 61 103  
 FT REPEAT 104 144  
 FT REPEAT 145 187  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180  
 FT NON\_TER 269  
 SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;  
 Query Match 15.5%; Score 110.5; DB 1; Length 269;  
 Best Local Similarity 29.8%; Pred. No. 0.0016;  
 Matches 34; Conservative 7; Mismatches 60; Indels 13; Gaps 5;  
 QY 9 CGPGRLLLTGTARCCRVHTRCCRDYPGEECCSEWDC-----CMCVQPEFHCGDPCCT 62  
 Db 62 CGKGEFLSTWNRKYC---HEHRYCNPNLRLTQSEGLTNTDTICVCEQG-HCTSHICE 117  
 QY 63 TCRHHP-CPPGQGVQSGKFSFGFCQICDASGTFSGGHEG--HCKPWTDCQTG 113  
 Db 118 SCTPHSLCLPGFGVKQIATGLLDTVCEPCPLGFGFSSVSSAFKCHRWTCERKG 171

RESULT 10  
CD40\_HUMAN STANDARD; PRT; 277 AA.  
AC P25942;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)  
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).  
GN TNFRSF5 OR CD40.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89356608; PubMed=2475341;  
RA Stamenkovic I., Clark E.A., Seed B.;  
RT "A B-lymphocyte activation molecule related to the nerve growth  
RT factor receptor and induced by cytokines in carcinomas.";  
RL EMBO J. 8:1403-1410(1989).  
RN [2]  
RP 3D-STRUCTURE MODELING OF 24-144.  
RX MEDLINE=97189482; PubMed=9037712;  
RA Bajorath J., Aruffo A.;  
RT "Construction and analysis of a detailed three-dimensional model of  
RT the ligand binding domain of the human B cell receptor CD40.";  
RL Proteins 27:59-70(1997).  
RN [3]  
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
RX MEDLINE=98266353; PubMed=9605317;  
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
RA Zheng Z., Naismith J.H., Thomas D.;  
RT "The role of polar interactions in the molecular recognition of CD40L  
RT with its receptor CD40.";  
RL Protein Sci. 7:1124-1135(1998).  
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
CC -!- SIMILARITY: CONTAINS A LA-NGER/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -!- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".  
CC  
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CC  
CC EMBL; X60592; CAA43045.1; -  
CC PIR; S04460; S04460.  
CC PDB; 1CDF; 01-APR-97.  
CC MIM; 109535; -  
CC InterPro; IPR001368; -  
CC Pfam; PF00020; TNFR\_c6; 4.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
CC PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
CC Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
KW 3D-structure.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 277 CD40L RECEPTOR.  
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 194 215 POTENTIAL.  
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 187 4 X TNFR-CYS.  
FT REPEAT 25 60 TNFR-CYS 1.  
FT REPEAT 61 103 TNFR-CYS 2.  
FT REPEAT 104 144 TNFR-CYS 3.  
FT REPEAT 145 187 TNFR-CYS 4.  
FT DISULFID 26 37

FT DISULFID 38 51  
FT DISULFID 41 59  
FT DISULFID 62 77  
FT DISULFID 83 103  
FT DISULFID 105 119  
FT DISULFID 111 116  
FT DISULFID 125 143  
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;  
  
Query Match 15.3%; Score 108.5; DB 1; Length 277;  
Best Local Similarity 29.4%; Pred. No. 0.0025;  
Matches 32; Conservative 8; Mismatches 58; Indels 11; Gaps 5;  
  
QY 9 CGPCRLLLTGTDAKCCRVHTTRCCRDYPG---EECCSEWDCMCVQPE-FHCGDPCCTT 63  
DB 62 CGSEFLDTWNRTHC---HQHKYCDPNLGRVQOKGTSETDTICTCEGWHCTSEACES 118  
QY 64 C-RHHPGPPGGVQSGQKFSFGFCIDCASGTFSGGHEG--HCKPWTDC 109  
DB 119 CVLHRSCTSPGFGVKQIATGVSDTICEPCVPGFFSNVSSAFEKCHPWTSC 167  
  
RESULT 11  
FBN2\_MOUSE STANDARD; PRT; 2907 AA.  
ID FBN2\_MOUSE STANDARD; PRT; 2907 AA.  
AC O61555; O63957;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE FIBRILLIN 2 PRECURSOR.  
GN FBN2 OR FBN-2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95263670; PubMed=7744963;  
RA Zhang H., Hu W., Ramirez F.;  
RT "Developmental expression of fibrillin genes suggests heterogeneity  
RT of extracellular microfibrils.";  
RL J. Cell Biol. 129:1165-1176(1995).  
RN [2]  
RP SEQUENCE OF 210-317 FROM N.A.  
RX MEDLINE=94140368; PubMed=8307578;  
RA Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,  
RA Francke U.;  
RT "Fibrillin genes map to regions of conserved mouse/human synteny on  
RT mouse chromosomes 2 and 18.";  
RL Genomics 18:667-672(1993).  
CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE  
CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
CC -!- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING  
CC EGF-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; L39790; AAA74908.1; -  
CC EMBL; S69359; AAC60685.1; -  
CC MGD; MGI:95490; Fbn2.  
CC InterPro; IPR000152; -  
CC InterPro; IPR000561; -

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FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 286 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
FT FT V).
FT DOMAIN 286 349 LAMININ EGF-LIKE 1.
FT DOMAIN 350 412 LAMININ EGF-LIKE 2.
FT DOMAIN 413 472 LAMININ EGF-LIKE 3.
FT DOMAIN 473 524 LAMININ EGF-LIKE 4.
FT DOMAIN 525 555 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 556 785 LAMININ DOMAIN IV.
FT DOMAIN 786 1192 8 X LAMININ EGF-LIKE REPEATS (DOMAIN
FT FT III).
FT DOMAIN 786 833 LAMININ EGF-LIKE 6.
FT DOMAIN 834 879 LAMININ EGF-LIKE 7.
FT DOMAIN 880 929 LAMININ EGF-LIKE 8.
FT DOMAIN 930 988 LAMININ EGF-LIKE 9.
FT DOMAIN 989 1040 LAMININ EGF-LIKE 10.
FT DOMAIN 1041 1097 LAMININ EGF-LIKE 11.
FT DOMAIN 1098 1145 LAMININ EGF-LIKE 12.
FT DOMAIN 1146 1192 LAMININ EGF-LIKE 13.
FT DOMAIN 1193 1412 DOMAIN II.
FT DOMAIN 1413 1445 DOMAIN ALPHA.
FT DOMAIN 1446 1801 COILED COIL (POTENTIAL).
FT DOMAIN 1259 1306 COILED COIL (POTENTIAL).
FT DOMAIN 1475 1529 COILED COIL (POTENTIAL).
FT DOMAIN 1576 1793 BY SIMILARITY.
FT DISULFID 286 295 BY SIMILARITY.
FT DISULFID 288 313 BY SIMILARITY.
FT DISULFID 315 324 BY SIMILARITY.
FT DISULFID 327 347 BY SIMILARITY.
FT DISULFID 350 359 BY SIMILARITY.
FT DISULFID 352 377 BY SIMILARITY.
FT DISULFID 380 389 BY SIMILARITY.
FT DISULFID 392 410 BY SIMILARITY.
FT DISULFID 413 426 BY SIMILARITY.
FT DISULFID 415 441 BY SIMILARITY.
FT DISULFID 443 452 BY SIMILARITY.
FT DISULFID 455 470 BY SIMILARITY.
FT DISULFID 473 487 BY SIMILARITY.
FT DISULFID 475 494 BY SIMILARITY.
FT DISULFID 496 505 BY SIMILARITY.
FT DISULFID 508 522 BY SIMILARITY.
FT DISULFID 508 522 BY SIMILARITY.
FT DISULFID 786 798 BY SIMILARITY.
FT DISULFID 788 805 BY SIMILARITY.
FT DISULFID 807 816 BY SIMILARITY.
FT DISULFID 819 831 BY SIMILARITY.
FT DISULFID 834 846 BY SIMILARITY.
FT DISULFID 836 853 BY SIMILARITY.
FT DISULFID 855 864 BY SIMILARITY.
FT DISULFID 867 877 BY SIMILARITY.
FT DISULFID 880 889 BY SIMILARITY.
FT DISULFID 882 896 BY SIMILARITY.
FT DISULFID 899 908 BY SIMILARITY.
FT DISULFID 911 927 BY SIMILARITY.
FT DISULFID 930 946 BY SIMILARITY.
FT DISULFID 932 957 BY SIMILARITY.
FT DISULFID 959 968 BY SIMILARITY.
FT DISULFID 971 986 BY SIMILARITY.
FT DISULFID 989 1003 BY SIMILARITY.
FT DISULFID 991 1010 BY SIMILARITY.
FT DISULFID 1013 1022 BY SIMILARITY.
FT DISULFID 1025 1038 BY SIMILARITY.
FT DISULFID 1098 1110 BY SIMILARITY.
FT DISULFID 1100 1117 BY SIMILARITY.
FT DISULFID 1119 1128 BY SIMILARITY.
FT DISULFID 1131 1143 BY SIMILARITY.
FT DISULFID 1146 1158 BY SIMILARITY.
FT DISULFID 1148 1165 BY SIMILARITY.
FT DISULFID 1167 1176 BY SIMILARITY.
FT DISULFID 1179 1190 BY SIMILARITY.
FT DISULFID 1193 1196 INTERCHAIN (PROBABLE).
FT DISULFID 1196 1196 INTERCHAIN (PROBABLE).
FT DISULFID 1800 1800 INTERCHAIN (PROBABLE).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1088 1088 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1252 1252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1311 1311 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1351 1351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1502 1502 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1801 AA; 196473 MW; 97AEF32F8F31FA75 CRC64;

Query Match 17.2%; Score 122; DB 1; Length 1801;
Best Local Similarity 27.5%; Pred.No. 0.0006;
Matches 47; Conservative 3; Mismatches 35; Indels 86; Gaps 10;

QY 5 GPGGCGP-----GRLLLTGTDAKRCRVHTTRC--CRDYPGEECCSEWDCMCVOPFHCGD 58
Db 873 GPPNCRPCVNCGR-----ADECDHAHTGACLGCRDVTGGEHCEH---CI-AGPH-GD 918

QY 59 PCCT---TCRHHPCPGQGVQSGKFS-----FGQCIDCASGTF 95
Db 919 PRLPYGGQCRPCPCPEPGG--SORHEATSCHRDGYSQQIVCHCRAGYTLGRCEACAPGHF 976

QY 96 -----SGHGHCKP 105
Db 977 GDPSPKPGRCQLCECSGNIDPTDPGACDPHTGQCLRLHHTGPHGCHCKP 1027

RESULT 7
LMB2_MOUSE
ID LMB2_MOUSE STANDARD; PRT; 1799 AA.
AC Q61292; Q62182;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR.
GN LAMB2 OR S-LAM OR LAMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/J;
RX MEDLINE=96278760; PubMed=8662701;
RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
RA Albrechtsen R., Wewer U.M.;
RT "Structural organization of the human and mouse laminin beta2 chain
genes, and alternative splicing at the 5' end of the human
transcript.";
RL J. Biol. Chem. 271:13407-13416(1996).
RN [2]
RP SEQUENCE OF 348-428 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94319092; PubMed=8043959;
RA Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;
RT "S-laminin gene (Lams) maps to F1 band of mouse chromosome 9.";
RL Mamm. Genome 5:393-394(1994).
RN [3]
RP FUNCTION.
RC STRAIN=129/J;
RX MEDLINE=95191650; PubMed=7885444;
RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
RT "Aberrant differentiation of neuromuscular junctions in mice lacking
s-laminin/laminin beta 2.";
RL Nature 374:258-262(1995).
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR
NERVE TERMINALS.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
```

CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
 CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT  
 CC MEMBRANES (MAJOR COMPONENT).  
 CC -1- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.  
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
 CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
 CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
 CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
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 CC -----  
 CC EMBL; U43541; AAC53535.1; -;  
 CC DR EMBL; U42624; AAC53535.1; JOINED.  
 CC DR EMBL; X75928; CAA53532.1; -;  
 CC DR HSSP; P02468; IKLO.  
 CC DR MGD; MGI:99916; Lamb2.  
 CC DR InterPro; IPR000561; -;  
 CC DR InterPro; IPR001886; -;  
 CC DR InterPro; IPR002049; -;  
 CC DR Pfam; PF00053; laminin\_EGF; 13.  
 CC DR Pfam; PF00055; laminin\_Nterm; 1.  
 CC DR PRINTS; PRO0011; EGF\_LAMININ.  
 CC DR PROSITE; PS00022; EGF\_1; 10.  
 CC DR PROSITE; PS01186; EGF\_2; 2.  
 CC DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
 CC KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 CC FT SIGNAL 1 35 POTENTIAL.  
 CC FT CHAIN 36 1799 LAMININ BETA-2 CHAIN.  
 CC FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).  
 CC FT DOMAIN 284 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 CC V).  
 CC FT DOMAIN 286 349 LAMININ EGF-LIKE 1.  
 CC FT DOMAIN 350 412 LAMININ EGF-LIKE 2.  
 CC FT DOMAIN 413 472 LAMININ EGF-LIKE 3.  
 CC FT DOMAIN 473 524 LAMININ EGF-LIKE 4.  
 CC FT DOMAIN 525 555 LAMININ EGF-LIKE 5 (INCOMPLETE).  
 CC FT DOMAIN 556 782 LAMININ DOMAIN IV.  
 CC FT DOMAIN 783 1191 8 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 CC III).  
 CC FT DOMAIN 784 831 LAMININ EGF-LIKE 6.  
 CC FT DOMAIN 832 877 LAMININ EGF-LIKE 7.  
 CC FT DOMAIN 878 927 LAMININ EGF-LIKE 8.  
 CC FT DOMAIN 928 986 LAMININ EGF-LIKE 9.  
 CC FT DOMAIN 987 1038 LAMININ EGF-LIKE 10.  
 CC FT DOMAIN 1039 1095 LAMININ EGF-LIKE 11.  
 CC FT DOMAIN 1096 1143 LAMININ EGF-LIKE 12.  
 CC FT DOMAIN 1144 1190 LAMININ EGF-LIKE 13.  
 CC FT DOMAIN 1191 1410 DOMAIN II.  
 CC FT DOMAIN 1411 1443 DOMAIN ALPHA.  
 CC FT DOMAIN 1444 1799 DOMAIN I.  
 CC FT DOMAIN 1257 1304 COILED COIL (POTENTIAL).  
 CC FT DOMAIN 1473 1527 COILED COIL (POTENTIAL).  
 CC FT DOMAIN 1577 1791 COILED COIL (POTENTIAL).  
 CC FT DISULFID 286 295 BY SIMILARITY.  
 CC FT DISULFID 288 313 BY SIMILARITY.  
 CC FT DISULFID 315 324 BY SIMILARITY.  
 CC FT DISULFID 327 347 BY SIMILARITY.  
 CC FT DISULFID 350 359 BY SIMILARITY.  
 CC FT DISULFID 352 377 BY SIMILARITY.  
 CC FT DISULFID 380 389 BY SIMILARITY.  
 CC FT DISULFID 392 410 BY SIMILARITY.  
 CC FT DISULFID 413 426 BY SIMILARITY.

FT DISULFID 415 441 BY SIMILARITY.  
 FT DISULFID 443 452 BY SIMILARITY.  
 FT DISULFID 455 470 BY SIMILARITY.  
 FT DISULFID 473 487 BY SIMILARITY.  
 FT DISULFID 475 494 BY SIMILARITY.  
 FT DISULFID 496 505 BY SIMILARITY.  
 FT DISULFID 508 522 BY SIMILARITY.  
 FT DISULFID 784 796 BY SIMILARITY.  
 FT DISULFID 786 803 BY SIMILARITY.  
 FT DISULFID 805 814 BY SIMILARITY.  
 FT DISULFID 817 829 BY SIMILARITY.  
 FT DISULFID 832 844 BY SIMILARITY.  
 FT DISULFID 834 851 BY SIMILARITY.  
 FT DISULFID 853 862 BY SIMILARITY.  
 FT DISULFID 865 875 BY SIMILARITY.  
 FT DISULFID 878 887 BY SIMILARITY.  
 FT DISULFID 880 894 BY SIMILARITY.  
 FT DISULFID 897 906 BY SIMILARITY.  
 FT DISULFID 909 925 BY SIMILARITY.  
 FT DISULFID 928 944 BY SIMILARITY.  
 FT DISULFID 930 955 BY SIMILARITY.  
 FT DISULFID 957 966 BY SIMILARITY.  
 FT DISULFID 969 984 BY SIMILARITY.  
 FT DISULFID 987 1001 BY SIMILARITY.  
 FT DISULFID 989 1008 BY SIMILARITY.  
 FT DISULFID 1011 1020 BY SIMILARITY.  
 FT DISULFID 1023 1036 BY SIMILARITY.  
 FT DISULFID 1096 1108 BY SIMILARITY.  
 FT DISULFID 1098 1115 BY SIMILARITY.  
 FT DISULFID 1117 1126 BY SIMILARITY.  
 FT DISULFID 1129 1141 BY SIMILARITY.  
 FT DISULFID 1144 1156 BY SIMILARITY.  
 FT DISULFID 1146 1163 BY SIMILARITY.  
 FT DISULFID 1165 1174 BY SIMILARITY.  
 FT DISULFID 1177 1188 BY SIMILARITY.  
 FT DISULFID 1191 1191 INTERCHAIN (PROBABLE).  
 FT DISULFID 1194 1194 INTERCHAIN (PROBABLE).  
 FT DISULFID 1798 1798 INTERCHAIN (PROBABLE).  
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1086 1086 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1250 1250 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1309 1309 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1349 1349 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1500 1500 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 1799 AA; 196352 MW; 1F28967A67AEDE33 CRC64;  
 Query Match 16.5%; Score 117; DB 1; Length 1799;  
 Best Local Similarity 26.9%; Pred. No. 0.0017;  
 Matches 46; Conservative 4; Mismatches 35; Indels 86; Gaps 10;  
 Qy 5 GGPGCGP-----GRLLGTGTDAACRCRVHTTRC--CRDYPGECCSEWDCMVCQVPEFHCGD 58  
 Db 871 GFPNCRPCVNGR-----ADECDTHGTACLCRDYTGGEHCE-----CI-AGFH-GD 916  
 Qy 59 PCCT--TCRHHPCCPGGVQSGKFS-----FGQCIDCASGTF 95  
 Db 917 PLPLPGGQCRPCPCPEPG--SQRHFTSCHRDGYSQIVCHCRAGYGLRCACAPGPF 974  
 Qy 96 -----SGGHEGCKP 105  
 Db 975 GDSKPGGRQCLCECSGNIDPMDPADCPHTGQCLRLCHNTEGPHGCKP 1025  
 RESULT 8  
 CD40\_MOUSE STANDARD; PRT; 289 AA.  
 ID CD40\_MOUSE  
 AC P27512;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 13-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).

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CC -----
DR EMBL; J04492; AAA40167.1; -
DR EMBL; U02567; AAA93113.1; -
DR PIR; B32393; B32393.
DR HSSP; P25942; ICDF.
DR MGD; MGI:1101059; Tnfrsf9.
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_C6; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 25 256 4-1BB LIGAND RECEPTOR.
FT DOMAIN 25 187 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 188 208 POTENTIAL.
FT DOMAIN 209 256 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 17 159 4 X TNFR-CYS.
FT REPEAT 17 45 TNFR-CYS 1.
FT REPEAT 46 85 TNFR-CYS 2.
FT REPEAT 86 117 TNFR-CYS 3.
FT REPEAT 118 159 TNFR-CYS 4.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 19.7%; Score 140; DB 1; Length 256;
Best Local Similarity 32.7%; Pred. No. 3.3e-06;
Matches 36; Conservative 15; Mismatches 41; Indels 18; Gaps 7;

QY 9 CGPGRLLGTGTARCRVHTTRCCRDYPGECSEW---DCMCVQPFHCGDCCTTC 64
DB 47 CPPSTFSSIGQPCNICRV---CAGFRKKFCSSTHNAECEIE-GFCLGFCQCTRC 101
QY 65 RHHPCCPGQVQSOGKFSFGQICDASGTFSGGH-EGHCKPWTDCQTFG 113
DB 102 -EKDCRPQQLTKG-----CKTCSLGTENDQNGTGVCRPWTNCSLDG 143

RESULT 4
ID 41BB_HUMAN
AC Q07011; STANDARD; PRT; 255 AA.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
GN TNFRSF9 OR ILA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand.";
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;

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RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor
RT family.";
RL Gene 134:295-298(1993).
RN [3]
RP REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA Kwon B.S.;
RT "Characterization of human homologue of 4-1BB and its ligand.";
RL Immunol. Lett. 45:67-73(1995).
CC -|- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
CC ACTIVE DURING T CELL ACTIVATION.
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -|- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
CC CELLS.
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -|- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
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CC -----
DR EMBL; U03397; AAA53133.1; -
DR EMBL; L12964; AAA62478.2; -
DR HSSP; P19438; 1EXT.
DR MIM; 602250; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 255 4-1BB LIGAND RECEPTOR.
FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 187 213 POTENTIAL.
FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 47 159 3 X TNFR-CYS.
FT REPEAT 47 86 TNFR-CYS 1.
FT REPEAT 87 118 TNFR-CYS 2.
FT REPEAT 119 159 TNFR-CYS 3.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EEF00460 CRC64;

Query Match 19.1%; Score 135.5; DB 1; Length 255;
Best Local Similarity 32.5%; Pred. No. 8.3e-06;
Matches 37; Conservative 9; Mismatches 41; Indels 27; Gaps 7;

QY 9 CGPGRLLGTGTARCRVHTTRCCRDYPG-----EBCCS-----EWDCMVQPFHCGDP 59
DB 48 CPPNSSFSSAGG--QRTCDI-----CRQCKGVFRTRKESSTNAECD---TFGFHCLGA 97
QY 60 CCTTCRHPCPGQVQSOGKFSFGQICDASGTFSGGHGCKPWTDCQTFG 113
DB 98 GCSMC-EQDCKQGQLTKG-----CKDCFCFTNDQKRGICRPWTNCSLOG 143

RESULT 5
OX40_HUMAN

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:22 ; Search time 43.78 Seconds  
(without alignments)  
89.199 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_139

Perfect score: 711

Sequence: 1 QPRTGPGCGPGRLLGTCT.....FSGHGEGCKPWTDTQFGF 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	143	20.1	272	1	OX40_MOUSE
2	141	19.8	271	1	OX40_RAT
3	140	19.7	256	1	41BB_MOUSE
4	135.5	19.1	255	1	41BB_HUMAN
5	123.5	17.4	277	1	OX40_HUMAN
6	122	17.2	1801	1	LMB2_RAT
7	117	16.5	1799	1	LMB2_MOUSE
8	116.5	16.4	289	1	CD40_MOUSE
9	110.5	15.5	269	1	CD40_BOVIN
10	108.5	15.3	277	1	CD40_HUMAN
11	105.5	14.8	2907	1	FBN2_MOUSE
12	104	14.6	1798	1	LMB2_HUMAN
13	103.5	14.6	2911	1	FBN2_HUMAN
14	99.5	14.0	2569	1	LMA3_MOUSE
15	98	13.8	3635	1	LMA3_MOUSE
16	97.5	13.7	1713	1	LMA3_HUMAN
17	96.5	13.6	581	1	IRR_RAT
18	95.5	13.4	1786	1	LMB1_HUMAN
19	94.5	13.3	435	1	TNRC_HUMAN
20	94.5	13.3	1297	1	IRR_HUMAN
21	93.5	13.2	212	1	AGI_HORVU
22	93.5	13.2	1786	1	LMB1_MOUSE
23	92.5	13.0	1370	1	IGLR_RAT
24	91.5	12.9	186	1	AGI3_WHEAT
25	91	12.8	2213	1	SORL_MOUSE
26	90.5	12.7	1210	1	EGFR_MOUSE
27	90.5	12.7	4289	1	TENX_HUMAN
28	90	12.7	169	1	KRUA_HUMAN
29	90	12.7	227	1	AGI_ORYSA
30	89	12.5	116	1	MCS_HUMAN
31	89	12.5	755	1	COMP_RAT
32	89	12.5	846	1	ITBX_DROME
33	88.5	12.4	212	1	AGIL_WHEAT
					147741 mus musculu
					P15725 rattus norv
					P20334 mus musculu
					Q07011 homo sapien
					P43489 homo sapien
					P15800 rattus norv
					Q61292 mus musculu
					P27512 mus musculu
					Q28203 bos taurus
					P25942 homo sapien
					Q61555 mus musculu
					P55268 homo sapien
					P35556 homo sapien
					Q61789 mus musculu
					Q61001 mus musculu
					Q16787 homo sapien
					Q64716 rattus norv
					P07942 homo sapien
					P36941 homo sapien
					P14616 homo sapien
					P15312 hordeum vul
					P02469 mus musculu
					P24062 rattus norv
					P10969 triticum ae
					Q95209 o sortilin
					Q01279 mus musculu
					P22105 homo sapien
					P26371 homo sapien
					P11219 oryza sativ
					P49901 homo sapien
					P35444 rattus norv
					P11584 drosophila
					P10968 triticum ae

RESULT 1

ID	OX40_MOUSE	STANDARD;	PRT;	272 AA.
AC	P47741;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).			
GN	TNFRSF4 OR TXGP1 OR OX40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=BA1B/C;			
RX	MEDLINE=94044750; PubMed=8228223;			
RA	Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,			
RA	Claassen E., Noelle R.J., Fell H.;			
RT	"Cloning of mouse OX40: a T cell activation marker that may mediate			
RT	T-B cell interactions."			
RL	J. Immunol. 151:5261-5271(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95255413; PubMed=7737295;			
RA	Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,			
RA	Barclay A.N.;			
RT	"Gene structure and chromosomal localization of the mouse homologue			
RT	of rat OX40 protein."			
RL	Eur. J. Immunol. 25:926-930(1995).			
CC	-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
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DR	EMBL; 221674; CAA79772.1; -			
DR	EMBL; X85214; CAA59476.1; -			
DR	HSP; P25942; 1CDF			
DR	MGD; MGI:104512; Tnfrsf4.			
DR	InterPro; IPR001368; -			
DR	Pfam; PF00020; TNFR_C6; 3.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.			
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;			
KW	Signal.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	272	OX40L RECEPTOR.
FT	DOMAIN	20	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	212	236	POTENTIAL.

ALIGNMENTS

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FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT REPEAT 144 144 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 20.1%; Score 143; DB 1; Length 272;
Best Local Similarity 27.8%; Pred. No. 1.8e-06;
Matches 40; Conservative 8; Mismatches 44; Indels 52; Gaps 7;

QY 14 LLLGTGTAR--CCRVHT-----TRCRD-YPG-----EECCSEWDCMCVQPEFHCGDPC-- 60
D 14 LALLGTARLLNCVRYTPSGHKHCKRCQCPGHGMYRCDHTRDTLC-----HPCET 65
QY 61 -----CCTCRHP-----CPCGGVOSQKFGFQCID 89
D 66 GFYNEAVNYDTCKQCQCNHRSGSELKQNCPTQDTVCRCPGTQPRQDSGYKLGVDVCP 125
QY 90 CASGTFSGGHEGCKEPTDCTQFG 113
D 126 CPFGHSPGNQACKPWTNCTLSG 149

RESULT 2
OX40_RAT
ID OX40_RAT STANDARD; PRT; 271 AA.
AC PI5725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RA MEDLINE=90214614; PubMed=2157591;
RX Mallett S., Fossum A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
lymphocytes -- a molecule related to nerve growth factor receptor."
RL EMBO J. 9:1063-1068(1990).
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
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DR EMBL; X17037; CAA34897.1; -.
DR PIR; S08036; S08036.
DR PIR; S12783; S12783.
DR HSP; P25942; ICDP.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
FT SIGNAL 1 19 POTENTIAL.
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FT CHAIN 20 271 OX40L RECEPTOR.
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 235 POTENTIAL.
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 164 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 102 TNFR-CYS 2.
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 124 164 TNFR-CYS 4.
FT CARBOHYD 143 143 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 19.8%; Score 141; DB 1; Length 271;
Best Local Similarity 29.3%; Pred. No. 2.8e-06;
Matches 44; Conservative 9; Mismatches 53; Indels 44; Gaps 8;

QY 1 ORPTGGPGCGPGRLLLG--TGTDARCCRVHT-----RCCRD-YPGEECCSEWD----- 46
D 6 QOPT-----AFLLGLSLGVTVKNCVDTYPSGHKCCRCQCPGHGMYRCDHTRDTV 58
QY 47 CMCVQPEFHCG-----DPC--CCTCRHH-----PCPPGQGVQSGKFSF 83
D 59 CHCEPGFYNEAVNYDTCKQCQCNHRSGSELKQNCPTEDTVCCRCGTQPRQDSHKL 118
QY 84 GFQCIDCASCTFSGGHEGCKEPTDCTQFG 113
D 119 GVDVCPGPHGFGSPGNSQACKPWTNCTLSG 148

RESULT 3
41BB_MOUSE
ID 41BB_MOUSE STANDARD; PRT; 256 AA.
AC P20334;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).
GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89184547; PubMed=2784565;
RA Kwon B.S., Weissman S.M.;
RT "cDNA sequences of two inducible T-cell genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94179805; PubMed=8133039;
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT "Genomic organization and chromosomal localization of the T-cell
antigen 4-1BB."
RL J. Immunol. 152:2256-2262(1994).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 25-29.
RX MEDLINE=93139510; PubMed=7678621;
RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
RA Kwon B.S.;
RT "Inducible T cell antigen 4-1BB. Analysis of expression and
function."
RL J. Immunol. 150:771-781(1993).
CC -!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
CC ACTIVE DURING T CELL ACTIVATION.
CC -!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
CC ASSOCIATES WITH P56-LCK.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
CC -!- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
CC -!- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
```





K; Loetscher, H.; Schlaeger, E.J.; Lamm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990

A;Residues: 1-474 <LEW>  
A:Cross-references: GR:M60469: NID:α199827: PTDN:AAA39752.1: PTD:α199828

A>Title: Purification and partial amino acid sequence analysis of two distinct tumor  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40;65-69;136-141;300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A>Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden  
A:Reference number: A35010; MUID:90110215  
A:Accession: B35010  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kuhnert, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A>Title: Cloning, sequencing and partial functional characterization of the 5' region  
A:Reference number: I38094; MUID:95121934  
A:Accession: I38094  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:Cross-references: GDB:I25914; OMIM:191191  
A:Map position: lp36.2-lp36.2  
A:Introns: 26/3  
A>Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <WAT>  
F:40-76/Domain: NGF receptor repeat homology <NG1>  
F:78-119/Domain: NGF receptor repeat homology <NG2>  
F:120-162/Domain: NGF receptor repeat homology <NG3>  
F:164-201/Domain: NGF receptor repeat homology <NG4>  
F:262-279/Domain: transmembrane #status predicted <TMN>  
F:280-461/Domain: intracellular #status predicted <INT>  
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.2%; Score 119; DB 1; Length 461;  
Best Local Similarity 26.3%; Pred. No. 0.023;  
Matches 41; Conservative 14; Mismatches 63; Indels 38; Gaps 8;

Qy 34 CGPG---RLLLGTGTDARC-----CRVHTRCCRDYVPGECCSEWD-- 71  
| | | : : : : : : : : : : : : : : : : :  
Db 57 CSPGHAKVFCTKTSDTVCDSCEDSTYTQLWNVPECLSCGRCSSDQVETQACTEQNR 116  
| | | : : : : : : : : : : : : : : : : :  
Qy 72 -CMCVQPEFHC-----GDPCCTTCRHHPCPGGVGVSQGKFSGFCIDCASFTSG-- 122  
| | | : : : : : : : : : : : : : : : : :  
Db 117 ICTC-RPGWCALSKQEGRCLAPLR--KCRPGFGVARPGTETSDVVCKPCAPGTFESNTT 173  
| | | : : : : : : : : : : : : : : : : :  
Qy 123 GHEGHCRTPTDCTQGFELTPFPGNKTHNAVCVGPSP 158  
| | | : : : : : : : : : : : : : : : : :  
Db 174 SSTICRPHQICN----VVAIPGNASHMDAVCTSTSP 205  
| | | : : : : : : : : : : : : : : : : :

RESULT 13  
B38634  
tumor necrosis factor receptor type 2 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
R:Accession: B38634; A40254; S54816  
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A>Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
A:Reference number: A38634; MUID:91187885  
A:Accession: B38634  
A:Molecule type: mRNA  
A:Residues: 1-474 <LEW>  
A:Cross-references: GR:M60469; NID:g199827; PIDN:AAA19752.1; PID:g199828

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
A:Reference number: A40254; MUID:91246168  
A:Accession: A40254  
A:Molecule type: mRNA  
A:Residues: 1-474 <GOO>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R:Kisssonerghis, M.; Followes, R.; Feldmann, M.; Chernajovsky, Y.  
Submitted to the EMBL Data Library, May 1995  
A:Description: Characterization of the promoter region of the murine p75-TNF receptor.  
A:Reference number: S54816  
A:Accession: S54816  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-22 <KIS>  
A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: cytokine receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F:40-77/Domain: NGF receptor repeat homology <NGL>  
F:79-120/Domain: NGF receptor repeat homology <NG2>  
F:166-203/Domain: NGF receptor repeat homology <NG4>  
  
Query Match 12.2%; Score 119; DB 2; Length 474;  
Best Local Similarity 31.0%; Pred. No. 0.023;  
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;  
  
QY 46 DARCCRVHTTCCRDYPERCCSEWDCMCVQPEFHCGDPCCTTC-RHHPCPPGGVQSOG 104  
Db 107 EIRACTKQNRVCAACEAGYCAL-----KTHSGS--CRQCMRLSKCGPGFGVASSR 155  
  
QY 105 KFSEFGQICDCASTFSG--GHEGCHKPWTDTCTQFGFLTPPGNKTNHNCVPCSP 158  
Db 156 APNGNVLCKACAPGTFTSDTSDVCRPHRCS----ILAIPGNASTDAVCAPESP 207  
  
RESULT 14  
A60771  
B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)  
C:Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
EMBO J. 8, 1403-1410, 1989  
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor.  
A:Reference number: S04460; MUID:89356608  
A:Accession: S04460  
A:Molecule type: mRNA  
A:Residues: 1-277 <STA>  
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851  
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
A:Reference number: A60771; MUID:8903941  
A:Accession: A60771  
A:Molecule type: protein  
A:Residues: 21-50 <BRA>  
A:Experimental source: Burkitt lymphoma cell line Raji  
C:Genetics:  
A:Gene: GDB:CD40  
A:Cross-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F:21-193/Domain: extracellular #status predicted <EXT>  
F:194-215/Domain: transmembrane #status predicted <TMN>  
F:216-277/Domain: intracellular #status predicted <CYT>

F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
Query Match 12.1%; Score 118.5; DB 2; Length 277;  
Best Local Similarity 27.7%; Pred. No. 0.018;  
Matches 36; Conservative 10; Mismatches 73; Indels 11; Gaps 5;  
  
QY 34 CGPGRLLGTGTARCCRVHTTCCRDYPG-----BECCSEWDCMCVQPE-FHCGDPCCTT 88  
Db 62 CGSEFFLDWTNRTHC---HQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACES 118  
  
QY 89 C-RHPPCPGGVQSOGKFSFGFCQICDCASTFSGHEG--HCKPWTDTCTQFGFLTVFPG 145  
Db 119 CVLHRSCSPGFGVKQIATGVSDTICEPCVPGFFSNVSSAFKCHPMTSCETKDLVVQQAG 178  
  
QY 146 NKTHNACVCP 155  
Db 179 TNKTDVVCPP 188  
  
RESULT 15  
A33837  
insulin-like growth factor I receptor precursor - rat  
N:Contains: insulin-like growth factor I alpha chain; insulin-like growth factor I be  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 16-Mar-1990 #sequence\_revision 03-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: JC2461; A33837; PC1131  
R:Pedrini, M.T.; Giorgio, F.; Smith, R.J.  
Biochem. Biophys. Res. Commun. 202, 1038-1046, 1994  
A:Title: cDNA cloning of the rat IGF I receptor: Structural analysis of rat and human  
A:Reference number: JC2461; MUID:94324926  
A:Accession: JC2461  
A:Molecule type: mRNA  
A:Residues: 1-1371 <PED>  
R:Werner, H.; Woloschak, M.; Adamo, M.; Shen-Orr, Z.; Roberts Jr., C.T.; LeRoith, D.  
Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989  
A:Title: Developmental regulation of the rat insulin-like growth factor I receptor ge  
A:Reference number: A33837; MUID:90017496  
A:Accession: A33837  
A:Molecule type: mRNA  
A:Residues: 1-364 <WER>  
R:Kurachi, H.; Jobo, K.; Ohta, M.; Kawasaki, T.; Itoh, N.  
Biochem. Biophys. Res. Commun. 187, 934-939, 1992  
A:Title: A new member of the insulin receptor family, insulin receptor-related recept  
A:Reference number: PC1130; MUID:92412145  
A:Accession: PC1131  
A:Molecule type: mRNA  
A:Residues: 913-984, 'PY', 987-1017 <KUR>  
A:Cross-references: GB:D12679; NID:g220918; PIDN:BAA20983.1; PID:g4433359  
C:Superfamily: insulin receptor; protein kinase homology  
C:Keywords: ATP; growth factor receptor; kinase-related transforming protein; transme  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-741/Product: insulin-like growth factor I alpha chain #status predicted <IGA>  
F:742-1371/Product: insulin-like growth factor I beta chain #status predicted <IGB>  
F:937-959/Domain: transmembrane #status predicted <TMN>  
F:971-974/Region: GPXY motif  
F:978-981/Region: NPXY motif  
F:998-1275/Domain: protein kinase homology <KIN>  
F:1006-1014/Region: protein kinase ATP-binding motif  
  
Query Match 11.8%; Score 115.5; DB 2; Length 1371;  
Best Local Similarity 27.18%; Pred. No. 0.087;  
Matches 57; Conservative 22; Mismatches 52; Indels 79; Gaps 20;  
  
QY 8 GAFAA-----LCGLA-----LLCAL-----LQRPCTGGPGCG---PGRL-----L 40  
Db 139 GAIRIEKNADICLSTIDWSLLIDAVSNYIVGNKPP--KEGDLCPGTLEKPMCKETTT 196  
  
QY 41 LGTGTADARCCRVHTTTC---CRDYPGECCSEWDCMCVQPEFHCGDPC-----CTTC 89

C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 15.4%; Score 151; DB 2; Length 271;  
Best Local Similarity 28.5%; Pred. No. 5.2e-05;  
Matches 47; Conservative 12; Mismatches 62; Indels 44; Gaps 8;  
QY 26 QRPTGPGGCGRLLLG--TGTDAACRCVHTT-----RCRD-YPGECCSEWD----- 71  
DB 6 QQPT-----AFLLGLSLGVTVKLVNKVDYTPSGHKCCRCQCGHGVSRCDHTRTDV 58  
QY 72 CMCVQPEFHCG----DPC--CTTCRHH-----PCPGQGVQSGQKFSF 108  
DB 59 CHPCPEGFYNEAVNYDTCKQCTQCNRSGSELKQNCPTPTEDVCQCRPGTPPQDSSHL 118  
QY 109 GRCQIDCASGTSGGHEGCKPWTCTQCGFLTVFPGNKTTHAVC 153  
DB 119 GVDVCPPEGFHSPGNSQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 6  
JC5559  
Lectin-B - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: JC5559  
R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)  
A:Reference number: JC5559; MUID:97290889  
A:Accession: JC5559  
A:Molecule type: protein  
A:Residues: 1-295 <YAM>  
A:Experimental source: root  
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharide  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p  
C:Keywords: glycoprotein  
F:96.139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.2%; Score 139; DB 2; Length 295;  
Best Local Similarity 28.8%; Pred. No. 0.00047;  
Matches 36; Conservative 18; Mismatches 41; Indels 30; Gaps 8;  
QY 20 CALSLGQRPTGGP-----GGCGRLLLGTGTDAACRCVHTTRCCRDYPG-----EECC 67  
DB 133 CGVDFGNRTCPNDLCCSEWGCWGTGEGYCGEGCQSQC---NHQRCGKDFAGRTCLNDLCC 189  
QY 68 SEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGQKFSFGQ-C---IDCASGTFSGG 123  
DB 190 SEWG-WCGSSEAHCGGQCSNCRNRC-----GR-NFGFRTCPNELCCSSGCGWS 238  
QY 124 HEGHC 128  
DB 239 NDAHC 243

RESULT 7  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C:Accession: A46476; A46515  
R:Torres, R.M.; Clark, E.A.  
J. Immunol. 148, 620-626, 1992  
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine B cell-associated surface molecule CD40, long splice form - mouse  
A:Reference number: A46476; MUID:92105763  
A:Accession: A46476  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-305 <TOR>  
A:Cross-references: GB:M83312; NID:g1553058  
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)  
A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0  
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay  
J. Immunol. 149, 3921-3926, 1992  
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A:Reference number: A46515; MUID:93094586  
A:Accession: A46515  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-287, LV' <GR>  
A:Cross-references: GB:M83312; NID:g1553058; PIDN:ANB08705.1; PID:g1553059; GB:M94126  
A:Experimental source: BALB/c, liver  
A:Note: sequence extracted from NCBI backbone (NCBI:P:120357)  
C:Comment: For an alternative splice form, see PIR:A46515.  
C:Comment: For an alternative splice form, see PIR:A46476.  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: alternative splicing; transmembrane protein  
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 13.8%; Score 135.5; DB 2; Length 305;  
Best Local Similarity 26.1%; Pred. No. 0.00091;  
Matches 49; Conservative 10; Mismatches 74; Indels 55; Gaps 8;  
QY 13 LCGIL--ALLCALSLGQRPTGGCGGRLLLGTGTDAAC-- 50  
DB 7 LCALWGCLLTAHLGQCVT----CSDKQYL----HDGCCDLQCPGSRKLTSHCTALEKTQ 58  
QY 51 -----RVHTTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 88  
DB 59 CHPCDSGEFSAQNNREIRHQHRCFNPQGLRVKKEGTAEEDTCTCKEGQHCTSKDCEA 118  
QY 89 C-RHHPCPPGQGVQSGQKFSFGFCIDCASGTFSGGHE--CHCKPWTCTQFGFLTVFPPG 145  
DB 119 CAQHTPCIPGFGVMEMATETTTDTHCPVPGFFSNQSLFEKCYPTWTSCEOKNLEVLQKG 178  
QY 146 NKTHNAVC 153  
DB 179 TSQTNVIC 186

RESULT 8  
MMRTS  
Laminin beta-2 chain precursor - rat  
N:Alternate names: laminin chain B3; S-laminin  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C:Accession: S03539  
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the ne  
A:Reference number: S03539; MUID:89159410  
A:Accession: S03539  
A:Molecule type: mRNA  
A:Residues: 1-1801 <HUN>  
A:Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin  
C:Function:  
A:Description: Interact with cells and with other basement membrane proteins to promo  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellu  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F:36-285/Domain: VI <DOM6>  
F:286-555/Domain: V <DOM5>  
F:286-347/Domain: laminin-type EGF-like homology <LE01>  
F:350-410/Domain: laminin-type EGF-like homology <LE02>  
F:413-470/Domain: laminin-type EGF-like homology <LE03>  
F:473-522/Domain: laminin-type EGF-like homology <LE04>  
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:556-784/Domain: IV <DOM4>

```
QY   121 --SCGHEGHCKPWTDCQTQFGFLTVFPGNKTHNAVCPVGSPPAEPL 163
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    176 QNTSPSARCPHTRCENOGILVEAAPQAOSDITC---KNPLEPL 217

RESULT 10
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
R:Accession: I48854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: I48854; MUID:95178848
A:Accession: I48854
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match          12.3%; Score 120.5; DB 2; Length 459;
Best Local Similarity 30.3%; Pred. No. 0.017;
Matches 37; Conservative 11; Mismatches 57; Indels 17; Gaps 6;

QY   48 RCRVHTTRCDRYPGECCSEWD---CMCVQPEF-----HCGDPCTTC-RHHPCPPQG 98
      ||:||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    77 RTCLSCSSCSSTDOVETRACTKQNRYCAGEAGRYCALKTSHSG--CRCQMRLSKCGGF 134

QY   99 GVQSOGNFSGFCIDCASGTESG--GHEHGCKPWTDCTQFGFLTVPGNKTHNAVCPVG 156
      ||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    135 GVASSRAPNGVLKACAPGTFSDTSSTDVCPRPHRICS----ILAIPGNASTDAVCAPE 190

QY   157 SP 158
      ||
Db    191 SP 192

RESULT 11
S53869
laminin beta-2 chain precursor (version 2) - human
N:Alternate names: s-laminin
C:Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
C:Accession: S53869
R:Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Sariola, H.; Tr
Matrix Biol. 14, 489-497, 1994
A:Title: The human laminin beta-2 chain (S-laminin); structure, expression in fetal
A:Reference number: S53869
A:Accession: S53869
A:Molecule type: mRNA
A:Residues: 1-1798 <II>
C:Genetics:
A:Gene: GDB:LAMB2
A:Cross-references: GDB:l32363; OMIM:150325
A:Map position: 3p21.3-p21.2
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-1798/Product: laminin beta-2 chain #status predicted <MAT>
F:283-344/Domain: laminin-type EGF-like homology <LEO1>
F:347-407/Domain: laminin-type EGF-like homology <LEO2>
F:410-467/Domain: laminin-type EGF-like homology <LEO3>
F:470-519/Domain: laminin-type EGF-like homology <LEO4>
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LEO5>
F:783-828/Domain: laminin-type EGF-like homology <LEO6>
F:831-874/Domain: laminin-type EGF-like homology <LEO7>
F:877-924/Domain: laminin-type EGF-like homology <LEO8>
F:927-983/Domain: laminin-type EGF-like homology <LEO9>
```



C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C;Accession: I37552  
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat  
Eur. J. Immunol. 24, 677-683, 1994  
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A;Reference number: I37552; MUID:94170844  
A;Accession: I37552  
A;Status: preliminary; translated from GB/EMBL/DDBBJ  
A;Molecule type: mRNA  
A;Residues: 1-277 <RES>  
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958  
C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match            16.5%; Score 162; DB 2; Length 277;  
Best Local Similarity 29.7%; Pred. No. 7.4e-06;  
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALGGLALLCALSLG-----QRPTGGPGCGPGRLLLTGTGDARCCRVHT 54  
||| ||| ||| ||| ||| : : : : : : : : : :  
Dd 4 GARRLRGPCAAALLLLGLSLTVTVLHCVGDTYPSNRDCHECR--PGNGVMVSRCSRSQN 61  
||| ||| ||| ||| ||| : : : : : : : : : :

QY 55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCD---PCCTTCRRHHPPCPGGVGQSQGKFSF 108  
||| ||| ||| ||| ||| : : : : : : : : : :  
Dd 62 TVCRPCGGFGFYNDVVYSKPKCPCTMCNLRSERKQLTATQDTVCRAGTQPLDSYKP 121  
||| ||| ||| ||| ||| : : : : : : : : : :

QY 109 GFQCICDASGFSGHGCHCKPWTDCTQFGELTVFPGNKTHNAVCPGPSPPA 160  
||| ||| ||| ||| ||| : : : : : : : : : :  
Dd 122 GVDCAPCPPGHFSGDNQACKPWTNCTLAGKHTLOPASNSSDAICEDRPDPA 173  
||| ||| ||| ||| ||| : : : : : : : : : :

RESULT 3  
I38426  
lymphocyte activation-induced receptor ILA precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C;Accession: I38426; JT0752  
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R  
Eur. J. Immunol. 24, 2219-2227, 1994  
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A;Reference number: I38426; MUID:94374434  
A;Accession: I38426  
A;Status: preliminary; translated from GB/EMBL/DDBBJ  
A;Molecule type: mRNA  
A;Residues: 1-255 <RES>  
A;Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321  
R;Schwarz, H.; Tuckwell, J.; Lotz, M.  
Gene 134, 295-298, 1993  
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne  
A;Reference number: JT0752; MUID:94085794  
A;Accession: JT0752  
A;Molecule type: mRNA  
A;Residues: 1-106,'R',108-255 <SCH>  
C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neuro  
C;Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <NAIT>  
F;187-213/Domain: transmembrane #status predicted <TMN>  
F;138,149/Binding site: carbohydate (Asn) (covalent) #status predicted  
F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict  
F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match            16.4%; Score 160.5; DB 2; Length 255;  
Best Local Similarity 30.9%; Pred. No. 9.2e-06;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTGDARCCRVHTTRCCRDYPG-----EECCS-----EWDCCMVQVEFFHCGRP 84  
||| ||| ||| ||| ||| : : : : : : : : : :  
Db 48 CPPNSFSAGG--QTCDI-----CROCKGVFTTRKCESTSNACDC--TFGFHCLGA 97  
||| ||| ||| ||| ||| : : : : : : : : : :

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QY   85 CQTTCRHHCPPGQGVQSQQKSFSGFCIDCASGTFFSGHGCHKPWTDTCTQFGFLTVPF 144
      G S M I : : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db   98 GCSC--EQDCKQGQLTKKG-----CKDCCGFTFNQDKRGICRPWNTCSLDGKSVLVN 149

QY   145 GNKTHNAVCPG-----SPPA---EP 162
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   150 GTKERDVVCGPSPADLSPGASSVTPAPAREP 181

RESULT 4
B32393
T-cell antigen 4-lbb precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: B32393; I48879
R:Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A:Title: cDNA sequence of two inducible T-cell genes.
A:Reference number: A32393; MUID:89184547
A:Accession: B32393
A:Molecule type: mRNA
A:Residues: 1-256 <KWOW>
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-lb
A:Reference number: I48879; MUID:94179805
A:Accession: I48879
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-256 <RES>
A:Cross-references: EMBL:U02567; NID:gl117783; PIDN:AAA93113.1; PID:g409178
C:Genetics:
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-256/Product: 4-lbb protein #status predicted <MAT>

Query Match          15.6%; Score 153; DB 2; Length 256;
Best Local Similarity 31.5%; Pred. No. 3.5e-05;
Matches 40; Conservative 17; Mismatches 52; Indels 18; Gaps 7;

QY   34 CGPGRL-LLGTTGDARCRVHTTRCCRDYPGECCSEW---DCMGVQPPEFHCGDPCTTC 89
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   47 CPPTFSSTGGQPNCRIV----CAGYFRFKFCSSSTHNAECEIE-GFHLGLGPQCTRC 101

QY   90 RHHPCCPPGQGVQSQRKSFSGFCIDCASGTFFSGGH-EGHCKPWTDTCTQFGFLTVPFNKT 148
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   102 -BKDCRPGQLTKQG-----CKTCSLIGTFNDQNGTGVCPRWTNCSLDGRSVLKGTTE 153

QY   149 HNAVCP 155
      : | | |
Db   154 KDVVCGP 160

RESULT 5
SI2783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: SI2783; S08036
R:Mallett, S.; Fossom, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of
A:Reference number: SI2783; MUID:90214614
A:Accession: SI2783
A:Molecule type: mRNA
A:Residues: 1-271 <NAL>
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C:Superfamily: CD27 antigen; NGF receptor repeat homology

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FT DOMAIN 831 876 LAMININ EGF-LIKE 7.
FT DOMAIN 877 946 LAMININ EGF-LIKE 8.
FT DOMAIN 927 985 LAMININ EGF-LIKE 9.
FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.
FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.
FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.
FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.
FT DOMAIN 1190 1409 DOMAIN 11.
FT DOMAIN 1410 1442 DOMAIN ALPHA.
FT DOMAIN 1443 1798 DOMAIN I.
FT DOMAIN 1253 1319 COILED COIL (POTENTIAL).
FT DOMAIN 1472 1526 COILED COIL (POTENTIAL).
FT DOMAIN 1577 1790 COILED COIL (POTENTIAL).
FT DISULFID 283 292 BY SIMILARITY.
FT DISULFID 285 310 BY SIMILARITY.
FT DISULFID 312 321 BY SIMILARITY.
FT DISULFID 324 344 BY SIMILARITY.
FT DISULFID 347 356 BY SIMILARITY.
FT DISULFID 349 374 BY SIMILARITY.
FT DISULFID 377 386 BY SIMILARITY.
FT DISULFID 389 407 BY SIMILARITY.
FT DISULFID 410 423 BY SIMILARITY.
FT DISULFID 412 438 BY SIMILARITY.
FT DISULFID 440 449 BY SIMILARITY.
FT DISULFID 452 467 BY SIMILARITY.
FT DISULFID 470 484 BY SIMILARITY.
FT DISULFID 472 491 BY SIMILARITY.
FT DISULFID 493 502 BY SIMILARITY.
FT DISULFID 505 519 BY SIMILARITY.
FT DISULFID 783 795 BY SIMILARITY.
FT DISULFID 785 802 BY SIMILARITY.
FT DISULFID 804 813 BY SIMILARITY.
FT DISULFID 816 828 BY SIMILARITY.
FT DISULFID 831 843 BY SIMILARITY.
FT DISULFID 833 850 BY SIMILARITY.
FT DISULFID 852 861 BY SIMILARITY.
FT DISULFID 864 874 BY SIMILARITY.
FT DISULFID 877 886 BY SIMILARITY.
FT DISULFID 879 893 BY SIMILARITY.
FT DISULFID 896 905 BY SIMILARITY.
FT DISULFID 908 924 BY SIMILARITY.
FT DISULFID 927 943 BY SIMILARITY.
FT DISULFID 929 954 BY SIMILARITY.
FT DISULFID 956 965 BY SIMILARITY.
FT DISULFID 968 983 BY SIMILARITY.
FT DISULFID 986 1000 BY SIMILARITY.
FT DISULFID 988 1007 BY SIMILARITY.
FT DISULFID 1010 1019 BY SIMILARITY.
FT DISULFID 1022 1035 BY SIMILARITY.
FT DISULFID 1095 1107 BY SIMILARITY.
FT DISULFID 1097 1114 BY SIMILARITY.
FT DISULFID 1116 1125 BY SIMILARITY.
FT DISULFID 1128 1140 BY SIMILARITY.
FT DISULFID 1143 1155 BY SIMILARITY.
FT DISULFID 1145 1162 BY SIMILARITY.
FT DISULFID 1164 1173 BY SIMILARITY.
FT DISULFID 1176 1187 BY SIMILARITY.
FT DISULFID 1190 1197 INTERCHAIN (PROBABLE).
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
FT DISULFID 1797 1797 INTERCHAIN (PROBABLE).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1348 1348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 914 914 R -> G (IN REF. 2).
FT CONFLICT 1179 1179 G -> A (IN REF. 2).
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1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;

Query Match

11.4%; Score 111.5; DB 1; Length 1798;

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Best Local Similarity 23.2%; Pred. No. 0.018;
Matches 55; Conservative 10; Mismatches 65; Indels 107; Gaps 13;
QY 8 GAFRALC----GLALLCALSLGQR-----PTGGPGCGGGRLLLTGTGDARC----- 49
Db 837 GALSLEKESGQCLCRGTGATGLRCDRCQRCQWGFPSCRP-----CVCNGHAD 884
QY 50 -CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFFHCGD--PCCTTCRHHPHPCPPGQGVQ--- 101
Db 885 ECNHTGTACLCGRDHTGGEHCEH-----CI-AGFHRDRLPYGGQCRPCPCPGSGQRHF 939
QY 102 ----SQKFS-----FGQCIDCASGTF----- 120
Db 940 ATSCHQDEYSQQIIVCHCRAGYTGLRCEACAPGHFGDPSRPGRCQLCECSGNIDPMDPDA 999
QY 121 -----SGGHEGHCCKPWTDTCTQFGFLTVPGNKTHNAV-----VPGSPPAE 161
Db 1000 CDPTGGQCLRLCHHTGEPHCAHCRP-----GFHGQAAROSCHRCTCNLLGTNPQQ 1049
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Search completed: September 4, 2001, 16:15:27  
Job time: 1139 sec





RT with its receptor CD40." ;  
 RL Protein Sci. 7:1124-1135(1998).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGER/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry; htm".  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".  
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 CC -----  
 CC EMBL: X60592; CAA43045.1; -  
 CC PIR: S04460; S04460.  
 CC FDB: ICDF; 01-APR-97.  
 CC MIM: 109535; -  
 CC InterPro: IPR001368; -  
 CC PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 CC PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 CC Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
 KW 3D-structure.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 277 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT DISULFID 26 37  
 FT DISULFID 38 51  
 FT DISULFID 41 59  
 FT DISULFID 62 77  
 FT DISULFID 83 103  
 FT DISULFID 105 119  
 FT DISULFID 111 116  
 FT DISULFID 125 143  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;  
 Query Match 12.1%; Score 118.5; DB 1; Length 277;  
 Best Local Similarity 27.7%; Pred. No. 0.0011;  
 Matches 36; Conservative 10; Mismatches 73; Indels 11; Gaps 5;  
 QY 34 CGPGRLLGTGTDAACRCVHTTRCCRDYGP-----EECCSEWDCMCVQPE-FHCDDPQCTT 88  
 DB 62 CGSEFLDTWNRTHC---HQHYKCDPNLGRVQOKTSETDICTCEGWHCTSEACES 118  
 QY 89 C-RHHFCPPCGQVQSGKSFQFCGDCASGTFSGGHEG--HCKPWTDCQFGLTVFPG 145  
 DB 119 CVLHRSCTPGVGVKQIATGVSDTICEPCPVGVFFSNVSSAFKCHPWTSCETKDLVQVQAG 178  
 QY 146 NKTHNAVCPV 155  
 DB 179 TNKTDVVCVP 188  
 RESULT 14  
 IGIR\_RAT  
 ID IGIR\_RAT STANDARD; PRT: 1370 AA.  
 AC P24062;  
 DT 01-NOV-1992 (Rel. 21, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).  
 GN IGFI.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95277910; PubMed=7758167;  
 RA Du J., Delafontaine P.;  
 RT "Inhibition of vascular smooth muscle cell growth through antisense  
 RL transcription of a rat insulin-like growth factor I receptor cDNA.";  
 RN Circ. Res. 76:963-972(1995).  
 CC [2]  
 RP SEQUENCE OF 1-364 FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=90017496; PubMed=2477843;  
 RA Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,  
 RA Leroith D.;  
 RT "Developmental regulation of the rat insulin-like growth factor I  
 RL receptor gene.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).  
 CC [3]  
 RP SEQUENCE OF 913-1017 FROM N.A.  
 RX MEDLINE=92412145; PubMed=1530648;  
 RA Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;  
 RT "A new member of the insulin receptor family, insulin  
 RL receptor-related receptor, is expressed preferentially in the  
 RL kidney.";  
 CC Biochem. Biophys. Res. Commun. 187:934-939(1992).  
 CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)  
 CC WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A  
 CC TYROSINE-PROTEIN KINASE ACTIVITY.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE  
 CC BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-  
 CC BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-  
 CC PROTEIN KINASES.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL: L29232; AAA43392.1; -  
 CC EMBL: M27293; AAA41384.1; -  
 CC PIR: A33837; A33837.  
 CC HSP: P06213; IIRK.  
 CC InterPro: IPR000494; -  
 CC InterPro: IPR000719; -  
 CC InterPro: IPR001245; -  
 CC InterPro: IPR001777; -  
 CC InterPro: IPR002011; -  
 CC InterPro: IPR002174; -  
 CC Pfam: PF00757; Furin-like; 1.  
 CC Pfam: PF01030; Recep\_L\_domain; 2.  
 CC Pfam: PF00041; fn3; 2.  
 CC Pfam: PF00069; pkinase; 1.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;  
 KW

KW Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 740  
FT CHAIN 742 1370  
FT DOMAIN 742 936  
FT TRANSMEM 937 960  
FT DOMAIN 961 1370  
FT DOMAIN 608 829  
FT DOMAIN 830 929  
FT DOMAIN 1000 1275  
FT NP\_BIND 1006 1014  
FT BINDING 1034 1034  
FT ACT\_SITE 1136 1136  
FT MOD\_RES 1166 1166  
FT CARBOHYD 51 51  
FT CARBOHYD 102 102  
FT CARBOHYD 135 135  
FT CARBOHYD 245 245  
FT CARBOHYD 314 314  
FT CARBOHYD 418 418  
FT CARBOHYD 439 439  
FT CARBOHYD 535 535  
FT CARBOHYD 608 608  
FT CARBOHYD 623 623  
FT CARBOHYD 641 641  
FT CARBOHYD 748 748  
FT CARBOHYD 757 757  
FT CARBOHYD 765 765  
FT CARBOHYD 901 901  
FT CARBOHYD 914 914  
FT CONFLICT 985 986  
SQ SEQUENCE 1370 AA; 155395 MW; A5946897A41CB145 CRC64;

Query Match 11.8%; Score 115.5; DB 1; Length 1370;  
Best Local Similarity 27.1%; Pred. No. 0.0066;  
Matches 57; Conservative 22; Mismatches 52; Indels 79; Gaps 20;

Qy 8 GAFA-----LCGLA-----LLCAL-----LQRPCTGPGCG-----PGR-----L 40  
Db 139 GAIRTEKNADLCYLTIDWSLIDAVSNYIVGNKPP--KEGDLCPGTLEKPMCKETT 196  
Qy 41 LGTGTDAACRHHVTRC---CRDYPGECCSEWDCMCVQPEHCGDPC-----CTTC 89  
Db 197 INNEYNYKWT--TNRCQKMPSCVCGKRACTE--NNECCHPE--CLGSCHTPPDNTTCVAC 251  
Qy 90 RHH-----PCPPGQGVQSGKFSEF-GFQCID---CAS-----GTFSGG---HEGHCK 129  
Db 252 RHYHYKGVCPACPP-----GTVRFEGWRCVDRDFCANIPNAESSDSGDPVIHDGEC- 303  
Qy 130 PWTDTQTGFLTVPGNKNTHAVCVGSGPP 159  
Db 304 -MQECPG-GFIR-----NSTQSMYICPCGP 327

RESULT 15  
LMB2\_HUMAN STANDARD; PRT; 1798 AA.  
AC P55268; Q16321;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).  
GN LMB2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95213013; PubMed=7698745;

RA Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,  
RT Champlaud M.F., Burgeson R.E., Albrechtsen R.;  
FT "Human beta 2 chain of laminin (formerly S chain): cDNA cloning,  
RL chromosomal localization, and expression in carcinomas.";  
RN Genomics 24:243-252(1994).  
RX SEQUENCE FROM N.A.  
RP MEDLINE=95316263; PubMed=7795887;  
RA Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,  
RT Sariola H., Tryggvason K.;  
FT "The human laminin beta 2 chain (S-laminin): structure, expression in  
RL fetal tissues and chromosomal assignment of the LAMB2 gene.";  
CC Matrix Biol. 14:489-497(1995).  
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, AND ORGANIZATION OF  
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
CC COMPRISING ONE LONG AND THREE SHORT ARMS WITH GLOBULES AT EACH END.  
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC  
CC CLEFT OF THE NEUROMUSCULAR JUNCTION.  
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC -!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
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CC EMBL; 268155; CAA92279.1; JOINED.  
DR EMBL; 268156; CAA92279.1; JOINED.  
DR EMBL; X79683; CAA56130.1; --  
DR EMBL; S77512; AAB34682.2; --  
DR HSP; P02468; IKLO.  
DR MIM; 150325; --  
DR InterPro; IPR000561; --  
DR InterPro; IPR001886; --  
DR InterPro; IPR002049; --  
DR Pfam; PF00053; laminin\_EGF; 13.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR PROSITE; PS00022; EGF\_1; 10.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 32  
FT CHAIN 33 1798  
FT DOMAIN 33 280  
FT DOMAIN 281 552  
FT DOMAIN 283 346  
FT DOMAIN 347 409  
FT DOMAIN 410 469  
FT DOMAIN 470 521  
FT DOMAIN 522 552  
FT DOMAIN 553 781  
FT DOMAIN 782 1190  
FT DOMAIN 783 830  
FT DOMAIN 830 830







DR Pfam: PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS0050; TNFR\_NGFR\_2; 1.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 >269 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 20 215 POTENTIAL.  
 FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 269 269  
 SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;  
 Query Match 12.5%; Score 122.5; DB 1; Length 269;  
 Best Local Similarity 28.7%; Pred. No. 0.00049;  
 Matches 37; Conservative 9; Mismatches 70; Indels 13; Gaps 5;  
 QY 34 CGPRLLLGTGTDARCCRVHTRCRDYPGECCSEWD-----CMCVQPEFHCGDPCCT 87  
 DB 62 CGKGEFTWNRKYC---HEHRYCNPNLRLRIQSEGLTNTDTICVCVEGO-HCTSHRCE 117  
 QY 88 TCRHHP-CPPGGVQSQGKSFSGFCIDCASGTFSGGHEG--HCKPMTDCTQFGELTVFP 144  
 DB 118 SCTPHSLCPGFGVQKIATGLLTDVCEPLGFFSNVSAFEKCHRWTSCKRKGGLVQHV 177  
 QY 145 GNKTHNAVY 153  
 DB 178 GTNKTDVVC 186  
 RESULT 10  
 TNRC\_HUMAN  
 ID TNRC\_HUMAN STANDARD; PRT; 435 AA.  
 AC P36941;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR  
 DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).  
 GN LTR OR TNFR OR TNFRSP3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93252381; PubMed=8486360;  
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
 RT "Construction and evaluation of a hncDNA library of human l2p  
 RT transcribed sequences derived from a somatic cell hybrid.";  
 RL Genomics 16:214-218(1993).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=94225209; PubMed=8171323;  
 RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
 RT "A lymphotoxin-beta-specific receptor."  
 RL Science 264:707-710(1994).  
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC IMMUNE DEVELOPMENT.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC -----  
 DR EMBL; L04270; AAA36757.1; -.  
 DR HSSP; P25942; ICDF.  
 DR MIM; 600979; -.  
 DR InterPro; IPR001368; -.  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS0050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30 POTENTIAL.  
 FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.  
 FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 228 248 POTENTIAL.  
 FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 42 211 4 X TNFR-CYS.  
 FT REPEAT 42 81 TNFR-CYS 1.  
 FT REPEAT 82 124 TNFR-CYS 2.  
 FT REPEAT 125 168 TNFR-CYS 3.  
 FT REPEAT 169 211 TNFR-CYS 4.  
 FT DISULFID 43 58 BY SIMILARITY.  
 FT DISULFID 59 72 BY SIMILARITY.  
 FT DISULFID 62 80 BY SIMILARITY.  
 FT DISULFID 83 98 BY SIMILARITY.  
 FT DISULFID 101 116 BY SIMILARITY.  
 FT DISULFID 104 124 BY SIMILARITY.  
 FT DISULFID 126 132 BY SIMILARITY.  
 FT DISULFID 139 148 BY SIMILARITY.  
 FT DISULFID 142 167 BY SIMILARITY.  
 FT DISULFID 170 185 BY SIMILARITY.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;  
 Query Match 12.4%; Score 121; DB 1; Length 435;  
 Best Local Similarity 26.1%; Pred. No. 0.00094;  
 Matches 43; Conservative 12; Mismatches 66; Indels 44; Gaps 10;  
 QY 34 CGPRLLLGTGTDARCCRVHTRC-----CRDYPGEE---C 66  
 DB 62 CPP-----GTYYSAKCSRIRDTVCATCAENSYNEHNNYLTICQLCRCPDPMVMSLEELAPC 116  
 QY 67 CS--EWDGCMVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FCIDCASGTF 120  
 DB 117 TSKRRITQCR-CQPGMFCAAWALECTHCELLSDCPPGTEAEKDEKGVGNHHCVPCKAGHF 175  
 QY 121 --SGGHEGHCKPTDCTQFGELTVFPKTNNAVCPGSPPAEPL 163  
 DB 176 QNTSSPSARCQPHTRCENOGLEVAAPGTAQSDTTC---KNPLEPL 217  
 RESULT 11  
 TNR2\_HUMAN  
 ID TNR2\_HUMAN STANDARD; PRT; 461 AA.  
 AC P20333;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
 DE BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; PubMed=2160731;







RN REVISION TO 107.  
 RA Schwarz H.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Blood;  
 RX MEDLINE=95347766; PubMed=7622190;  
 RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,  
 RA Kwon B.S.;  
 RL "Characterization of human homologue of 4-lbb and its ligand";  
 RL Immunol. Lett. 45:67-73(1995).  
 CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-LBBL. POSSIBLY  
 CC ACTIVE DURING T CELL ACTIVATION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T  
 CC CELLS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdwl37.htm".  
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 CC -----  
 DR EMBL; U03397; AAA53133.1; -;  
 DR EMBL; LI2984; AAA62478.2; -;  
 DR HSP; P19438; 1EXT.  
 DR MIM; 602250; -;  
 DR InterPro: IPR001368; -;  
 DR Pfam: PF00020; TNFR\_C6; 2;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1;  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 1;  
 KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 255 4-LBB LIGAND RECEPTOR.  
 FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 187 213 POTENTIAL.  
 FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 47 159 3 X TNFR-CYS.  
 FT REPEAT 47 86 TNFR-CYS 1.  
 FT REPEAT 87 118 TNFR-CYS 2.  
 FT REPEAT 119 159 TNFR-CYS 3.  
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;  
 SQ  
 Query Match 16.4%; Score 160.5; DB 1; Length 255;  
 Best Local Similarity 30.9%; Pred. No. 2.4e-07;  
 Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;  
 QY 34 CGPGRLLLTGTDAACRCHVHTTCCRDYGP-----ECCCS-----EWDCCMCVQPEFHCGDP 84  
 Db 48 CPNSSFSSAGG--QRTCDI-----CQCKGVFTRKCSSTSNACDC---TFGFHCLGA 97  
 QY 85 CCTCRHHPCPGQGVQSGKFSFGQCIDCASGTSGGHEGCKPWTDCQTQFGFLTVFP 144  
 Db 98 GCSMC-EQDCKQKQELTKG-----CKDCCFGTNDQKRGICRPWNCSLDGKSLVN 149  
 QY 145 GNKTHNAVCPG-----SPPA---EP 162  
 Db 150 GTRKDVWCGSPADLSPGASSVTPPAPAREP 181  
 RESULT 4  
 ID 41BB\_MOUSE  
 AC P20334;

DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 4-LBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-LBB).  
 GN TNFRSP9 OR ILA OR LY63 OR CD137 OR CD157.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=89184547; PubMed=2784565;  
 RA Kwon B.S., Weissman S.M.;  
 RL "cDNA sequences of two inducible T-cell genes";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=94179805; PubMed=8133039;  
 RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;  
 RL "Genomic organization and chromosomal localization of the T-cell  
 RL antigen 4-LBB";  
 RL J. Immunol. 152:2256-2262(1994).  
 RN [3]  
 RP CHARACTERIZATION, AND SEQUENCE OF 25-29.  
 RX MEDLINE=93139510; PubMed=7678621;  
 RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T.,  
 RA Kwon B.S.;  
 RL "Inducible T cell antigen 4-LBB. Analysis of expression and  
 RL function";  
 RL J. Immunol. 150:771-781(1993).  
 CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-LBBL. POSSIBLY  
 CC ACTIVE DURING T CELL ACTIVATION.  
 CC -1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.  
 CC ASSOCIATES WITH P56-LCK.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.  
 CC -1- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 DR EMBL; J04492; AAA40167.1; -;  
 DR EMBL; U02567; AAA93113.1; -;  
 DR PIR; B32393; B32393.  
 DR HSP; P25942; ICDF.  
 DR MGD; MGI:1101059; Tnfrsf9.  
 DR InterPro: IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
 KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24  
 FT CHAIN 25 256 4-LBB LIGAND RECEPTOR.  
 FT DOMAIN 25 187 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 188 208 POTENTIAL.  
 FT DOMAIN 209 256 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 17 159 4 X TNFR-CYS.  
 FT REPEAT 17 45 TNFR-CYS 1.  
 FT REPEAT 46 85 TNFR-CYS 2.  
 FT REPEAT 86 117 TNFR-CYS 3.  
 FT REPEAT 118 159 TNFR-CYS 4.  
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;  
 SQ



GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: September 4, 2001, 16:15:26 ; Search time 43.78 Seconds  
(without alignments)  
128.321 Million cell updates/sec

Title: us-09-512-363-2\_copy\_1\_164

Perfect score: 979

Sequence: 1 MAQHGAMGAFRALCGLALC.....GNKTHNAVCPGSPAPPLG 164

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	162	16.5	272	1	OX40_MOUSE
2	162	16.5	277	1	OX40_HUMAN
3	160.5	16.4	255	1	41BB_HUMAN
4	153	15.6	256	1	41BB_MOUSE
5	151	15.4	271	1	OX40_RAT
6	135.5	13.8	289	1	CD40_MOUSE
7	134.5	13.7	1801	1	LMB2_RAT
8	127.5	12.5	1799	1	LMB2_MOUSE
9	122.5	12.5	269	1	CD40_BOVIN
10	121	12.4	435	1	TNRC_HUMAN
11	121	12.4	461	1	TNR2_HUMAN
12	119	12.2	474	1	TNR2_MOUSE
13	118.5	12.1	277	1	CD40_HUMAN
14	115.5	11.8	1370	1	IG1R_RAT
15	111.5	11.4	1798	1	LMB2_HUMAN
16	110.5	11.3	2907	1	FN2_MOUSE
17	109.5	11.2	2531	1	NTC1_MOUSE
18	109	11.1	3635	1	LM5_MOUSE
19	108.5	11.1	1373	1	IG1R_MOUSE
20	106.5	10.9	2911	1	FN2_HUMAN
21	105	10.7	1172	1	TSP2_HUMAN
22	104.5	10.7	684	1	FBL1_CHICK
23	102.5	10.5	956	1	TSP3_MOUSE
24	102	10.4	186	1	AG13_WHEAT
25	101.5	10.4	1367	1	IG1R_HUMAN
26	101.5	10.4	2318	1	NTC3_MOUSE
27	101	10.3	4543	1	LRP1_CHICK
28	100.5	10.3	2531	1	NTC1_RAT
29	100	10.2	581	1	IRR_RAT
30	100	10.2	1106	1	STC_DROME
31	99.5	10.2	169	1	KRUA_HUMAN
32	99.5	10.2	227	1	AG1_ORYSA
33	99.5	10.2	2569	1	LM3_MOUSE

RESULT 1					
OX40_MOUSE					
ID	OX40_MOUSE	STANDARD;	PRT;	272 AA.	
AC	P47741;				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).				
GN	TNFRSF4 OR TXGP1 OR OX40.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C;				
RX	MEDLINE=94044750; PubMed=8228223;				
RA	Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,				
RA	Claassen E., Noelle R.J., Fell H.;				
RT	"Cloning of mouse OX40: a T cell activation marker that may mediate				
RT	T-B cell interactions."				
RL	J. Immunol. 151:5261-5271(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95255413; PubMed=7737295;				
RA	Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,				
RA	Barclay A.N.;				
RT	"Gene structure and chromosomal localization of the mouse homologue				
RT	of rat OX40 protein."				
RL	Eur. J. Immunol. 25:926-930(1995).				
CC	-I- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.				
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; Z21674; CAA79772.1; -				
DR	EMBL; X85214; CAA59476.1; -				
DR	HSSP; P25942; ICDF.				
DR	MGI; M104512; Tnfrsf4.				
DR	InterPro; IPR001368; -				
DR	Pfam; PF00020; TNFR_C6; 3.				
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.				
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.				
DR	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;				
Signal.					
KW	SIGNAL	1	19	POTENTIAL.	
FT	CHAIN	20	272	OX40L RECEPTOR.	
FT	DOMAIN	20	211	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	212	236	POTENTIAL.	

34	99	10.1	213	1	AG12_WHEAT	P02876	triticum ae
35	99	10.1	454	1	LRP1_HUMAN	Q07954	homo sapien
36	98.5	10.1	755	1	COMP_RAT	P35444	rattus norv
37	98.5	10.1	2139	1	CRB_DROME	P10040	drosophila
38	98	10.0	212	1	AG1_HORVU	P15312	hordeum vul
39	97.5	10.0	416	1	NGFR_CHICK	P18519	gallus gall
40	97.5	10.0	1713	1	LM3_HUMAN	Q16787	homo sapien
41	97	9.9	2871	1	FBNI_BOVIN	P98133	bos taurus
42	96	9.8	212	1	AG11_WHEAT	P10968	triticum ae
43	96	9.8	4289	1	TENX_HUMAN	P22105	homo sapien
44	95.5	9.8	415	1	TNRC_MOUSE	P50284	mus musculu
45	95.5	9.8	1210	1	EGFR_MOUSE	Q01279	mus musculu

ALIGNMENTS

```

CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL).
A -> G (IN REF. 2).
SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match
Best Local Similarity 16.58; Score 162; DB 1; Length 272;
Matches 45; Conservative 28.3%; Pred. No. 1.9e-07;
Matches 11; Mismatches 51; Indels 52; Gaps 7;

QY 39 LLLGTGTDAR---CRVHT---TRCRRD-YPG-----ECCSEWDCMVQPEFHCGDPC-- 85
DB 14 LALLVGTARLNCVKHTYPSGHHKCRQCQGHGMSVRCDHTRDTLC-----HPCET 65
QY 86 -----CTTCRRHP-----CPGGGVQSGKFSGFQCID 114
DB 66 GFYNEAVNYDFCKCTOCNHRSGSELKNCNCTPTQDTCVCRREGTQPRQDSGYKLGVDVCP 125
QY 115 CASTFTFGGHEGHCQPTWDTCTQFGFLTVFPCKTHNAVC 153
DB 126 CPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 2
OX40_HUMAN
ID OX40_HUMAN STANDARD; PRT; 277 AA.
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
GN TNFRSF4 OR TXGPIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=94170844; PubMed=7510240;
RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
RA Hummel M., Fonatsch C., Stein H.;
RT "The human OX40 homolog: cDNA structure, expression and chromosomal
RT assignment of the ACT35 antigen."
RL Eur. J. Immunol. 24:677-683(1994).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=95219871; PubMed=7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA Watson M.L., Selidin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of
RT its activities on OX40 receptor."
RL Circ. Shock 44:30-34(1994).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
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CC or send an email to license@isb-sib.ch).
CC EMBL; X75962; CAA53576.1; -

```

[illegible]



A>Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal

A:Reference number: S53869

A:Accession: S53869

A:Molecule type: mRNA

A:Residues: 1-1798 <II>

C:Genetics:

A:Gene: GDB:LAMB2

A:Cross-references: GDB:132363; OMIM:150325

A:Map position: 3p21.3-3p21.2

C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer

F:1-32/Domain: signal sequence #status predicted <SIG>

F:33-1798/Product: laminin beta-2 chain #status predicted <MAT>

F:283-344/Domain: laminin-type EGF-like homology <LE01>

F:347-407/Domain: laminin-type EGF-like homology <LE02>

F:410-467/Domain: laminin-type EGF-like homology <LE03>

F:470-519/Domain: laminin-type EGF-like homology <LE04>

F:522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>

F:783-828/Domain: laminin-type EGF-like homology <LE06>

F:831-874/Domain: laminin-type EGF-like homology <LE07>

F:877-924/Domain: laminin-type EGF-like homology <LE08>

F:927-983/Domain: laminin-type EGF-like homology <LE09>

F:986-1035/Domain: laminin-type EGF-like homology <LE10>

F:1038-1092/Domain: laminin-type EGF-like homology <LE11>

F:1095-1140/Domain: laminin-type EGF-like homology <LE12>

F:1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match 15.2%; Score 112; DB 2; Length 1798;

Best Local Similarity 24.9%; Pred. No. 0.058;

Matches 44; Conservative 8; Mismatches 47; Indels 78; Gaps 10;

QY 5 CRVHTRC--CRDYPGECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPGGQVQ--- 56

DB 886 CWNTHGACLGCRDHTGHEHCR---CI-AGFHPYGGQCRPCPCPEGPGSRHF 939

QY 57 ----SOKGES-----FGQCIDCASGTF----- 75

DB 940 ATSCHODEYSQQIVCHCRAGYTGRLCEACAPGHGDPSPGRCQLCESGNIDPMDPDA 999

QY 76 -----SGGHEGHCKPWDTQFGPLTVFPNGKNTNAVQ-VPGSPPAE 116

DB 1000 CDPHTGQCLRLHHTGEPHCAHKP-----GPHQAARQSCHRCTNLLGTNPQQ 1049

RESULT 13

154182

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000

C:Accession: I54182

R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P. Genomics 16, 214-218, 1993

A>Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq

A:Reference number: I54182; MUID:93252381

A:Accession: I54182

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-435 <RES>

A:Cross-references: GB:L04270; NID:G339761; PIDN:AAA36757.1; PID:G339762

C:Genetics:

A:Gene: GDB:LTBR

A:Cross-references: GDB:1230195; OMIM:600979

A:Map position: 12p13.3-12p13.1

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 15.1%; Score 111.5; DB 2; Length 435;

Best Local Similarity 25.7%; Pred. No. 0.024;

Matches 39; Conservative 12; Mismatches 62; Indels 39; Gaps 9;

QY 2 ARCCVHTTRC-----CRDYPGEE---CCS--EWDGCMCVQP 32

Db 70 AKCSRIIDTVCATCAENSYNEHWNLYTICQLCRPCDPVMGLEELIAPCTSKRKTCORC-OP 128  
Qy 33 EFHCGDPC--CTTCR-HHCPDPGQGVQSGKFSFG-FQCIDCASGTF--SGHGEHGCKPW 86  
Db 129 GMFAAALAECTHCELLSDCPGTEALKDEVGKNNHCVCPCAKAGHFONTSSPSARCOQH 188  
Qy 87 TDCQFGFLIVFPCKNTHNAVCPGSPAPPL 118  
Db 189 TRCENQGLVEAAPTQSDTTC----KNPLEPL 217

RESULT 14  
A60771  
B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)  
C:Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
A:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
EMBO J. 8, 1403-1410, 1989  
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A:Reference number: S04460; MUID:89356608  
A:Accession: S04460  
A:Molecule type: mRNA  
A:Residues: 1-277 <STA>  
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851  
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
A:Reference number: A60771; MUID:89093941  
A:Accession: A60771  
A:Molecule type: protein  
A:Residues: 21-50 <BRA>  
A:Experimental source: Burkitt lymphoma cell line Raji  
A:Genetics:  
A:Gene: GDB:CD40  
A:Cross-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F:21-193/Domain: extracellular #status predicted <EXT>  
F:194-215/Domain: transmembrane #status predicted <TM>  
F:216-277/Domain: intracellular #status predicted <CYT>  
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.1%; Score 111; DB 2; Length 277;  
Best Local Similarity 31.5%; Pred. No. 0.02;  
Matches 29; Conservative 6; Mismatches 53; Indels 4; Gaps 3;  
Qy 23 SEWDCMCVQPE-FHCGDPCCTTC-RHHCPDPGQGVQSGKFSFGFQCIDCASGTFSGGHE 80  
Db 97 SETDITCTCEGWHCTSEACSVLHRSCTSPGFGVKQIATGVSDTICEPCVPVGFNSVS 156  
Qy 81 G--HCKPWIDCTQFGFLTVFPCKNTHNAVCP 110  
Db 157 AFKCHFWTSCETKVDIVVQAGTNKTDVCCP 188

RESULT 15  
A33837  
insulin-like growth factor I receptor precursor - rat  
N:Contains: insulin-like growth factor I alpha chain; insulin-like growth factor I beta  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 16-Mar-1990 #sequence\_revision 03-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: JC2461; A33837; PC1131  
R:Pedrini, M.T.; Giorgino, F.; Smith, R.J.  
Biochem. Biophys. Res. Commun. 202, 1038-1046, 1994  
A:Title: CDNA cloning of the rat IGF I receptor: Structural analysis of rat and human IG  
A:Reference number: JC2461; MUID:94324926

A:Accession: JC2461  
A:Molecule type: mRNA  
A:Residues: 1-1371 <PED>  
R:Werner, H.; Woloschak, M.; Adamo, M.; Shen-Orr, Z.; Roberts Jr., C.T.; LeRoith, D.  
Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989  
A:Title: Developmental regulation of the rat insulin-like growth factor I receptor ge  
A:Reference number: A33837; MUID:90017496  
A:Accession: A33837  
A:Molecule type: mRNA  
A:Residues: 1-364 <WER>  
A:Cross-references: GB:M27293  
R:Kurachi, H.; Jobo, K.; Ohta, M.; Kawasaki, T.; Itoh, N.  
Biochem. Biophys. Res. Commun. 187, 934-939, 1992  
A:Title: A new member of the insulin receptor family, insulin receptor-related recept  
A:Reference number: PC1130; MUID:92412145  
A:Accession: PC1131  
A:Molecule type: mRNA  
A:Residues: 913-984, 'PY', 987-1017 <KUP>  
A:Cross-references: GB:DI2679; NID:g220918; PIDN:BAA20983.1; PID:g4433359  
C:Superfamily: insulin receptor; protein kinase homology  
C:Keywords: ATP; growth factor receptor; kinase-related transforming protein; transme  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-741/Product: insulin-like growth factor I alpha chain #status predicted <IGA>  
F:742-1371/Product: insulin-like growth factor I beta chain #status predicted <IGB>  
F:937-959/Domain: transmembrane #status predicted <TM>  
F:971-974/Region: GPXY motif  
F:978-981/Region: NPXY motif  
F:998-1275/Domain: protein kinase homology <KIN>  
F:1006-1014/Region: protein kinase ATP-binding motif

Query Match 14.9%; Score 110; DB 2; Length 1371;  
Best Local Similarity 28.5%; Pred. No. 0.071;  
Matches 39; Conservative 15; Mismatches 35; Indels 48; Gaps 13;  
Qy 9 TTRC---CRDYPGECCSEWDCMCVQPEFHCGDPC-----CTTCRH-----PC 49  
Db 208 TNRQKMCPSVCGKRACTE-NNECCHPE--CLGSCHTDPDNTTCVACRHHYYKGVCPAC 264  
Qy 50 PPGQGVQSGKFSF-GFQCID---CAS-----GTFSGG---HEGHCKPWIDCTQFGFLTV 97  
Db 265 PP-----GTYREGWRCVDRDFCANIPNAESSDSGFGVIHDGEC--MQECPS-GFIR- 313  
Qy 98 FPGNKTNAVCPGSP 114  
Db 314 ---NSTQSMYCIPCEGP 327

Search completed: September 4, 2001, 16:12:13  
Job time: 1110 sec





A:Accession: B38634  
A:Molecule type: mRNA  
A:Residues: 1-474 <LEW>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A>Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
A:Reference number: A40254; MUID:91246168  
A:Accession: A40254  
A:Molecule type: mRNA  
A:Residues: 1-474 <GO>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R:Kisssnerghis, M.; Fellowes, R.; Feldmann, M.; Chernaajovsky, Y.  
submitted to the EMBL Data Library, May 1995  
A:Description: Characterization of the promoter region of the murine p75-TNF receptor.  
A:Reference number: S54816  
A:Accession: S54816  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-22 <KIS>  
A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: cytokine receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F:40-777/Domain: NGF receptor repeat homology <NG1>  
F:79-120/Domain: NGF receptor repeat homology <NG2>  
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 16.1%; Score 119; DB 2; Length 474;  
Best Local Similarity 31.0%; Pred. NO. 0.0062;  
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;

Qy 1 DARCVRHTTRCCRDYGECCSEWDCMCVQPERHCGDPCCCTC-RHHPCPPGQGVQSOG 59  
Db 107 EIRACTKQKNVCAACAGRYCAL-----KTHSGS--CRQCMRLSKCGPGFGVASSR 155

Qy 60 KFSFGFCIDCASCFTSG--GHEGHCXKPTWDTQFGFLTFPPGNKTHNAVCPVGPSP 113  
Db 156 APNGVNLKACAPCTFSDTSSDVCPRHICS----ILAIPGNASTDAVCAPESP 207

RESULT 10  
MMRTS  
laminin beta-2 chain precursor - rat  
N:Alternate names: laminin chain B3; S-laminin  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A>Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro  
A:Reference number: S03539; MUID:89159410  
A:Accession: S03539  
A:Molecule type: mRNA  
A:Residues: 1-1801 <HUN>  
A:Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: Interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F:36-285/Domain: VI <DOM6>  
F:286-555/Domain: V <DOM5>  
F:286-347/Domain: laminin-type EGF-like homology <LE01>  
F:350-410/Domain: laminin-type EGF-like homology <LE02>  
F:413-470/Domain: laminin-type EGF-like homology <LE03>  
F:473-522/Domain: laminin-type EGF-like homology <LE04>  
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:556-784/Domain: laminin-type IV <DOM4>

F:786-831/Domain: laminin-type EGF-like homology <LE06>  
F:788-1196/Domain: III <DOM3>  
F:834-877/Domain: laminin-type EGF-like homology <LE07>  
F:880-927/Domain: laminin-type EGF-like homology <LE08>  
F:930-986/Domain: laminin-type EGF-like homology <LE09>  
F:989-1038/Domain: laminin-type EGF-like homology <LE10>  
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>  
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>  
F:1197-1412/Domain: II <DOM2>  
F:1197-1412/Region: heptad repeats  
F:1413-1445/Domain: alpha <ALP>  
F:1446-1801/Region: heptad repeats  
F:1446-1801/Domain: I <DOM1>  
F:45-50/Disulfide bonds: #status predicted  
F:251,371,1088,1252,1311,1351,1502/Binding site: carboxylate (Asn) (covalent) #statu  
F:1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 16.0%; Score 118; DB 1; Length 1801;  
Best Local Similarity 26.0%; Pred. NO. 0.019;  
Matches 46; Conservative 5; Mismatches 44; Indels 82; Gaps 10;

Qy 5 CRVHTTRC--CRDYGECCSEWDCMCVQPERHCGDPCCCT---TCRHHPCPPGQGVQSOG 59  
Db 889 CDAHTGACLCGRDYGGEHCER----CI-AGPH-GDRLPYGGQCRPCPCPEPG--SOR 940  
Qy 60 KFS-----FGFCIDCASCFTSG-----FGHQAARQSCRCCTCNLLGTDP 1050

Db 941 HFATSCHRDGYSQIVCHCRAGYTGRLCEACAPGHGDPSPKGGRCQCECSGNIDPTDP 1000

Qy 76 -----SGHHEGHCXKPTWDTQFGFLTFPPGNKTHNAVCPVGPSP 114  
Db 1001 GACDPHTGQCLRLHHTGPHGCHCKP-----GFHQAARQSCRCCTCNLLGTDP 1050

RESULT 11  
A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower,  
Science 248, 1019-1023, 1990  
A>Title: A receptor for tumor necrosis factor defines an unusual family of cellular a  
A:Reference number: A35356; MUID:90260639  
A:Accession: A35356  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir  
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A>Title: A second tumor necrosis factor receptor gene product can shed a naturally oc  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195; R, 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,  
Cytokine 2, 231-237, 1990  
A>Title: Two human TNF receptors have similar extracellular, but distinct intracellular  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:g235648; PIDN:AA819824.1; PID:g235649  
A>Note: sequence extracted from NCBI backbone (NCBI:63368, NCBIP:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:12 ; Search time 80.15 Seconds  
(without alignments)  
113.098 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DARCRRVHTTRCCRDYPGEE.....GNKTHNAVCPGSPAPBLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159.5	21.6	255	2	I38426 lymphocyte activat
2	158	21.4	272	2	I48700 gene OX40 protein
3	150	20.4	277	2	I37532 OX40 homolog - hum
4	149.5	20.3	256	2	B32393 T-cell antigen 4-1
5	149	20.2	271	2	S12783 OX40 antigen precu
6	127	17.2	295	2	JC5559 lectin-B - Virgini
7	123	16.7	305	2	A46476 B cell-associated
8	120.5	16.4	459	2	I48854 gene murine tumour
9	119	16.1	474	2	B38634 tumor necrosis fac
10	118	16.0	1801	1	MMRTS laminin beta-2 cha
11	117	15.9	461	1	A35356 laminin beta-2 cha
12	112	15.2	1798	2	S53869 laminin beta-2 cha
13	111.5	15.1	435	2	I54182 tumor necrosis fac
14	111	15.1	277	2	A50711 B-cell activation
15	110	14.9	1371	2	A33837 insulin-like growt
16	109	14.8	329	2	A48805 insulin-like growt
17	108	14.7	1574	2	T13954 MEGF6 protein - ra
18	103	14.0	1797	2	A55677 laminin beta-2 cha
19	99	13.4	1367	1	IGHUR1 insulin-like growt
20	94	12.8	152	2	T18975 hypothetical prote
21	93	12.6	3635	2	T10053 laminin alpha 5 ch
22	92	12.5	416	1	JN0006 nerve growth facto
23	92	12.5	1172	1	T5HUP2 thrombospondin 2 p
24	92	12.5	1820	2	A55494 latent transformat
25	91.5	12.4	1106	2	T13938 gene shuttle craft
26	91.5	12.4	2318	2	S45306 notch 3 protein -
27	91	12.3	956	1	A46016 thrombospondin 3 -
28	90.5	12.3	1106	2	T44598 hypothetical prote
29	90.5	12.3	2150	2	T32497 hypothetical prote

## ALIGNMENTS

RESULT 1

I38426

lymphocyte activation-induced receptor ILA precursor - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000

C:Accession: I38426; JT0752

R:Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.

Eur. J. Immunol. 24, 2219-2227, 1994

A:Title: Molecular and biological characterization of human 4-1BB and its ligand.

A:Reference number: I38426; MUID:94374434

A:Accession: I38426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-255 <RES>

A:CROSS-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321

R:Schwarz, H.; Tuckwell, J.; Lotz, M.

Gene 134, 295-298, 1993

A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human

A:Reference number: JT0752; MUID:94085794

A:Accession: JT0752

A:Molecule type: mRNA

A:Residues: 1-106, 'R', 108-255 <SCH>

C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-ne

C:Comment: This receptor recognizes soluble, cell-surface bound or extracellular mat

C:Superfamily: CD27 antigen; Ngf receptor repeat homology

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>

F:187-213/Domain: transmembrane #status predicted <TM>

F:138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status pred

F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte

Query Match 21.6%; Score 159.5; DB 2; Length 255;

Best Local Similarity 31.9%; Pred. NO. 1.8e-06;

Matches 44; Conservative 12; Mismatches 43; Indels 39; Gaps 8;

QY 3 RCRVHTTRCCRDYPG-----EECCS-----EWDCMCVQPEFHGCDPCCTTCRHHPCPPGQ 53

Db 60 RUCDI-----CROCKGVFRTRKESSTSNAECDG---TPGFHCLGACSMC-EDQCKQGQ 110

QY 54 GVQSQKFSFGFCIDCASGTGSGHGHCKPMTDCTQFGFLTVFPGNKTHNAVCPG-- 111

Db 111 ELTKKG-----CKDCCFGTFENDQKRGICRPWTNCSLDGKSVLVNCTKRDVVCGSPSA 163

QY 112 -----SPPA---EP 117

Db 164 DLSPGASSVTPPAPAREP 181

RESULT 2

Insulin receptor-r  
Insulin receptor-r  
fibrillin-2 precu  
hypothetical prote  
thrombospondin 3 p  
laminin beta-1 cha  
notch3 protein - h  
fibrillin-2 precu  
Notch homolog prot  
crumbs protein - f  
Notch-1 protein -  
hypothetical prote  
disintegrin-like m  
hypothetical prote  
thrombospondin 2 p  
notch4 - mouse

30 90 12.2 540 2 B47417  
31 90 12.2 1268 2 B36502  
32 90 12.2 2907 2 A57278  
33 89 12.1 164 2 T24272  
34 89 12.1 956 2 A57121  
35 89 12.1 1786 1 MMHUB1  
36 89 12.1 2321 2 S78549  
37 89 12.1 2918 2 A54105  
38 88.5 12.0 2352 2 T30201  
39 88 11.9 2139 2 A35672  
40 88 11.9 2531 2 A46019  
41 87.5 11.9 259 2 T21011  
42 87.5 11.9 814 2 G02390  
43 87.5 11.9 1111 2 T26972  
44 87.5 11.9 1172 2 A42587  
45 87.5 11.9 1964 2 T09059

I48700  
gene ox40 protein - mouse  
N:Alternate names: OX40 antigen  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
C:Accession: I48700; I48334; S34377  
R:Calderhead, D.M.; Buhlmann, J.E.; van den Bortwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993  
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell int  
A:Reference number: I48700; MUID:94044750  
A:Accession: I48700  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-272 <RES>  
A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828  
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. Eur. J. Immunol. 25, 926-930, 1995  
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40  
A:Reference number: I48334; MUID:95255413  
A:Accession: I48334  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-14,'G',16-272 <RE2>  
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819  
C:Genetics:  
A:Gene: ox40  
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 21.4%; Score 158; DB 2; Length 272;  
Best Local Similarity 27.4%; Pred. No. 2.5e-06;  
Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;

QY 5 CRVHT-----TRCCRD-YPG-----ECCSEWDCMCVQPEFFHCGDPC----- 40  
DB 27 CVKHTPSGHKKCCRECPQGHGWSRCDHTDTC-----HPCETGFYNEAVNYDTCK 78  
QY 41 -CTCRHHP-----CPPGQGVQSGKFSFGFCIDCASGTFSGGHEGH 82  
DB 79 OCTQCNHRSGSELKQNCPTQDTVCRCPGTOPRDSGYKLGVDVCPCPGPHFSGNQNA 138  
QY 83 CKPWTDCTQFGFLTVFNGKTHNAV 108  
DB 139 CKPWTNCTLQSGKQTRHPASDSDAVC 164

RESULT 3  
I37552  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durrkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat  
Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment c  
A:Reference number: I37552; MUID:94170844  
A:Accession: I37552  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 20.4%; Score 150; DB 2; Length 277;  
Best Local Similarity 30.8%; Pred. No. 1.2e-05;  
Matches 41; Conservative 11; Mismatches 53; Indels 28; Gaps 7;

QY 11 RCRRD-YPG-----ECCSEWDCMC--VQPEFH-----CGDPC--CTTC-----RHHPCP 50  
DB 41 RCCHCRPGNGMVSRCSSRNTVCRPGFGYNDVVSCKPKCPCTWCNLRSGSERKQLCT 100

QY 51 PGQ-----GVQSQKFSFGFCIDCASGTFSGGHEGHCKPWTDTCTQFGFLTVFPGNK 102  
DB 101 ATQDTVCRCRAGTQPLDSYKPGVDCAPCPPGPHFSPGDNQACKPWTNCTLAGKHTLPASN 160  
QY 103 THNAVCPGSPPA 115  
DB 161 SSDAICEDRDPPA 173

RESULT 4  
B32393  
T-cell antigen 4-1BB precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R:Kwon, B.S.; Weissman, S.M. Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A:Title: cDNA sequence of two inducible T-cell genes.  
A:Reference number: A32393; MUID:89184547  
A:Accession: B32393  
A:Molecule type: mRNA  
A:Residues: 1-256 <KWO>  
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T. J. Immunol. 152, 2256-2262, 1994  
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B  
A:Reference number: I48879; MUID:94179805  
A:Accession: I48879  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-256 <RES>  
A:Cross-references: EMBL:U02567; NID:g117783; PIDN:AAA93113.1; PID:g409178  
C:Genetics:  
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 20.3%; Score 149.5; DB 2; Length 256;  
Best Local Similarity 33.6%; Pred. No. 1.2e-05;  
Matches 37; Conservative 15; Mismatches 41; Indels 17; Gaps 6;

QY 5 CRVHTTRCCRDYPGEECCSEW---DCMCVQPEFFHCGDPCCTTCRHHPCPPGQGVQSGKRF 61  
DB 64 CRV---CAGYFRFKKFCSSTHNAECIE-GFCHLGQCTRC-EKDCRPGQELTKQG--- 115  
QY 62 SFGFCIDCASGTFSGGH-EGHCKPWTDTCTQFGFLTVFPGKTHNAVCP 110  
DB 116 -----CKTCSLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP 160

RESULT 5  
SI2783  
OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: SI2783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N. EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc  
A:Reference number: SI2783; MUID:90214614  
A:Accession: SI2783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TMM>





[illegible]

QY 33 EFHCGDPC--CTTCR-HHPGPPGVOSQKFSFG-FQCIDCASGTF--SGHGHCKPWP 86  
 DB 129 GMFCAAWALECTHCELLSDCPPGTEALKEVGNHNCVPCAKAGHFQNTSSPSARCQPH 188  
 QY 87 TDCTQFGFLVFPNGKTHNAVCPGSPAPLEPL 118  
 DB 189 TRCENQGLVEAFCQAQSDTTC---KNPLEPL 217

RESULT 12  
 CD40\_HUMAN STANDARD; PRT; 277 AA.  
 ID CD40\_HUMAN  
 AC P25942;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)  
 DE (TUMOR NECROSIS FACTOR RECEPTOR 5).  
 GN TNFRSF5 OR CD40.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89356608; PubMed=2475341;  
 RA Stamenkovic I., Clark E.A., Seed B.;  
 RT "A B-lymphocyte activation molecule related to the nerve growth  
 factor receptor and induced by cytokines in carcinomas";  
 RL ENBO J. 8:1403-1410(1989).  
 RN [2]  
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 RX MEDLINE=97189482; PubMed=9037712;  
 RA Bajorath J., Aruffo A.;  
 RT "Construction and analysis of a detailed three-dimensional model of  
 the ligand binding domain of the human B cell receptor CD40.";  
 RL Proteins 27:59-70(1997).  
 RN [3]  
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 RX MEDLINE=98266353; PubMed=9605317;  
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
 RA Zheng Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".  
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 CC -----  
 DR EMBL; X60592; CAA43045.1; -;  
 DR PIR; S04460; S04460.  
 DR PDB; 1CDF; 01-APR-97.  
 DR MIM; 109535; -;  
 DR InterPro: IPR001368; -;  
 DR Pfam; PF000020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
 KW 3D-structure. 1 19 POTENTIAL.  
 FT SIGNAL 20 277 CD40L RECEPTOR.  
 FT CHAIN

FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT DISULFID 26 37  
 FT DISULFID 38 51  
 FT DISULFID 41 59  
 FT DISULFID 62 77  
 FT DISULFID 83 103  
 FT DISULFID 105 119  
 FT DISULFID 111 116  
 FT DISULFID 125 143  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180  
 SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 Query Match 15.1%; Score 111; DB 1; Length 277;  
 Best Local Similarity 31.5%; Pred. No. 0.0019;  
 Matches 29; Conservative 6; Mismatches 53; Indels 4; Gaps 3;  
 QY 23 SEWDCMCVQPE-FHCGDPCCTTC-RHHPGPPGVOSQKFSFGFQCIDCASGTFSGGHE 80  
 DB 97 SETDTICTCEGWHCTSEACSVLHRSCTPGVSKQIATGVSDTICEPCPVGFFSNVSS 156  
 QY 81 G-HCKPWTDCQFGFLVFPNGKTHNAVCP 110  
 DB 157 AFEKCHPWTSCETKDLVVQQAGTKNTKTDVVVCGP 188

RESULT 13  
 IG1R\_RAT STANDARD; PRT; 1370 AA.  
 ID IG1R\_RAT  
 AC P24062;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).  
 GN IGFI.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95277910; PubMed=7758167;  
 RA Du J., Delafontaine P.;  
 RT "Inhibition of vascular smooth muscle cell growth through antisense  
 transcription of a rat insulin-like growth factor I receptor cDNA.";  
 RL Circ. Res. 76:963-972(1995).  
 RN [2]  
 RP SEQUENCE OF 1-364 FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=90017496; PubMed=2477843;  
 RA Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,  
 RA Leroith D.;  
 RT "Developmental regulation of the rat insulin-like growth factor I  
 receptor gene";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).  
 RN [3]  
 RP SEQUENCE OF 913-1017 FROM N.A.  
 RX MEDLINE=92412145; PubMed=1530648;  
 RA Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;  
 RT "A new member of the insulin receptor family, insulin  
 receptor-related receptor, is expressed preferentially in the  
 RT kidney.";  
 RL Biochem. Biophys. Res. Commun. 187:934-939(1992).  
 CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)



FT DISULFID 443 452 BY SIMILARITY.  
 FT DISULFID 455 470 BY SIMILARITY.  
 FT DISULFID 477 487 BY SIMILARITY.  
 FT DISULFID 475 494 BY SIMILARITY.  
 FT DISULFID 496 505 BY SIMILARITY.  
 FT DISULFID 508 522 BY SIMILARITY.  
 FT DISULFID 784 796 BY SIMILARITY.  
 FT DISULFID 786 803 BY SIMILARITY.  
 FT DISULFID 805 814 BY SIMILARITY.  
 FT DISULFID 817 829 BY SIMILARITY.  
 FT DISULFID 832 844 BY SIMILARITY.  
 FT DISULFID 834 851 BY SIMILARITY.  
 FT DISULFID 853 862 BY SIMILARITY.  
 FT DISULFID 865 875 BY SIMILARITY.  
 FT DISULFID 880 894 BY SIMILARITY.  
 FT DISULFID 897 906 BY SIMILARITY.  
 FT DISULFID 909 925 BY SIMILARITY.  
 FT DISULFID 928 944 BY SIMILARITY.  
 FT DISULFID 930 955 BY SIMILARITY.  
 FT DISULFID 957 966 BY SIMILARITY.  
 FT DISULFID 969 984 BY SIMILARITY.  
 FT DISULFID 987 1001 BY SIMILARITY.  
 FT DISULFID 989 1008 BY SIMILARITY.  
 FT DISULFID 1011 1020 BY SIMILARITY.  
 FT DISULFID 1023 1036 BY SIMILARITY.  
 FT DISULFID 1096 1108 BY SIMILARITY.  
 FT DISULFID 1098 1115 BY SIMILARITY.  
 FT DISULFID 1117 1126 BY SIMILARITY.  
 FT DISULFID 1129 1141 BY SIMILARITY.  
 FT DISULFID 1144 1156 BY SIMILARITY.  
 FT DISULFID 1146 1163 BY SIMILARITY.  
 FT DISULFID 1165 1174 BY SIMILARITY.  
 FT DISULFID 1177 1188 BY SIMILARITY.  
 FT DISULFID 1191 1191 INTERCHAIN (PROBABLE).  
 FT DISULFID 1194 1194 INTERCHAIN (PROBABLE).  
 FT DISULFID 1798 1798 INTERCHAIN (PROBABLE).  
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1086 1086 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1250 1250 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1309 1309 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1349 1349 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1500 1500 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1799 AA; 196352 MW; 1F28967A67AEDE33 CRC64;

Query Match . 15.3%; Score 113; DB 1; Length 1799;  
 Best Local Similarity 25.4%; Pred. No. 0.0054;  
 Matches 45; Conservative 6; Mismatches 44; Indels 82; Gaps 10;

QY 5 CRVHTTRC--CRDYPGEECCSWDCMVCVOPFHGCDPCT---TCRHPCPGQGVQSG 59  
 DB 887 CDTHTGACLGCRDYGGEHCER----CI-AGFH-GDPLPYGGQCRPCPCPGPG--SQR 938  
 QY 60 KFS-----FGQCIDCAGTF----- 75  
 DB 939 HFATSCHRDGYSSQIVCHCRAGYTLGRCEACAPFGDPSKPGGRGQLECSGNDPMDP 998  
 QY 76 -----SGGHEGCHKPWTDCQFGFLTVPFGKTHNAVC-VPGSP 114  
 DB 999 DACDPHTGQCLRLHNTGEPHCGYCKP-----GFHGQAARQSHRCRCNLLGTDP 1048

RESULT 11  
 TNRC\_HUMAN STANDARD; PRT; 435 AA.  
 AC P36941;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR  
 DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).

GN LTBR OR TNFR OR TNFRSF3.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93252381; PubMed=8486360;  
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
 RT "Construction and evaluation of a hncDNA library of human 12p  
 transcribed sequences derived from a somatic cell hybrid.";  
 RL Genomics 16:214-218(1993).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=94225209; PubMed=8171323;  
 RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
 RA Ehrenfelds B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
 RT "A lymphotoxin-beta-specific receptor.";  
 RL Science 264:707-710(1994).  
 CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC IMMUNE DEVELOPMENT.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC -----  
 CC EMBL; L04270; AAA36757.1; --  
 DR HSP; P25942; LCDF.  
 DR MIM; 600979; --  
 DR InterPro; IPR001368; --  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30 POTENTIAL.  
 FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.  
 FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 228 248 POTENTIAL.  
 FT DOMAIN 42 211 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 42 81 4 X TNFR-CYS.  
 FT REPEAT 82 124 TNFR-CYS 1.  
 FT REPEAT 125 168 TNFR-CYS 2.  
 FT REPEAT 169 211 TNFR-CYS 3.  
 FT DISULFID 43 58 BY SIMILARITY.  
 FT DISULFID 59 72 BY SIMILARITY.  
 FT DISULFID 62 80 BY SIMILARITY.  
 FT DISULFID 83 98 BY SIMILARITY.  
 FT DISULFID 101 116 BY SIMILARITY.  
 FT DISULFID 104 124 BY SIMILARITY.  
 FT DISULFID 126 132 BY SIMILARITY.  
 FT DISULFID 139 148 BY SIMILARITY.  
 FT DISULFID 142 167 BY SIMILARITY.  
 FT DISULFID 170 185 BY SIMILARITY.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 15.1%; Score 111.5; DB 1; Length 435;  
 Best Local Similarity 25.7%; Pred. No. 0.0025;  
 Matches 39; Conservative 12; Mismatches 62; Indels 39; Gaps 9;

QY 2 ARCCRVHTTRC-----CRDYPGEE-----CCS---EWDCMVCQP 32  
 DB 70 AKCSIRDVTCAENSYNEHWNLYTICQLCRPCDPVMGLEETAPCTSKRKTCRC-QP 128

FT	CARBOHYD	1088	1088	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1252	1252	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1311	1311	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1351	1351	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1502	1502	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1801 AA;	196473 MR;	97AEF32F831FA75 CRC64;

  

Query Match	16.0%;	Score 118;	DB 1;	Length 1801;	
Best Local Similarity	26.0%;	Pred. No. 0.0019;			
Matches 46;	Conservative	5;	Mismatches 44;	Indels 82;	Gaps

  

QY	5	CRVHTTRC--CRDYPGEBCSCSDWCMCVQPEHFGCDPCT---	TCRHHPCPGQGVOSQ	59
DB	889	CDAAHTGACLCGRDVTGGEHCE---	CI-AGFH-GDRLPYGGCQPCPCPEGPG--	SQR 940
QY	60	KFS-----	FGQCIDCASGTF-----	75
DB	941	HFAT5CHRDRGYSQIIVCHCRAGYTGRLCEACAPGHGDPSPKPGRCQLCESGNIDPTDP	1000	
QY	76	-----	SGHGEGHCKPMTDCTQCFGLTVFPFNKTHNAVCS-VPGSPP	114
DB	1001	GACDPHTGQCLRLHHTGEPHCGHCKP-----	GFHQQAARQSCHRCTCNLLGTDP	1050

  

RESULT 10					
LMB2_MOUSE					
IC	LMB2_MOUSE	STANDARD;	PRT;	1799	AA.
AD	O61292;	O62182;			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	LAMININ BETA-2 CHAIN PRECURSOR.				
GN	LAMININ BETA-2 CHAIN PRECURSOR.				
GN	LAMB2 OR S-LAM OR LAMS.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
ON	NCBI_Taxid=10090;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129/J;				
RC	MEDLINE=96278760; PubMed=8662701;				
RX	Durkin M.E., Gautam M., Loechele S., Sanes J.R., Merlie J.P.,				
RA	Albrechtsen R., Wewer U.M.;				
RT	"Structural organization of the human and mouse laminin beta2 chain				
RT	genes, and alternative splicing at the 5' end of the human				
RT	transcript.;"				
RL	J. Biol. Chem. 271:13407-13416(1996).				
RL	[2]				
RP	SEQUENCE OF 348-428 FROM N.A.				
RC	TISSUE=Lung;				
RX	MEDLINE=94319092; PubMed=8043959;				
RA	Aberdam D., Galliano M.F., Mattel M.-G., Ortonne J.P., Meneguzzi G.;				
RT	"S-laminin gene (lams) maps to F1 band of mouse chromosome 9.;"				
RL	Mamm. Genome 5:393-394(1994).				
RL	[3]				
RP	FUNCTION.				
RC	STRAIN=129/J;				
RX	MEDLINE=953191650; PubMed=7885444;				
RA	Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;				
RT	"Aberrant differentiation of neuromuscular junctions in mice lacking				
RT	s-laminin/laminin beta 2.;"				
RL	Nature 374:258-262(1995).				
CC	-1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ OF				
CC	CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT, MIGRATION, & ORGANIZATION OF				
CC	WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.				
CC	-1- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR				
CC	NERVE TERMINALS.				
CC	-1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE				
CC	DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND				
CC	TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE				
CC	COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.				

CC	THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC	(S-SUBCELLULAR), AND LAMININ-7 (KS-LAMININ).
CC	-1- MEMBRANE LOCATION; EXTRACELLULAR; FOUND IN THE BASEMENT
CC	MEMBRANES (MAJOR COMPONENT).
CC	-1- TISSUE SPECIFICITY; NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.
CC	-1- DOMAIN; THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC	WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC	-1- DOMAIN; DOMAINS VI AND IV ARE GLOBULAR.
CC	-1- SIMILARITY; CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC	-1- SIMILARITY; CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC	-1- SIMILARITY; CONTAINS 1 LAMININ DOMAIN IV.
CC	-----
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CC	-----
DR	EMBL; U43541; AAC53535.1; .
DR	EMBL; U42624; AAC53535.1; JOINED.
DR	EMBL; X75928; CAA53532.1; .
DR	HSSP; P02468; IKLO.
DR	MGI; MGI:99916; Lamb2.
DR	InterPro; IPR000561; .
DR	InterPro; IPR001886; .
DR	InterPro; IPR002049; .
DR	Pfam; PF00053; laminin_EGF_13.
DR	Pfam; PF00055; laminin_Nterm; 1.
DR	PRINTS; PR00011; EGFLAMININ.
DR	PROSITE; PS00022; EGF_1; 10.
DR	PROSITE; PS01186; EGF-2; 2.
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
KW	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW	Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT	SIGNAL 1 35 POTENTIAL.
FT	CHAIN 36 1799 LAMININ BETA-2 CHAIN.
FT	DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).
FT	DOMAIN 284 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
FT	V).
FT	DOMAIN 286 349 LAMININ EGF-LIKE 1.
FT	DOMAIN 350 412 LAMININ EGF-LIKE 2.
FT	DOMAIN 413 472 LAMININ EGF-LIKE 3.
FT	DOMAIN 473 524 LAMININ EGF-LIKE 4.
FT	DOMAIN 525 555 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT	DOMAIN 556 782 LAMININ DOMAIN IV.
FT	DOMAIN 783 1191 8 X LAMININ EGF-LIKE REPEATS (DOMAIN
FT	III).
FT	DOMAIN 784 831 LAMININ EGF-LIKE 6.
FT	DOMAIN 832 877 LAMININ EGF-LIKE 7.
FT	DOMAIN 878 927 LAMININ EGF-LIKE 8.
FT	DOMAIN 928 986 LAMININ EGF-LIKE 9.
FT	DOMAIN 987 1038 LAMININ EGF-LIKE 10.
FT	DOMAIN 1039 1095 LAMININ EGF-LIKE 11.
FT	DOMAIN 1096 1143 LAMININ EGF-LIKE 12.
FT	DOMAIN 1144 1190 LAMININ EGF-LIKE 13.
FT	DOMAIN 1191 1410 DOMAIN II.
FT	DOMAIN 1411 1443 DOMAIN ALPHA.
FT	DOMAIN 1444 1799 DOMAIN I.
FT	DOMAIN 1257 1304 COILED COIL (POTENTIAL).
FT	DOMAIN 1473 1527 COILED COIL (POTENTIAL).
FT	DOMAIN 1577 1791 COILED COIL (POTENTIAL).
FT	DISULFID 286 295 BY SIMILARITY.
FT	DISULFID 288 313 BY SIMILARITY.
FT	DISULFID 315 324 BY SIMILARITY.
FT	DISULFID 327 347 BY SIMILARITY.
FT	DISULFID 350 359 BY SIMILARITY.
FT	DISULFID 352 377 BY SIMILARITY.
FT	DISULFID 380 389 BY SIMILARITY.
FT	DISULFID 392 410 BY SIMILARITY.
FT	DISULFID 413 426 BY SIMILARITY.
FT	DISULFID 415 441 BY SIMILARITY.





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DR PIR: A23666; A23666.
DR PDB: 1CA9; 12-APR-99.
DR MIM: 191191; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_NGFR_1; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00652; TNFR_NGFR_2; 4.
DR PROSITE: PS00650; TNFR_NGFR_2; 4.
KW Receptor; transmembrane; Glycoprotein; Repeat; Signal;
KW Phosphorylation; Pharmaceutical; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 258 287 POTENTIAL.
FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 201 4 X TNFR-CYS.
FT REPEAT 39 76 TNFR-CYS 1.
FT REPEAT 77 118 TNFR-CYS 2.
FT REPEAT 119 162 TNFR-CYS 3.
FT REPEAT 163 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 141 141 R -> P (IN REF. 4).
FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).
FT CONFLICT 363 363 A -> T (IN REF. 4).
SQ SEQUENCE 461 AA; 48316 MW; 603580ECD67636F CRC64;

Query Match 16.1%; Score 119; DB 1; Length 461;
Best Local Similarity 30.4%; Pred. No. 0.00055;
Matches 35; Conservative 11; Mismatches 51; Indels 18; Gaps 6;

QY 10 TRCDYRPGECSEWD--CMVQPFHC-----GDPCTTCRHHPGPPGQVQSGK 60
DB 98 SRGSSQVETQACTREQNRICTC-RPGWYKALSKQECRLCAPLR--KCRPGFGVARPGT 154
QY 61 FSGFGCIDCASGTFSG--GHEGCKRWTDCTQGTFTVFPGNKTHNAVCPVGPSP 113
DB 155 ETSDDVCKPCAPGTFSTSTSDICRPHQICN----VVAIPGNASRDVACTSTSP 205

RESULT 8
TNR2_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
GN TNRSF1B OR TNR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91187885; PubMed-1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]

SEQUENCE FROM N.A.
MEDLINE-91246168; PubMed-1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN-NOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Kissnerghis M., Fellows R., Feldmann M., Chernajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M60469; AAA39752.1; -.
CC EMBL: M59378; AAA40463.1; -.
CC EMBL: U39488; AAA85021.1; -.
CC EMBL: X87128; CAA60618.1; -.
CC PIR: B38634; B38634.
CC HSP: P19438; INCF.
CC MGI: MGI:1314883; Tnfrsf1b.
CC InterPro: IPR001368; -.
CC Pfam: PF00020; TNFR_C6; 4.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS00650; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462AE398C4D6563 CRC64;

Query Match 16.1%; Score 119; DB 1; Length 474;
Best Local Similarity 31.0%; Pred. No. 0.00056;
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;

QY 1 DARCRVHTTRCCRDYPCGECSEWDCMCVQPFHCPCCTTC-RHHPGPPGQVQSGK 59
DB 107 EIRACTRQQRNVKACEAGRYCAL-----KTHSGS--CRQCMRLSKCGPGFGVASSR 155

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Matches	37;	Conservative	10;	Mismatches	51;	Indels	30;	Gaps	5;
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QY	11	RCCRD-YPGEECCSEWD-----CMCVQPEFHCG-----DPC---CTTCRRH-----	47
DB	36	KCCEQCQPGHGVMVSRCDHTDRDTVCHCEFCGFYEAVNYDTCKOCTOCNHRSGSELKONCT	95
QY	48	-----PCPBGOGVGQQSKFSGFOCIDACASGTFFGGHGHEGCKPWTDCTQFGFLTVFP	100
DB	96	PTEDTVCQCRPGTPQRQDSHKGLGVDCVCPGPHFSPGSNQACKPWTNCTLSGKQIRHPA	155
QY	101	NKTHNAV	108
DB	156	SNSLDTV	163

  

RESULT 6

CD40_MOUSE	STANDARD;	PRT;	289 AA.
ID CD40_MOUSE P27512;			
AC AC			
DT DT	01-AUG-1992 (Rel. 23, Created)		
DT DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE DE	CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).		
GN GN	TNFRSF5 OR CD40.		
OS OS	Mus musculus (Mouse).		
OC OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX OX	NCBI_TaxID=10090;		
[1]			
RP RP	SEQUENCE FROM N.A.		
RP RP	MEDLINE=G21105763; PubMed=1370315;		
RX RX	Torres R.M., Clark E.A.;		
RA RA	"Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";		
RT RT	J. Immunol. 148:620-626(1992).		
RL RL	[2]		
RN RN	REVSIONS.		
RP RP	STRAIN=BALB/C;		
RC RC	Torres R.M.;		
RL RL	Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.		
RN RN	[3]		
RP RP	SEQUENCE FROM N.A.		
RP RP	STRAIN=BALB/C; TISSUP=Liver;		
RC RC	MEDLINE=G3094586; PubMed=1281194;		
RX RX	Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,		
RA RA	Howard M., Cockayne D.A.;		
RA RA	"Genomic structure and chromosomal mapping of the murine CD40 gene.";		
RT RT	J. Immunol. 149:3921-3926(1992).		
CC CC	- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.		
CC CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC CC	- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.		
CC CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensel@isb-sib.ch).		
CC CC	EMBL; M83312; AB087051; -		
CC CC	EMBL; M94126; AAA37404.1; -		
DR DR	EMBL; M94129; AAA37404.1; JOINED.		
DR DR	EMBL; M94128; AAA37404.1; JOINED.		
DR DR	EMBL; M94127; AAA37404.1; JOINED.		
DR DR	PIR; A46476; A46476.		
DR DR	HSSP; P25942; ICDF.		
DR DR	MGI; MGI:88336; Tnfrsf5.		
DR DR	InterPro: IPR001368; -		
DR DR	Pfam: PF00020; TNFR_c6; 4.		
DR DR	PROSITE: PS00652; TNFR_NGFR_1; 1.		
DR DR	PROSITE: PS00500; TNFR_NGFR_2; 4.		
KW KW	Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.		

RA Latza U., Duerkop H., Schmittger S., Ringeling J., Eitelbach F.,  
 RA Hummel M., Fonatsch C., Stein H.;  
 RT "The human OX40 homolog: cDNA structure, expression and chromosomal  
 RT assignment of the ACT35 antigen.";  
 RL Eur. J. Immunol. 24:677-683(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95219871; PubMed=7704935;  
 RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,  
 RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K.R., Alderson M.R.;  
 RT "Identification of OX40 ligand and preliminary characterization of  
 RT its activities on OX40 receptor.";  
 RL Circ. Shock 44:30-34(1994).  
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide cd134 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".  
 CC -----  
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 CC -----  
 DR EMBL; X75962; CAA53576.1; -;  
 DR EMBL; S76792; AAB33944.1; ALT\_INIT.  
 DR HSSP; P25942; ICDF.  
 DR MIW; 600315; -;  
 DR InterPro: IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 277  
 FT CHAIN 29 277  
 FT DOMAIN 29 214  
 FT TRANSMEM 29 214  
 FT DOMAIN 236 277  
 FT DOMAIN 30 169  
 FT DOMAIN 30 169  
 FT REPEAT 30 65  
 FT REPEAT 66 107  
 FT REPEAT 108 126  
 FT REPEAT 127 167  
 FT REPEAT 146 146  
 FT CARBOHYD 160 160  
 FT CARBOHYD 160 160  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 20.4%; Score 150; DB 1; Length 277;  
 Best Local Similarity 30.8%; Pred. No. 6.2e-07;  
 Matches 41; Conservative 11; Mismatches 53; Indels 28; Gaps 7;  
 Qy 11 RCRRD-YPG-----EBCCEWDCMC--VQPEFH-----CGDPC--CTTC-----RHHPGP 50  
 Db 41 RCCECRPGNGVMVSRCSQNTVCRPCGPGFYNDVVSSKPKCPCTWCLNRSRSGERKQLCT 100  
 Qy 51 PQQ-----GVQSQGFSGFCQIDCASGTFSGHGHECHKPWTCTQFGFLTVPPGNK 102  
 Db 101 ATQDFTVCRAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLPASN 160  
 Qy 103 THNAVCPGSPPA 115  
 Db 161 SSDAICEDRDPPA 173  
 RESULT 4  
 ID 41BB\_MOUSE  
 AC P20334; STANDARD; PRT; 256 AA.

DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).  
 GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89184547; PubMed=2784565;  
 RA Kwon B.S., Weissman S.M.;  
 RT "cDNA sequences of two inducible T-cell genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=BALE/C;  
 RX MEDLINE=94179805; PubMed=8133039;  
 RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;  
 RT "Genomic organization and chromosomal localization of the T-cell  
 RT antigen 4-1BB.";  
 RL J. Immunol. 152:2256-2262(1994).  
 RN [3]  
 RP CHARACTERIZATION, AND SEQUENCE OF 25-29.  
 RX MEDLINE=93139510; PubMed=7678621;  
 RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T.,  
 RA Kwon B.S.;  
 RT "Inducible T cell antigen 4-1BB. Analysis of expression and  
 RT function.";  
 RL J. Immunol. 150:771-781(1993).  
 CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY  
 CC -1- ACTIVE DURING T CELL ACTIVATION.  
 CC -1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.  
 CC -1- ASSOCIATES WITH P56-LCK.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.  
 CC -1- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 DR EMBL; J04492; AAA40167.1; -;  
 DR EMBL; U02567; AAA93113.1; -;  
 DR PIR; B32393; B32393.  
 DR HSSP; P25942; ICDF.  
 DR MGD; MGI:1101059; Tnfrsf9.  
 DR InterPro: IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; FALSE\_NEG.  
 KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24  
 FT CHAIN 25 256  
 FT DOMAIN 25 187  
 FT DOMAIN 188 208  
 FT TRANSMEM 188 208  
 FT DOMAIN 209 256  
 FT DOMAIN 17 159  
 FT REPEAT 17 45  
 FT REPEAT 46 85  
 FT REPEAT 86 117  
 FT REPEAT 118 159  
 FT REPEAT 128 128  
 FT CARBOHYD 138 138  
 FT CARBOHYD 138 138  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:23 ; Search time 43.78 Seconds  
(without alignments)  
93.111 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DARCRRVHTRCRDYPGE.....GNKTHNAVCPGSPAPLEPLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	159.5	21.6	255	1 41BB_HUMAN	Q07011 homo sapien
2	158	21.4	272	1 OX40_MOUSE	P47741 mus musculu
3	150	20.4	277	1 OX40_HUMAN	P43489 homo sapien
4	149.5	20.3	256	1 41BB_MOUSE	P20334 mus musculu
5	149	20.2	271	1 OX40_RAT	P15725 rattus norv
6	123	16.7	289	1 CD40_MOUSE	P27512 mus musculu
7	119	16.1	461	1 TNFR2_HUMAN	P20333 homo sapien
8	119	16.1	474	1 TNFR2_MOUSE	P25119 mus musculu
9	118	16.0	1801	1 LMB2_RAT	P15800 rattus norv
10	113	15.3	1799	1 LMB2_MOUSE	O61292 mus musculu
11	111.5	15.1	435	1 TNRC_HUMAN	P36941 homo sapien
12	111	15.1	277	1 CD40_HUMAN	P25942 homo sapien
13	110	14.9	1370	1 IG1R_RAT	P24062 rattus norv
14	109	14.8	269	1 CD40_BOVIN	Q28203 bos taurus
15	104	14.1	1798	1 LMB2_HUMAN	P55268 homo sapien
16	103	14.0	1373	1 IG1R_MOUSE	O60751 mus musculu
17	99	13.4	1367	1 IG1R_HUMAN	P08069 homo sapien
18	93	12.6	3635	1 LMA5_MOUSE	O61001 mus musculu
19	92	12.5	416	1 NGFR_CHICK	P18519 gallus gall
20	92	12.5	1172	1 TSP2_HUMAN	P35442 homo sapien
21	91.5	12.4	1106	1 SPC_DROME	P40798 drosophila
22	91.5	12.4	2318	1 NTC3_MOUSE	O61982 mus musculu
23	91	12.3	956	1 TSP3_MOUSE	O5895 mus musculu
24	90	12.2	581	1 IRR_RAT	Q64716 rattus norv
25	90	12.2	1297	1 FBN2_HUMAN	P14616 homo sapien
26	90	12.2	2907	1 FBN2_MOUSE	O61555 mus musculu
27	89	12.1	116	1 MCS_HUMAN	P49901 homo sapien
28	89	12.1	956	1 TSP3_HUMAN	P49746 homo sapien
29	89	12.1	1786	1 LMB1_HUMAN	P07942 homo sapien
30	89	12.1	2911	1 FBN2_HUMAN	P35556 homo sapien
31	88.5	12.0	2569	1 LMA3_MOUSE	O61789 mus musculu
32	88	11.9	810	1 NELL1_HUMAN	Q92832 homo sapien
33	88	11.9	2139	1 CRB_DROME	P10040 drosophila

RESULT 1

ID	41BB_HUMAN	STANDARD;	PRT;	255 AA.
AC	Q07011;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)			
DE	(T-CELL ANTIGEN ILA) (CD137 ANTIGEN).			
GN	TNFRSF9 OR ILA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RX	MEDLINE=94374434; PubMed=8088337;			
RA	Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,			
RA	Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;			
RT	"Molecular and biological characterization of human 4-1BB and its			
RT	ligand."			
RL	Eur. J. Immunol. 24:2219-2227(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RX	MEDLINE=94085794; PubMed=8262389;			
RA	Schwarz H., Tuckwell J., Lotz M.;			
RT	"A receptor induced by lymphocyte activation (ILA): a new member of			
RT	the human nerve-growth-factor/tumor-necrosis-factor receptor			
RT	family."			
RN	[3]			
RP	REVISION TO 107.			
RA	Schwarz H.;			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95347766; PubMed=7622190;			
RA	Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,			
RA	Kwon B.S.;			
RT	"Characterization of human homologue of 4-1BB and its ligand.";			
RT	Immunol. Lett. 45:67-73(1995).			
CC	- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY			
CC	ACTIVE DURING T CELL ACTIVATION.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T			
CC	CELLS.			
CC	- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry.			
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			

34	88	11.9	2531	1	NTCL_MOUSE	Q01705 mus musculu
35	87.5	11.9	867	1	SSPO_BOVIN	P98167 bos taurus
36	87.5	11.9	1172	1	TSP2_MOUSE	Q03390 mus musculu
37	87.5	11.9	1964	1	NTC4_MOUSE	P31695 mus musculu
38	87	11.8	415	1	TNRC_MOUSE	P50284 mus musculu
39	87	11.8	961	1	TSPA_HUMAN	P35443 homo sapien
40	87	11.8	1394	1	TGFB_HUMAN	P22084 homo sapien
41	87	11.8	1786	1	LMB1_MOUSE	P02459 mus musculu
42	86	11.7	169	1	KRUA_HUMAN	P26371 homo sapien
43	86	11.7	1170	1	TSP2_BOVIN	Q95116 bos taurus
44	86	11.7	1173	1	TSP1_XENLA	P35448 xenopus lae
45	86	11.7	1210	1	EGFR_MOUSE	Q01279 mus musculu

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CC EMBL; U03397; AAA53133.1; -;  
 DR EMBL; L12964; AAA62478.2; -;  
 DR HSSP; P19438; 1EXT.  
 DR MIM; 602250; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 2;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1;  
 DR PROSITE; PS00652; TNFR\_NGFR\_2; 1;  
 KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 17  
 FT CHAIN 18 255  
 FT DOMAIN 18 186  
 FT TRANSMEM 187 213  
 FT DOMAIN 214 255  
 FT REPEAT 47 159  
 FT REPEAT 47 86  
 FT REPEAT 87 118  
 FT REPEAT 119 159  
 FT CARBOHYD 138 138  
 FT CARBOHYD 149 149  
 SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;

Query Match 21.6%; Score 159.5; DB 1; Length 255;  
 Best Local Similarity 31.9%; Pred. No. 8.2e-08;  
 Matches 44; Conservative 12; Mismatches 43; Indels 39; Gaps 8;  
 QY 3 RCRVHTTCRDYPG-----EECCS-----EWDCMCVQPEFHCGDPCCTTCRHHPCPPGQ 53  
 Db 60 RTCDI-----CRCKGVFTKESSTNSAECDC---TPGFHCLGAGCSMC-EQDCKQGG 110  
 QY 54 GVSQKSFSGFCIDCASGTFSGGHEGCHKPWTDCTQFGFLTVFPNGKTHNAVCPVG-- 111  
 Db 111 ELTKKG-----CKDCFGTFNDKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPA 163  
 QY 112 -----SPPA---RP 117  
 Db 164 DLSPGASSVTPPAPAREP 181

RESULT 2  
 OX40\_MOUSE  
 ID OX40\_MOUSE STANDARD; PRT; 272 AA.  
 AC P47741;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).  
 GN TNFRSF4 OR TXGP1 OR OX40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Caldarhead D.M., Buhlmann J.E., van den Eertwegh A.J.,  
 RA Claassen E., Noelle R.J., Fell H.;  
 RT "Cloning of mouse OX40: a T cell activation marker that may mediate  
 RT T-B cell interactions";  
 RL J. Immunol. 151:5261-5271(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Barclay A.N.;  
 RT "Gene structure and chromosomal localization of the mouse homologue

RT of rat OX40 protein.";  
 RL Eur. J. Immunol. 25:926-930(1995).  
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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CC EMBL; Z21674; CAA79772.1; -;  
 DR EMBL; X85214; CAA59476.1; -;  
 DR HSSP; P25942; 1CDF.  
 DR MGD; MGI:104512; Tnfrsf4.  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 3;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3;  
 DR PROSITE; PS00652; TNFR\_NGFR\_2; 2;  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 272  
 FT DOMAIN 20 211  
 FT TRANSMEM 212 236  
 FT DOMAIN 237 272  
 FT DOMAIN 26 165  
 FT REPEAT 26 61  
 FT REPEAT 62 103  
 FT REPEAT 104 124  
 FT REPEAT 125 165  
 FT CARBOHYD 144 144  
 FT CONFLICT 15 15  
 SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 21.4%; Score 158; DB 1; Length 272;  
 Best Local Similarity 27.4%; Pred. No. 1.2e-07;  
 Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;  
 QY 5 CRVHT---TRCCRD-YPG-----EECCSEWDCMCVQPEFHCGDPC----- 40  
 Db 27 CVKHTYPSGHKCCRECQPGHGMVSRCDHTDITLC-----HPCETGFYNEAVNYDTCK 78  
 QY 41 -CTTCRHHP-----CPPGQGVQSGKFSFGFCIDCASGTFSGGHEGH 82  
 Db 79 QCTQCNRHRSSELKQNCCTPTQDVTVCRCRPGTQPRQDSGYKLGVCVCPGPPHSPGNNOA 138  
 QY 83 CKPWTDCTQFGFLTVFPNGKTHNAV 108  
 Db 139 CKPWNTCTLSGKQTRHPASDSDAVC 164

RESULT 3  
 OX40\_HUMAN  
 ID OX40\_HUMAN STANDARD; PRT; 277 AA.  
 AC P43489; Q13663;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY  
 DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).  
 GN TNFRSF4 OR TXGP1L.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=941170844; PubMed=7510240;





```

F:2488-2523/Domain: EGF homology <EGF>

Query Match      14.0%; Score 105.5; DB 2; Length 2907;
Best Local Similarity 26.8%; Pred. No. 0.25;
Matches 33; Conservative 11; Mismatches 40; Indels 39; Gaps 8;

QY 2 CGPGRLLLTGTDAKCC-----RVHTTRCCRDYPGEECCSEWDCMCVQPEFHCG 50
Db 677 CPPG---LAVGVDRVCVDTHTMRSTCYGEIKKGVCVRPFPGAVTKSE--CCCANDPDYGF 731
QY 51 DPCTTTCRHHPCPPGQGVQSQGKFSFGF-----QC-ID---CASG---TFSGGHE 93
Db 732 EPC-----QPCPAKNSAEFHGLCSGGIGITVDGRDINECALDPDICANGICENLRGT 785
QY 94 GNC 96
Db 786 CNC 788

Search completed: September 4, 2001, 16:12:13
Job time: 1110 sec

```

A:Molecule type: mRNA

A:Residues: 1-277 <RES>

A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958

C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 19.3%; Score 145.5; DB 2; Length 277;  
Best Local Similarity 31.0%; Pred. No. 2.7e-05;  
Matches 39; Conservative 10; Mismatches 66; Indels 11; Gaps 4;

QY 2 CGPGRLLLTGTDAACRCRVTTRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCT 55

Db 46 CRP-----GNGMVSKRSQNTVCRPGEGFNVVSSRPCKPCTWCNLSRSGERKQLCT 100

QY 56 TCRHHPCPPGGVQSGKFSFGQICDASGTFSGHGHCKPWTCTDCTQFGFLTVPNGK 115

Db 101 ATQDTVCRACGTQPLDSYKPGVDCAPCPGPHGSPCDNACKPWTNCTLAGKHTLPASN 160

QY 116 THNAVC 121

Db 161 SSDAIC 166

RESULT 6

JC5559

lectin-B - Virginian pokeweed

C:Species: Phytolacca americana (Virginian pokeweed)

C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000

C:Accession: JC5559

R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.

Biosci. Biotechnol. Biochem. 61, 690-698, 1997

A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)

A:Reference number: JC5559; MUID:97290889

A:Accession: JC5559

A:Molecule type: protein

A:Residues: 1-295 <YAM>

A:Experimental source: root

C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharide

C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase

C:Keywords: glycoprotein

F:96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.4%; Score 138.5; DB 2; Length 295;

Best Local Similarity 31.7%; Pred. No. 0.00011;

Matches 33; Conservative 17; Mismatches 31; Indels 23; Gaps 7;

QY 2 CGPGRLLLTGTDAACRCRVTTRCCRDYPG-----EECCSEWDCM-CVQPEFHCGDPCCT 56

Db 154 CGITEGYCGEGCQSQC---NHQRCCKDFAGRTCLNDLCCSENG-WCGSSEAHCGGCGSQSN 209

QY 57 CRHHPCPPGGVQSGKFSFGTQ-C---IDCASGTFSGGHEHC 96

Db 210 CNYNRC-----GR-NFGFRTCPNELCCSSGGMGCSNDAHC 243

RESULT 7

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000

C:Accession: A46476; A46515

R:Torres, R.M.; Clark, E.A.

J. Immunol. 148, 620-626, 1992

A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine

A:Reference number: A46476; MUID:92105763

A:Accession: A46476

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305 <TOR>

A:Cross-references: GB:M83312; NID:g1553058

A:Note: sequence extracted from NCBI backbone (NCBI:75206, NCBIP:75207)

A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0

R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay  
J. Immunol. 149, 3921-3926, 1992

A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A:Reference number: A46515; MUID:93094586

A:Accession: A46515

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-287, 'IV' <GRI>

A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126

A:Experimental source: BALB/c, liver

A:Note: sequence extracted from NCBI backbone (NCBI:120357)

C:Comment: For an alternative splice form, see PIR:A46515.

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: alternative splicing; transmembrane protein

F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 16.9%; Score 127.5; DB 2; Length 305;

Best Local Similarity 28.9%; Pred. No. 0.00089;

Matches 37; Conservative 8; Mismatches 72; Indels 11; Gaps 5;

QY 2 CGPGRLLLTGTDAACRCRVTTRCCRDYPG-----EECCSEWDCM-CVQPE-FHCGDPCCTT 56

Db 62 CDSGEFSAOWNRETRC---HQHRCPEPNQGLRVKKEGTAEEDTCTCKEGQHCSTKDEA 118

QY 57 C-RHHPCPPGGVQSGKFSFGQICDASGTFSGGHE--GHCKPWTCTQFGFLTVPNG 113

Db 119 CAQHTPCIPGFGVEMWEMATETDTVCHPCVPVGFSSNOSLFKCYPMWTSCEBDKNLEVLQKG 178

QY 114 NKTHNAVC 121

Db 179 TSOTNVIC 186

RESULT 8

MMRTS

laminin beta-2 chain precursor - rat

N:Alternate names: laminin chain B3; S-laminin

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999

C:Accession: S03539

R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.

Nature 338, 229-234, 1989

A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the ne

A:Reference number: S03539; MUID:89159410

A:Accession: S03539

A:Molecule type: mRNA

A:Residues: 1-1801 <HUN>

A:Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251

C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin

C:Function:

A:Description: Interact with cells and with other basement membrane proteins to promo

C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellu

F:1-35/Domain: signal sequence #status predicted <SIG>

F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>

F:36-285/Domain: VI <DOM6>

F:286-555/Domain: V <DOM5>

F:286-347/Domain: laminin-type EGF-like homology <LEO1>

F:350-410/Domain: laminin-type EGF-like homology <LEO2>

F:413-470/Domain: laminin-type EGF-like homology <LEO3>

F:473-522/Domain: laminin-type EGF-like homology <LEO4>

F:525-555/Domain: laminin-type EGF-like homology #status atypical <LEO5>

F:556-784/Domain: IV <DOM4>

F:786-831/Domain: laminin-type EGF-like homology <LEO6>

F:788-1196/Domain: III <DOM3>

F:834-877/Domain: laminin-type EGF-like homology <LEO7>

F:880-927/Domain: laminin-type EGF-like homology <LEO8>

F:930-986/Domain: laminin-type EGF-like homology <LEO9>

F:989-1038/Domain: laminin-type EGF-like homology <LEO10>

F:1041-1095/Domain: laminin-type EGF-like homology <LEO11>

F:1098-1143/Domain: laminin-type EGF-like homology <LEO12>

F;1146-1190/Domain: laminin-type EGF-like homology <LE13>

F;1197-1412/Domain: II <DOM2>

F;1197-1412/Region: heptad repeats

F;1413-1445/Domain: alpha <ALP>

F;1446-1801/Region: heptad repeats

F;1446-1801/Domain: I <DOM1>

F;45-50/Disulfide bonds: #status predicted

F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status F

F;1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 15.6%; Score 117.5; DB 1; Length 1801;

Best Local Similarity 25.9%; Pred. No. 0.019;

Matches 44; Conservative 3; Mismatches 42; Indels 81; Gaps 9;

QY 18 CRVHTTRC--CRDYPGEGECSEWDCMCVQPEFHCGDPCCT---TCRHPCPPGGQVQSG 72

DB 889 CDATGACGLGRDTGGEHCEB-----CI-AGFH-GDPLPYGGQRCPCPCPEGFG--SQR 940

QY 73 KFS-----FGQCIDCASGTF----- 88

DB 941 HFATSCHRDGYSQIVCHCRAGYTGRLCEACAPGHGDPSPKPGRCQLCECSGNIDPTDP 1000

QY 89 -----SGGHEGCHKPWTCTQFGFLTVPFGKTHNAVC 121

DB 1001 GACDPHTGQCLRLHHTGPHGCHKP-----GFHGQAARQSCHRCTC 1043

RESULT 9

A60771

B-cell activation protein CD40 precursor - human

N;Alternate names: B-cell surface antigen Bp50

C;Species: Homo sapiens (man)

C;Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000

C;Accession: S04460; A60771

R;Stamenkovic, I.; Clark, E.A.; Seed, B.

EMBO J. 8, 1403-1410, 1989

A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor

A;Reference number: S04460; MUID:89356608

A;Molecule type: mRNA

A;Residues: 1-277 <STA>

A;Cross-references: EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:g29851

R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.

J. Immunol. 142, 562-567, 1989

A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like

A;Reference number: A60771; MUID:89093941

A;Accession: A60771

A;Molecule type: protein

A;Residues: 21-50 <BRA>

A;Experimental source: Burkitt lymphoma cell line Raji

C;Genetics:

A;Gene: GDB:CD40

A;Cross-references: GDB:215268; OMIM:109535

A;Map position: 20q12-20q13.2

C;Superfamily: CD27 antigen; NGF receptor repeat homology

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-27/Product: B-cell activation protein CD40 #status experimental <MAT>

F;21-193/Domain: extracellular #status predicted <EXT>

F;194-215/Domain: transmembrane #status predicted <TM>

F;216-277/Domain: intracellular #status predicted <CYT>

F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.2%; Score 114.5; DB 2; Length 277;

Best Local Similarity 27.3%; Pred. No. 0.0099;

Matches 35; Conservative 10; Mismatches 72; Indels 11; Gaps 5;

QY 2 CGPRLLLGTGTARCRVHTTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 56

DB 62 CGESEFLDTWNRTHC---HQHKYCDNLGLRVQOKGTSETDTTICTCEGWHCTSEACES 118

QY 57 C-RHHPCPPGGQVQSGKFSFGFCQICDCASGTFSGGHEG--HCKPWTCTQFGFLTVPFG 113

DB 119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGFGFNSVSAFEKCHPWTSCETKDLVVQAG 178

QY 114 NKTHNAVC 121

DB 179 TNKTDVVC 186

RESULT 10

I54182

tumor necrosis factor receptor 2-related protein - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000

C;Accession: I54182

R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

Genomics 16, 214-218, 1993

A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq

A;Reference number: I54182; MUID:93252381

A;Accession: I54182

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-435 <RES>

A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762

C;Genetics:

A;Gene: GDB:LTBR

A;Cross-references: GDB:1230195; OMIM:600979

A;Map position: 12p13.3-12p13.1

C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 14.9%; Score 112.5; DB 2; Length 435;

Best Local Similarity 25.2%; Pred. No. 0.019;

Matches 39; Conservative 12; Mismatches 63; Indels 41; Gaps 9;

QY 2 CGPRLLLGTGTARCRVHTTRC-----CRDYPGEE-----C 34

DB 62 CPP-----GTVSARKSRIRDTVCATCAENSNEHWNLTTCQLCRPCDPVPMGLEEIAFC 116

QY 35 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGGQVQSGKFSFG--FQCIDCASGTF 88

DB 117 TSKRKTQRC--QPMFCAAWALECTHCELLSDCPGCTAELEKDEVGKGNHCVPCAGHF 175

QY 89 --SGGHEGCHKPWTCTQFGFLTVPFGKTHNAVC 121

DB 176 QNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 210

RESULT 11

T18975

hypothetical protein C06A1.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T18975

R;McMurray, A.

submitted to the EMBL Data Library, June 1995

A;Reference number: Z19054

A;Accession: T18975

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-152 <WIL>

A;Cross-references: EMBL:Z49886; PIDN:CAA90055.1; GSPDB:GN00020; CESP:C06A1.6

A;Experimental source: clone C06A1

C;Genetics:

A;Gene: CESP:C06A1.6

A;Map position: 2

A;Introns: 22/3

Query Match 14.9%; Score 112; DB 2; Length 152;

Best Local Similarity 34.9%; Pred. No. 0.011;

Matches 30; Conservative 0; Mismatches 32; Indels 24; Gaps 5;

Result No.	Score	Query Match	Length	ID	Description
1	162	21.5	272	2	gene ox40 protein
2	152.5	20.3	255	2	lymphocyte activat
3	149.5	19.9	271	2	OX40 antigen precu
4	149	19.8	256	2	T-cell antigen 4-1
5	145.5	19.3	277	2	OX40 homolog - hum
6	138.5	18.4	295	2	lectin-B - Virgini
7	127.5	16.9	305	2	B cell-associated
8	117.5	15.6	1801	1	laminin beta-2 cha
9	114.5	15.2	277	2	B-cell activation
10	112.5	14.9	435	2	tumor necrosis fac
11	112	14.9	152	2	hypothetical prote
12	111.5	14.8	1798	2	laminin beta-2 cha
13	111	14.7	461	1	tumor necrosis fac
14	107	14.2	164	2	hypothetical prote
15	105.5	14.0	2907	2	fibrillin-2 precur
16	104.5	13.9	459	2	gene murine tumour
17	103.5	13.7	1574	2	MEGF6 protein - ra
18	103.5	13.7	2918	2	fibrillin-2 precur
19	103	13.7	474	2	tumor necrosis fac
20	103	13.7	1797	2	laminin beta-2 cha
21	102.5	13.6	188	2	hypothetical prote
22	102	13.5	1371	2	insulin-like growt
23	98	13.0	329	2	insulin-like growt
24	97	12.9	1820	2	latent transformin
25	96.5	12.8	540	2	insulin receptor-r
26	96.5	12.8	1713	2	adhesive ligand ep
27	96	12.7	416	1	nerve growth facto
28	95	12.6	1268	2	insulin receptor-r
29	93	12.4	212	2	agglutinin isolact

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C;Accession: I38426; JT0752  
R;Alfredson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R  
Eur. J. Immunol. 24, 2219-2227, 1994  
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A;Reference number: I38426; MUID:94374434  
A;Accession: I38426  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-255 <RES>  
A;Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA5313.1; PID:g571321  
Gene 134, 295-298, 1993  
R;Schwarz, H.; Tuckwell, J.; Lotz, M.  
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne  
A;Reference number: JT0752; MUID:94085794  
A;Accession: JT0752  
A;Molecule type: mRNA  
A;Residues: 1-106, R', 108-255 <SCH>  
C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
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F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict  
F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

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QY 2 CGPGRLLGGTGDARCCRVHTTCCRDYPG-----EBCCS-----EWDGCMVQPEFHCGDP 52  
Db 48 CPPNSFSSAGG--QRTCDI-----CROCKGVFRKCKSTSNACDC---TPGFHCLGA 97  
QY 53 CCTTCRHHPPGQVQSGQKFSFGFCIDCASGTFSGGHEGCKPWTCTQFGFLTVFP 112  
Db 98 GCSMC-EQDCKQGELTKG-----CKDCCFCFTNDQKRGICRPWTNCLDGSKSLVN 149  
QY 113 GNKTHNAV 121  
Db 150 GTRERDVVC 158

RESULT 3  
SL2783  
OX40 antigen precursor - rat  
N;Alternate names: nerve growth factor receptor homolog  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C;Accession: SL2783; S08036  
R;Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte  
A;Reference number: SL2783; MUID:90214614  
A;Accession: SL2783  
A;Molecule type: mRNA  
A;Residues: 1-271 <NAL>  
A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: growth factor receptor; transmembrane protein  
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QY 7 LLLG--TGTDAKCCRVHTT-----RCCRD-YPGEECCSEWD-----CMCVOPEFHCG-- 50  
Db 12 LLLGLSGVTVKLNCVKTDPGSHKCCRECPQGHGWSRCDHTRTVTHPCPGPGYNEAV 71  
QY 51 --DPC--CTTCRRH-----PCPPGQVQSGQKFSFGFCIDCASGTF 89  
Db 72 NYDTCKQCTQCNRHSRSGSELKONCTPTEDTVQCRRGTQPRQDSSHKLGVDVCPGPHFS 131  
QY 90 GGHEGCKPWTCTQFGFLTVFPGNKTHNAV 121  
Db 132 PGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 4  
B32393  
T-cell antigen 4-1BB precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C;Accession: B32393; I48879  
R;Kwon, B.S.; Weissman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A;Title: cDNA sequence of two inducible T-cell genes.  
A;Reference number: A32393; MUID:89184547  
A;Accession: B32393  
A;Molecule type: mRNA  
A;Residues: 1-256 <KWO>  
A;Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994  
A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B  
A;Reference number: I48879; MUID:94179805  
A;Accession: I48879  
A;Status: preliminary; translated from GB/EMBL/DBJ  
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A;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: transmembrane protein  
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QY 58 RHHPCCPGQVQSGQKFSFGFCIDCASGTFSGGH-EGHCKPWTCTQFGFLTVFPGNKT 116  
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QY 117 HNAV 121  
Db 154 KDVC 158

RESULT 5  
I37552  
OX40 homolog - human  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C;Accession: I37552  
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo  
Eur. J. Immunol. 24, 677-683, 1994  
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen  
A;Reference number: I37552; MUID:94170844  
A;Accession: I37552  
A;Status: preliminary; translated from GB/EMBL/DBJ



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FT DOMAIN 1072 1113 EGF-LIKE 15, CALCIUM-BINDING.
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CC EMBL; L04270; AAA36757.1; -.
DR HSSP; P25942; ICDF.
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DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
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DR PROSITE; PS00050; TNFR_NGFR_2; 3.
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RESULT 12

Id LMB2\_MOUSE STANDARD; PRT: 1799 AA.

AC Q61292; Q62182;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE LAMININ BETA-2 CHAIN PRECURSOR.

GN LAMB2 OR S-LAM OR LAMS.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/J;

RX MEDLINE=96278760; PubMed=8662701;

RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,  
 RA Albrechtsen R., Wewer U.M.;  
 RT "Structural organization of the human and mouse laminin beta2 chain  
 RT genes, and alternative splicing at the 5' end of the human  
 RT transcript.";  
 RL J. Biol. Chem. 271:13407-13416(1996).  
 RN [2]  
 RP SEQUENCE OF 348-428 FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=94319092; PubMed=8043959;  
 RA Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Menesquzzi G.;  
 RT "S-laminin gene (Lams) maps to F1 band of mouse chromosome 9.";  
 RL Mamm. Genome 5:393-394(1994).  
 RN [3]  
 RP FUNCTION.  
 RC STRAIN=129/J;  
 RX MEDLINE=95191650; PubMed=7885444;  
 RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;  
 RT "Aberrant differentiation of neuromuscular junctions in mice lacking  
 RT s-laminin/laminin beta 2.";  
 RL Nature 374:258-262(1995).  
 CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
 CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
 CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT.  
 CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
 CC -!- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR  
 CC NERVE TERMINALS.  
 CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
 CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
 CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
 CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
 CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT  
 CC MEMBRANES (MAJOR COMPONENT).  
 CC -!- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.  
 CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
 CC -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
 CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
 CC -!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
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EMBL; U43541; AAC53535.1; -.

EMBL; U42624; AAC53535.1; JOINED.

EMBL; X75928; CAA53532.1; -.

HSSP; P02468; 1KLO.

MGD; MGI:99916; Lamb2.

InterPro; IPR000561; -.

InterPro; IPR001886; -.

InterPro; IPR002049; -.

Pfam; PF00053; laminin\_EGF; 13.

Pfam; PF00055; laminin\_Nterm; 1.

PRINTS; PR00011; EGFLAMININ.

PROSITE; PS00022; EGF\_1; 10.

PROSITE; PS01186; EGF\_2; 2.

PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.

PROSITE; PS01248; LAMININ\_NTERM; 1.

PROSITE; PS01248; LAMININ\_NTERM; 1.

PROSITE; PS01248; LAMININ\_NTERM; 1.

PROSITE; PS01248; LAMININ\_NTERM; 1.

PROSITE; PS01248; LAMININ\_NTERM; 1.

FT	DOMAIN	350	412	.LAMININ EGF-LIKE 2.
FT	DOMAIN	413	472	.LAMININ EGF-LIKE 3.
FT	DOMAIN	473	524	.LAMININ EGF-LIKE 4.
FT	DOMAIN	525	555	.LAMININ EGF-LIKE 5 (INCOMPLETE).
FT	DOMAIN	556	782	.LAMININ DOMAIN IV.
FT	DOMAIN	783	1191	8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).
FT	DOMAIN	784	831	.LAMININ EGF-LIKE 6.
FT	DOMAIN	832	877	.LAMININ EGF-LIKE 7.
FT	DOMAIN	878	927	.LAMININ EGF-LIKE 8.
FT	DOMAIN	928	986	.LAMININ EGF-LIKE 9.
FT	DOMAIN	987	1038	.LAMININ EGF-LIKE 10.
FT	DOMAIN	1039	1095	.LAMININ EGF-LIKE 11.
FT	DOMAIN	1096	1143	.LAMININ EGF-LIKE 12.
FT	DOMAIN	1144	1190	.LAMININ EGF-LIKE 13.
FT	DOMAIN	1191	1410	DOMAIN II.
FT	DOMAIN	1411	1443	DOMAIN ALPHA.
FT	DOMAIN	1444	1799	DOMAIN I.
FT	DOMAIN	1257	1304	COILED COIL (POTENTIAL).
FT	DOMAIN	1473	1527	COILED COIL (POTENTIAL).
FT	DOMAIN	1577	1791	COILED COIL (POTENTIAL).
FT	DISULFID	286	295	BY SIMILARITY.
FT	DISULFID	288	313	BY SIMILARITY.
FT	DISULFID	315	324	BY SIMILARITY.
FT	DISULFID	327	347	BY SIMILARITY.
FT	DISULFID	350	359	BY SIMILARITY.
FT	DISULFID	352	377	BY SIMILARITY.
FT	DISULFID	380	389	BY SIMILARITY.
FT	DISULFID	392	410	BY SIMILARITY.
FT	DISULFID	413	426	BY SIMILARITY.
FT	DISULFID	415	441	BY SIMILARITY.
FT	DISULFID	443	452	BY SIMILARITY.
FT	DISULFID	455	470	BY SIMILARITY.
FT	DISULFID	473	487	BY SIMILARITY.
FT	DISULFID	475	494	BY SIMILARITY.
FT	DISULFID	496	505	BY SIMILARITY.
FT	DISULFID	508	522	BY SIMILARITY.
FT	DISULFID	784	796	BY SIMILARITY.
FT	DISULFID	786	803	BY SIMILARITY.
FT	DISULFID	805	814	BY SIMILARITY.
FT	DISULFID	817	829	BY SIMILARITY.
FT	DISULFID	832	844	BY SIMILARITY.
FT	DISULFID	834	851	BY SIMILARITY.
FT	DISULFID	853	862	BY SIMILARITY.
FT	DISULFID	865	875	BY SIMILARITY.
FT	DISULFID	878	887	BY SIMILARITY.
FT	DISULFID	880	894	BY SIMILARITY.
FT	DISULFID	897	906	BY SIMILARITY.
FT	DISULFID	909	925	BY SIMILARITY.
FT	DISULFID	928	944	BY SIMILARITY.
FT	DISULFID	930	955	BY SIMILARITY.
FT	DISULFID	957	966	BY SIMILARITY.
FT	DISULFID	969	984	BY SIMILARITY.
FT	DISULFID	987	1001	BY SIMILARITY.
FT	DISULFID	989	1008	BY SIMILARITY.
FT	DISULFID	1011	1020	BY SIMILARITY.
FT	DISULFID	1023	1036	BY SIMILARITY.
FT	DISULFID	1036	1108	BY SIMILARITY.
FT	DISULFID	1098	1115	BY SIMILARITY.
FT	DISULFID	1117	1126	BY SIMILARITY.
FT	DISULFID	1129	1141	BY SIMILARITY.
FT	DISULFID	1144	1156	BY SIMILARITY.
FT	DISULFID	1146	1163	BY SIMILARITY.
FT	DISULFID	1165	1174	BY SIMILARITY.
FT	DISULFID	1177	1188	BY SIMILARITY.
FT	DISULFID	1191	1191	INTERCHAIN (PROBABLE).
FT	DISULFID	1194	1194	INTERCHAIN (PROBABLE).
FT	DISULFID	1798	1798	INTERCHAIN (PROBABLE).
FT	CARBOHYD	251	251	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	371	371	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1086	1086	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1250	1250	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1309	1309	N-LINKED (GLCNAC. . .)

[illegible]





RP CHARACTERIZATION.  
RX MEDLINE=93016040; PubMed=1328224;  
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
RT Lipari M.T., Goeddel D.V.;  
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
RT Characterization of ligand binding, internalization, and receptor  
RT phosphorylation.";  
RL J. Biol. Chem. 267:21172-21178(1992).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
RX MEDLINE=99221490; PubMed=10206649;  
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
RT "Structural basis for self-association and receptor recognition of  
RT human TRAF2.";  
RL Nature 398:533-538(1999).  
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND  
CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
CC LEVEL ON THREONINE RESIDUES.  
CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND  
CC WYETH-AVERT). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING  
CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO  
CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".  
CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
CC WWW="http://www.enbrelinfo.com/".  
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CC -----  
DR EMBL; M32315; AAA59929.1; -  
DR EMBL; M35857; AAA63262.1; -  
DR EMBL; U52165; AAC50622.1; -  
DR EMBL; U52156; AAC50622.1; JOINED.  
DR EMBL; U52157; AAC50622.1; JOINED.  
DR EMBL; U52158; AAC50622.1; JOINED.  
DR EMBL; U52159; AAC50622.1; JOINED.  
DR EMBL; U52160; AAC50622.1; JOINED.  
DR EMBL; U52161; AAC50622.1; JOINED.  
DR EMBL; U52162; AAC50622.1; JOINED.  
DR EMBL; U52163; AAC50622.1; JOINED.  
DR EMBL; U52164; AAC50622.1; JOINED.  
DR EMBL; M55994; AAA36755.1; -  
DR PIR; A35356; A35356.  
DR PIR; A36007; A36007.  
DR PIR; A36475; A36475.  
DR PIR; B35010; B35010.  
DR PIR; A23666; A23666.  
DR PDB; 1CA9; 12-APR-99.  
DR MIM; 191191; -  
DR InterPro; IPR001368; -  
DR Pfam; PF00020; TNFR\_C6; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 4.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
KW Phosphorylation; Pharmaceutical; 3D-structure.  
FT SIGNAL 1 22  
FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.  
FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 258 287 POTENTIAL.  
FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 39 201 4 X TNFR-CYS.  
FT REPEAT 39 76 TNFR-CYS 1.  
FT REPEAT 77 118 TNFR-CYS 2.

FT REPEAT 119 162 TNFR-CYS 3.  
FT REPEAT 163 201 TNFR-CYS 4.  
FT DISULFID 40 53 BY SIMILARITY.  
FT DISULFID 54 67 BY SIMILARITY.  
FT DISULFID 57 75 BY SIMILARITY.  
FT DISULFID 78 93 BY SIMILARITY.  
FT DISULFID 96 110 BY SIMILARITY.  
FT DISULFID 100 118 BY SIMILARITY.  
FT DISULFID 120 126 BY SIMILARITY.  
FT DISULFID 134 143 BY SIMILARITY.  
FT DISULFID 137 161 BY SIMILARITY.  
FT DISULFID 164 179 BY SIMILARITY.  
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 193 193 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 141 141 R -> P (IN REF. 4).  
FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).  
FT CONFLICT 363 363 A -> T (IN REF. 4).  
SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;  
Query Match 15.0%; Score 113; DB 1; Length 461;  
Best Local Similarity 25.8%; Pred. No. 0.0016;  
Matches 39; Conservative 14; Mismatches 60; Indels 38; Gaps 8;  
QY 2 CGPG---RLLTGTGDARC-----CRVHTRCRDYPGECCSEWD-- 39  
DB 57 CSPQGHARVCTKTSDTVDCSDSTYTQLWNWVPECLSCGSSDQVETQACTREQNR 116  
QY 40 -CMCVQPEFHC-----GDPCCCTCRHHPCPPGGQVSGQKFSFGFCIDCASGTFSG-- 90  
DB 117 ICTC-RGWYCALSKQECRCALPLR--KCRPGGVARPGTETSDVCKPCAPGFSNTT 173  
QY 91 GHEGHCPRWTDCTQFGTLTFPGNKNTHNAV 121  
DB 174 SSTDCRPHQICN---VVAIPGNASRDVAV 200  
RESULT 11  
TNRC HUMAN STANDARD; PRT; 435 AA.  
ID P36941;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR  
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).  
GN LTBR OR TNFR OR TNFRSF3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
RA "Construction and evaluation of a hncDNA library of human 12p  
RT transcribed sequences derived from a somatic cell hybrid.";  
RL Genomics 16:214-218(1993).  
RN [2]  
RP FUNCTION.  
RX MEDLINE=94225209; PubMed=8171323;  
RX Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
RT "A lymphotoxin-beta-specific receptor.";  
RL Science 264:707-710(1994).  
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
CC IMMUNE DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -----  
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Pfam: PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 289 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;  
 SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;  
 Query Match 16.9%; Score 127.5; DB 1; Length 289;  
 Best Local Similarity 28.9%; Pred. No. 5.4e-05;  
 Matches 37; Conservative 8; Mismatches 72; Indels 11; Gaps 5;  
 QY 2 CGPGRLLLTGTDCRCRVHTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 56  
 DB 62 CDSGEFSAQWNRREIRC---HQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQCHTSKDCEA 118  
 QY 57 C-RHHPCPGGVQSGQKFSFGFCIDCASGTFSGGHE--GHCKPWTDCQFGFLTVPFG 113  
 DB 119 CAQHTPCIPGFGVEMETATETDTVCHPCPVGFFSNQSSLFKCYPTWSCEDKNLEVLQKG 178  
 QY 114 NKTHNAVC 121  
 DB 179 TSQTNVIC 186  
 RESULT 7  
 CD40\_BOVIN STANDARD; PRT; 269 AA.  
 AC Q28203;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).  
 GN TNFRSF5 OR CD40.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97281252; PubMed=9135560;  
 RA Hirano A., Brown W.C., Estes D.M.;  
 RT "Cloning, expression and biological function of the bovine CD40  
 RT homologue: role in B-lymphocyte growth and differentiation in  
 RT cattle.";  
 RL Immunology 90:294-300(1997).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 CC EMBL; U57745; AAC48710.1; -  
 DR HSSP; P25942; 1CDF.  
 DR InterPro; IPR001368; -  
 DR Pfam; PF00020; TNFR\_C6; 4.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 289 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 289 AA; 29983 MW; 745903F30F95F387 CRC64;  
 SQ SEQUENCE 289 AA; 29983 MW; 745903F30F95F387 CRC64;  
 Query Match 16.3%; Score 122.5; DB 1; Length 269;  
 Best Local Similarity 28.7%; Pred. No. 0.00015;  
 Matches 37; Conservative 9; Mismatches 70; Indels 13; Gaps 5;  
 QY 2 CGPGRLLLTGTDCRCRVHTRCCRDYPGEECCSEWD-----CMCVQPEFHCGDPCCT 55  
 DB 62 CGKGEFLSTWNRKYC---HEHRYCNPNLGLRIQSEGLTNTDTICVVEGQ-HCTSHTC 117  
 QY 56 TCRHHP-CPGGVQSGQKFSFGFCIDCASGTFSGGHEG--HCKPWTDCQFGFLTVP 112  
 DB 118 SCTPSHLCPLGFGVQKQIATGLDTCVCPGLGFFSNVSSAFKCRHWTSCKRGLVQHV 177  
 QY 113 GNKTHNAVC 121  
 DB 178 GTNKDVVC 186  
 RESULT 8  
 LMB2\_RAT STANDARD; PRT; 1801 AA.  
 AC P15800;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).  
 GN LMB2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89159410; PubMed=2922051;  
 RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;  
 RT "A laminin-like adhesive protein concentrated in the synaptic cleft  
 RT of the neuromuscular junction.";  
 RL Nature 338:229-234(1989).  
 CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
 CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
 CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
 CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
 CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
 CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
 CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
 CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
 CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
 CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC  
 CC CLEFT OF THE NEUROMUSCULAR JUNCTION.  
 CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.



RA Mallett S., Fossum S., Barclay A.N.;  
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T  
RT lymphocytes -- a molecule related to nerve growth factor receptor.";  
RL EMOB J. 9:1063-1068(1990).  
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -----  
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CC -----  
DR EMBL: X17037; CAA34897.1; .  
DR PIR: S08036; S08036.  
DR PIR: S12783; S12783.  
DR HSP: P25942; ICDF.  
DR InterPro: IPR001368; .  
DR Pfam: PF00020; TNFR\_C6; 3.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
KW Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 271  
FT DOMAIN 20 210  
FT TRANSMEM 211 235  
FT DOMAIN 236 271  
FT DOMAIN 25 164  
FT REPEAT 25 60  
FT REPEAT 61 102  
FT REPEAT 103 123  
FT REPEAT 124 164  
FT CARBOHYD 143 143  
FT SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;  
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Query Match 19.8%; Score 149.5; DB 1; Length 271;  
Best Local Similarity 28.9%; Pred. No. 5.3e-07;  
Matches 4; Conservative 11; Mismatches 60; Indels 37; Gaps 7;  
-----  
QY 7 LLLG--TCTDARCCRVHT-----RCCRD-YPGECCSEWD-----CMCVOPEFHCG-- 50  
DB 12 LLLGLSLGTVKLVCKDTPSGHKCCRCQPGHGMVSRCDHTRDTVCHPCPGFGYNEAV 71  
QY 51 --DPC--CTTCRHH-----PCPPGQGVQSGKFSFGFCIDCASGTFSS 89  
DB 72 NYDTCKOCTQCNHRSGSELKQNCPTEDTVQCRCRGTQPRQDSSHKLGVDCVPCPPGHFS 131  
QY 90 GGHEGCHKPWTDCQFGFLTVFPGNKTHNAV 121  
DB 132 PCSNQACKPWTNCTLSGRQIRHPASNSLDTVC 163  
-----  
RESULT 4  
41BB\_MOUSE STANDARD; PRT; 256 AA.  
ID 41BB\_MOUSE  
AC P20334;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 4-LBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-LBB).  
GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=89184547; PubMed=2784565;  
RA Kwon B.S., Weissman S.M.;  
RT "cDNA sequences of two inducible T-cell genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).  
RN [2]  
RC SEQUENCE FROM N.A.  
RC STRAIN=BALB/C.  
RX MEDLINE=94179805; PubMed=8133039;  
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;  
RT "Genomic organization and chromosomal localization of the T-cell  
RT antigen 4-LBB.";  
RN J. Immunol. 152:2256-2262(1994).  
RN [3]  
RP CHARACTERIZATION, AND SEQUENCE OF 25-29.  
RX MEDLINE=93139510; PubMed=7678621;  
RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T.,  
RA Kwon B.S.;  
RT "Inducible T cell antigen 4-LBB. Analysis of expression and  
RT function.";  
RL J. Immunol. 150:771-781(1993).  
CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-LBB. POSSIBLY  
CC ACTIVE DURING T CELL ACTIVATION.  
CC -1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.  
CC -1- ASSOCIATES WITH P56-LCK.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.  
CC -1- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -----  
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CC -----  
DR EMBL: J04492; AAA40167.1; .  
DR EMBL: U02567; AAA93113.1; .  
DR PIR: B32393; B32393.  
DR HSP: P25942; ICDF.  
DR MGD: MGI:1101059; Tnfrsf9.  
DR InterPro: IPR001368; .  
DR Pfam: PF00020; TNFR\_C6; 1.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; FALSE\_NEG.  
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 24  
FT CHAIN 25 256  
FT DOMAIN 25 187  
FT TRANSMEM 188 208  
FT DOMAIN 209 256  
FT DOMAIN 17 159  
FT REPEAT 17 45  
FT REPEAT 46 85  
FT REPEAT 86 117  
FT REPEAT 118 159  
FT CARBOHYD 128 128  
FT CARBOHYD 138 138  
FT SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;  
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Query Match 19.8%; Score 149; DB 1; Length 256;  
Best Local Similarity 31.2%; Pred. No. 5.6e-07;  
Matches 39; Conservative 17; Mismatches 51; Indels 18; Gaps 7;  
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QY 2 CGPGRLL-LLGTGTDAACRVHTTRCCRDYPGECCSEW----DCMCVOPEFHCGDPCCTTC 57  
DB 47 CPSTFSSIGGQPNCTCRV----CAGYFRKFKCSSTHNAECIEB-GFHCGLGPOCTRC 101  
QY 58 RHHPCPGQGVQSGKFSFGFCIDCASGTFSGGH-EGHCKPWTDCQFGFLTVFPGNK 116  
DB 102 -EKDCRPGBELTKQG-----CKTCSLGTGTFNDONGTGVCRPWTNCSLDGRSVLKTGTE 153



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:24 ; Search time 43.78 Seconds  
(without alignments)  
95,458 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_154

Perfect score: 753

Sequence: 1 GCGPRLLLGTGTARCCRV.....TQFGFLTVFPGKTHNAVCV 122

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	162	21.5	272	1	OX40_MOUSE
2	152.5	20.3	255	1	41BB_HUMAN
3	149.5	19.9	271	1	OX40_RAT
4	149	19.8	256	1	41BB_MOUSE
5	145.5	19.3	277	1	OX40_HUMAN
6	127.5	16.9	289	1	CD40_MOUSE
7	122.5	16.3	269	1	CD40_BOVIN
8	117.5	15.6	1801	1	LMB2_RAT
9	114.5	15.2	277	1	CD40_HUMAN
10	113	15.0	461	1	TNR2_HUMAN
11	112.5	14.9	435	1	TNR2_MOUSE
12	112.5	14.9	1799	1	LMB2_MOUSE
13	105.5	14.0	2907	1	FN2_MOUSE
14	103.5	13.7	1798	1	LMB2_HUMAN
15	103.5	13.7	2911	1	FN2_HUMAN
16	103	13.7	474	1	TNR2_MOUSE
17	102	13.5	1370	1	IG1R_RAT
18	99.5	13.2	2569	1	LMA3_MOUSE
19	96.5	12.8	581	1	IRR_RAT
20	96.5	12.8	1713	1	LMA3_HUMAN
21	96	12.7	416	1	NGFR_CHICK
22	95	12.6	1297	1	IRR_HUMAN
23	95	12.6	1373	1	IG1R_MOUSE
24	93	12.4	212	1	AG1_HORVU
25	93	12.4	3635	1	LMA5_MOUSE
26	92	12.2	956	1	TSP3_MOUSE
27	92	12.2	1367	1	IG1R_HUMAN
28	92	12.2	2871	1	FN1_BOVIN
29	92	12.2	2871	1	FN1_HUMAN
30	92	12.2	4289	1	TENX_HUMAN
31	91.5	12.2	213	1	AG12_WHEAT
32	91.5	12.2	1106	1	STC_DROME
33	91	12.1	186	1	AG13_WHEAT
					P47741 mus musculus
					Q07011 homo sapien
					P15725 rattus norv
					P20334 mus musculus
					P43489 homo sapien
					P27512 mus musculus
					Q28203 bos taurus
					P15800 rattus norv
					P25942 homo sapien
					P20333 homo sapien
					P36941 homo sapien
					Q61292 mus musculus
					Q61555 mus musculus
					P5268 homo sapien
					P35556 homo sapien
					P25119 mus musculus
					P24062 rattus norv
					Q61789 mus musculus
					Q64716 rattus norv
					P16787 homo sapien
					P18519 gallus gall
					P14616 homo sapien
					Q60751 mus musculus
					P15312 hordeum vul
					Q61001 mus musculus
					Q05895 mus musculus
					P08069 homo sapien
					P98133 bos taurus
					P35555 homo sapien
					P22105 homo sapien
					P02876 triticum ae
					P40798 drosophila
					P10969 triticum ae

## RESULT 1

ID	OX40_MOUSE	STANDARD;	PRT;	272 AA.
AC	P47741;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).			
GN	TNFRSF4 OR TXGP1 OR OX40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RN	[1]			
RC	STRAIN=BALB/C;			
RX	MEDLINE=94044750; PubMed=8228223;			
RA	Calderhead D.M., Buhlmann J.E., van den Bortwegh A.J.,			
RA	Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,			
RA	Barclay A.N.;			
RT	"Gene structure and chromosomal localization of the mouse homologue			
RT	of rat OX40 protein.";			
RL	Eur. J. Immunol. 25:926-930(1995).			
CC	-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; Z21674; CAA59476.1; -.			
DR	EMBL; X85214; CAA59476.1; -.			
DR	HSP; P25942; ICDP.			
DR	MGI; MGI:104512; Tnfrsf4.			
DR	InterPro; IPR001368; -.			
DR	Pfam; PF00020; TNFR_c6; 3.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.			
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;			
KW	Signal.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	272	OX40L RECEPTOR.
FT	DOMAIN	20	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	212	236	POTENTIAL.

## ALIGNMENTS

P50284 mus musculus  
Q95209 O sortilin-  
P31695 mus musculus  
P11219 oryza sativ  
P07942 homo sapien  
P49901 homo sapien  
P11364 drosophila  
P37889 mus musculus  
P10040 drosophila  
P26371 homo sapien  
P10968 triticum ae  
Q92832 homo sapien

34 91 12.1 415 1 TNRC\_MOUSE  
35 91 12.1 2213 1 SORL\_RABIT  
36 90.5 12.0 1964 1 NTC4\_MOUSE  
37 90 12.0 227 1 AGL\_ORYZA  
38 89.5 11.9 1786 1 LMB1\_HUMAN  
39 89 11.8 116 1 MCS\_HUMAN  
40 89 11.8 846 1 ITBX\_DROME  
41 88.5 11.8 1221 1 FBL2\_MOUSE  
42 88.5 11.8 2139 1 CRB\_DROME  
43 88 11.7 169 1 KRUH\_HUMAN  
44 88 11.7 212 1 AGL1\_WHEAT  
45 88 11.7 810 1 NEIL\_HUMAN

```
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 21.5%; Score 162; DB 1; Length 272;
Best Local Similarity 28.3%; Pred. No. 3.9e-08;
Matches 45; Conservative 11; Mismatches 51; Indels 52; Gaps 7;

QY 7 LLALGTGTAR--CCRVHT-----TRCCRD-YPG-----ECCSEWDCMVQPEFHGCDPC-- 53
DB 14 LALTLGVTARLNCVHKYTPSGHKCCRECPGHGMVSRCDHTRTLIC-----HFCET 65

QY 54 -----CTTCRHHP-----CPPGGVQSOGKFSFGFCID 82
DB 66 GFYNEAVNYDTCKQCTNHRSGSELKQNCPTPTDTCRCRPGTQPRQDSYKLGVDVCP 125

QY 83 CASGTFSGGEGHCKPWTCTQGTGFLTVFGNKTHNAVC 121
DB 126 CPPGHFSPGNQACKPWTCTLSGKQTRHPASDSDAVC 164

RESULT 2
41BB_HUMAN STANDARD; PRT; 255 AA.
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
GN TNFRSF9 OR ILA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand.";
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor
RT family.";
RL Gene 134:295-298(1993).
RN [3]
RP REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou B.S., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RT "Characterization of human homologue of 4-1BB and its ligand.";
RL Immunol. Lett. 45:67-73(1995).
CC -I- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
```

```
CC ACTIVE DURING T CELL ACTIVATION.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
CC CELLS.
CC -I- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U03397; AAA53133.1; -.
CC EMBL: L12964; AAA62478.2; -.
CC HSP; P19438; TEXT.
CC MIM; 602250; -.
CC InterPro; IPR001368; -.
CC Pfam; PF00020; TNFR_C6; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00050; TNFR_NGFR_2; 1.
CC Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
CC SIGNAL 1 17 POTENTIAL.
CC CHAIN 18 255 4-1BB LIGAND RECEPTOR.
CC DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 187 213 POTENTIAL.
CC DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 47 159 3 X TNFR-CYS.
CC REPEAT 47 86 TNFR-CYS 1.
CC REPEAT 87 118 TNFR-CYS 2.
CC REPEAT 119 159 TNFR-CYS 3.
CC CARBOHYD 138 138 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 149 149 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 255 AA; 27899 MW; F3A563F85EF00460 CRC64;

Query Match 20.3%; Score 152.5; DB 1; Length 255;
Best Local Similarity 31.8%; Pred. No. 2.7e-07;
Matches 41; Conservative 11; Mismatches 50; Indels 27; Gaps 7;

QY 2 CGPGRLLGTGTARCCRVHTTRCCRDYPG-----EECCS-----EWDCCMVQPEFHGCDP 52
DB 48 CPPNFSFSSAGG--QRTCDI-----CROCKGVFTRKCSSTSNABCDG---TPGFHCLGA 97

QY 53 CCTTCRHHPCPPGGVQSOGKFSFGFCIDCASGTFSGGEGHCKPWTCTQGTGFLTVFP 112
DB 98 GCSMC-BQDCKQGOELTKKG-----CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVN 149

QY 113 GNKTHNAVC 121
DB 150 GTKERDVVC 158

RESULT 3
OX40_RAT STANDARD; PRT; 271 AA.
ID OX40_RAT
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=90214614; PubMed=2157591;
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```

Db      29  CGPG-----GHGTPVDELDRCCRIHDD--CYGEAGKKGCFPKLTLYSWKC 71
|||||  |||  |||::||  ||::||  ||::||  |||  |||  |||
RESULT  10
JC6547
high sulfur protein B2E - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C:Accession: JC6547
R:Mitsui, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tsuboi, R.; Ogawa, H.
Gene 208, 123-129, 1998
A:Title: Structure and hair follicle-specific expression of genes encoding the rat h
A:Reference number: JC6547; MUID:98201605
A:Accession: JC6547
A:Molecule type: DNA
A:Residues: 1-188 <MIT>
A:Cross-references: DDBJ:AB003753; NID:g3046870; PIDN:BA25573.1; PID:g3046871
C:Comment: This protein is a cysteine-rich, keratin associated protein.
C:Genetics:
A:Gene: b2E
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: hair

Query Match      24.1%; Score 61.5; DB 2; Length 188;
Best Local Similarity 38.7%; Pred. No. 6.4;
Matches 12; Conservative 4; Mismatches 12; Indels 3; Gaps 2;

Qy  13  TDARCCRVHTTR--CCR-DYPGECCECCSEWDC 40
      |  |||::|  :  |||  |  |  |  |  |  |
Db  140  TPPTCCQLLHHAQASCCRPSPYCGQSCCRPACC 170

RESULT  11
A57474
extracellular matrix protein 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 08-Dec-1995
C:Accession: A57474
R:Bhalerao, J.; Tytlzanowski, P.; Filie, J.D.; Kozak, C.A.; Merregaert, J.
J. Biol. Chem. 270, 16385-16394, 1995
A:Title: Molecular cloning, characterization, and genetic mapping of the cDNA coding
A:Reference number: A57474; MUID:95332352
A:Accession: A57474
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-559 <BHA>
A:Cross-references: GB:I33416
A:Experimental source: stromal osteogenic cell line MN7
C:Genetics:
A:Gene: Ecml
A:Map position: 3
C:Keywords: alternative splicing; extracellular matrix

Query Match      24.1%; Score 61.5; DB 2; Length 559;
Best Local Similarity 37.8%; Pred. No. 14;
Matches 14; Conservative 3; Mismatches 19; Indels 1; Gaps 1;

Qy   2  CGPRLLLGTGDARCCRVHTTRCCR-DYPGEECCSE 37
      |||||  :  |||  |  |  |  |  |  |
Db  445  CGSRLVSKHKHQPGLIGNMTVRCELPPYEQACCGE 481

RESULT  12
C34860
phospholipase A2 (EC 3.1.1.4), Pa 5 - mulga snake
C:Species: Pseudechis australis (mulga snake)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 24-Jul-1997
C:Accession: C34860
R:Takasaki, C.; Yutani, F.; Kajiyashiki, T.
Toxicol 28, 329-339, 1990

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QY      2  CGPG-----RLLLG-TGTDARCR---VHTTRCCRDYPGECC--SEW 38
      |||| | | | | | | | | | | | | | | | | | | | | | |
Db      667  CGPGQRTTRTCGLSPNGQEATTCQGSIIETLC-----EGQSCCNSEW 710

RESULT      5
T24272
hypothetical protein T01B7.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C:Accession: T24272
R:Sims, M.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19867
A:Accession: T24272
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-164 <WIL>
A:Cross-references: EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00022
A:Experimental source: clone T01B7
C:Genetics:
A:Gene: CESP:T01B7.8
A:Map position: 2
A:Introns: 20/3; 90/2

Query Match      24.9%; Score 63.5; DB 2; Length 118
Best Local Similarity 38.9%; Pred. No. 3.5;
Matches 14; Conservative 1; Mismatches 12; Indels

QY      1  GCGPGRLLLTGTDA RCRVHTTRCCRDYPGECCS 36
      |||| | | | | | | | | | | | | | | | |
Db      74  GCGGG-----GGGCGCCCRPRCCCR-----RCCT 100

RESULT      6
H34860
phospholipase A2 (EC 3.1.1.4), Pa 15 - mulga snake
C:Species: Pseudechis australis (mulga snake)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change
C:Accession: H34860
R:Takasaki, C.; Yutani, F.; Kajiyashiki, T.
Toxicol 28, 329-339, 1990
A:Title: Amino acid sequences of eight phospholipases A-2 from
A:Reference number: A34860; MUID:90760881
A:Accession: H34860
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-118 <TAK>
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:48,92/Active site: His, Asp #status predicted

Query Match      24.7%; Score 63; DB 2; Length 118
Best Local Similarity 32.7%; Pred. No. 3.2;
Matches 16; Conservative 4; Mismatches 13; Indels

QY      2  CGPGRLLLTGTDA----RCR VHTTRCCRDYPGECC-----SEWDC 40
      |||| | | | | | | | | | | | | | | | |
Db      29  CGPG----GRGTPVDELDRCKIHD--CYIEAGKGCYPKLTWYSWQC 71

RESULT      7
T18975
hypothetical protein C06A1.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C:Accession: T18975
R:McMurray, A.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19054
A:Accession: T18975

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Result No.	Score	Query Match	Length	DB	ID	Description
1	70	27.5	118	2	E34860	phospholipase A2 (
2	69	27.1	118	1	PSSNK3	phospholipase A2 (
3	66	25.9	416	2	G86232	hypothetical prote
4	64.5	25.3	788	2	T25061	hypothetical prote
5	63.5	24.9	164	2	T24272	hypothetical prote
6	63	24.7	118	2	H34860	phospholipase A2 (
7	63	24.7	152	2	T18975	hypothetical prote
8	63	24.7	295	2	JC5559	lectin-B - Virgini
9	62	24.3	117	2	B32416	phospholipase A2 (
10	61.5	24.1	188	2	JC6547	high sulfur protei
11	61.5	24.1	559	2	A57474	extracellular matr
12	61	23.9	118	2	C34860	phospholipase A2 (
13	61	23.9	188	2	T15651	hypothetical prote
14	60.5	23.7	177	2	SP37650	high-sulfur kerati
15	60	23.5	119	1	PSNOAT	phospholipase A2 (
16	60	23.5	119	1	PSNOAS	phospholipase A2 (
17	59.5	23.3	122	2	JC6548	high sulfur protei
18	59.5	23.3	227	1	LN9Z	lectin precursor -
19	59	23.1	117	2	A3416	phospholipase A2 (
20	59	23.1	118	1	PSOXB	phospholipase A2 h
21	59	23.1	118	1	PSSNK1	phospholipase A2 (
22	59	23.1	118	2	F34860	phospholipase A2 (
23	59	23.1	152	1	KRSHHC	keratin high-sulfu
24	59	23.1	152	2	I47111	high-sulfur wool m
25	59	23.1	152	2	I47108	high-sulfur wool m
26	59	23.1	156	1	KRSHHB	keratin high-sulfu
27	59	23.1	172	2	I47106	high-sulfur wool m
28	59	23.1	182	1	KRSHHD	keratin high-sulfu
29	59	23.1	212	2	T05936	agglutinin isolct

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

[illegible]

```

Query Match      23.1%; Score 59; DB 1; Length 181;
Best Local Similarity 29.4%; Pred. No. 2,3;
Matches 15; Conservative 6; Mismatches 18; Indels 12; Gaps 3;

QY  2  CGPGRLLGTTG-----TDARCCRVHTTR--CCR-DYPGECCSEWDC 40
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  112 CRPDRCRVGTLPPCCVWCTSTPSCOLYYAQASCCRPSTYCGSCCRPACC 162

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Search completed: September 4, 2001, 16:15:25  
Job time: 1137 sec

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RESULT	11
PA22_OXYS	
ID	PA22_OXYSC STANDARD; PRT; 118 AA.
AC	P00615;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	PHOSPHOLIPASE A2 HOMOLOG, TAPOXIN BETA CHAIN.
OS	Oxyuranus scutellatus scutellatus (Australian taipan).
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Elapidae; Acanthophinae; Oxyuranus.
OX	NCBI_TaxID=8667;
RN	[1]
RP	SEQUENCE.
TX	TISSUE=Venom;
RC	MEDLINE=83079319; PubMed=6755920;
RA	Lind P.;
RT	"Amino-acid sequence of the beta 1 isosubunit of taipoxin, an extremely potent presynaptic neurotoxin from the Australian snake taipan ( <i>Oxyuranus s. scutellatus</i> ).";
RL	Eur J Biochem 128:71-75(1982).
CC	-I- FUNCTION: TAPOXIN IS THE MOST POTENT ANIMAL TOXIN KNOWN. THE BETA CHAIN IS NEITHER TOXIC NOR ENZYMATICALLY ACTIVE BY ITSELF. IT DOES NOT BIND CALCIUM.
CC	-I- SUBUNIT: CONTAINS THREE NONCOVALENTLY BOUND CHAINS (ALPHA, BETA, AND GAMMA), EACH RELATED TO PHOSPHOLIPASE A2.
CC	-I- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. PIR; A00755; PS0XB.
DR	HSP; P00593; 4BP2.
DR	InterPro; IPR001211; .
DR	Pfam; PF00068; phoslip; 1.
DR	PRINTS; PR00389; PHEHLIPASEA2.
DR	PROSITE; PS00118; PA2_HIS; 1.
DR	PROSITE; PS00119; PA2_ASP; 1.
KW	Presynaptic neurotoxin; Multigene family; Venom.
FT	DISULFID 11 71 BY SIMILARITY.

Query Match 23.1%; Score 59; DB 1; Length 118;  
Best Local Similarity 32.7%; Pred. No. 1.7;  
Matches 16: Conservative 5; Mismatches 12; Indels 16; Gaps 4;

CC -1- FUNCTION: N-ACETYL-D-GLUCOSAMINE BINDING LECTIN.  
CC -1- SIMILARITY: CONTAINS FOUR COPIES OF A CHITIN-BINDING DOMAIN.  
CC -----  
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CC -----  
DR EMBL; M24504; AAA20873.1; -  
DR PIR; J01102; LNRZ.  
DR PIR; A23616; A23616.  
DR HSSP; P10968; IWGC.  
DR InterPro: IPR001002; -  
DR Pfam; PF00187; chitin\_binding; 4.  
DR PRINTS; PR00451; CHITINBINDING.  
DR PROSITE; PS00026; CHITIN\_BINDING; 4.  
KW Lectin; Duplication; Chitin-binding; Glycoprotein; signal.  
FT SIGNAL 1 28  
FT CHAIN 29 201  
FT PROPEP 202 227  
FT CHAIN 29 122  
FT CHAIN 123 201  
FT DOMAIN 29 72  
FT DOMAIN 73 115  
FT DOMAIN 116 158  
FT DOMAIN 159 201  
FT MOD\_RES 29 29  
FT DISULFID 31 46  
FT DISULFID 40 52  
FT DISULFID 45 59  
FT DISULFID 63 68  
FT DISULFID 74 89  
FT DISULFID 88 95  
FT DISULFID 106 111  
FT DISULFID 117 132  
FT DISULFID 126 138  
FT DISULFID 131 145  
FT DISULFID 149 154  
FT DISULFID 160 175  
FT DISULFID 169 181  
FT DISULFID 174 188  
FT DISULFID 192 197  
FT CARBOHYD 211 211  
SQ SEQUENCE 227 AA; 22795 MW; 691EB39F6690BAF1 CRC64;  
  
Query Match 23.3%; Score 59.5; DB 1; Length 227;  
Best Local Similarity 20.2%; Pred. No. 2.4;  
Matches 17; Conservative 3; Mismatches 17; Indels 47; Gaps 3;  
  
QY 2 CGPGRLLLTGTDA-RCC-----RVHTTRCCRDY----- 29  
DB 52 CGLGRDYCTGCGGACCSQRCSGGGATCSNNQCCSQYGYCGFGSEYCGSGCNGPC 111  
QY 30 -----PGEECCSEW 38  
DB 112 RADIKGRNANGELCPNNWCCSQW 135  
  
RESULT 9  
ID PA2A\_PSEPO STANDARD; PRT; 117 AA.  
AC P20258;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE PHOSPHOLIPASE A2 (EC 3.1.1.4) (PSEUDEKIN A CHAIN) (PHOSPHATIDYLCHOLINE  
DE 2-ACYLHYDROLASE).  
OS Pseudechis porphyriacus (Red-bellied black snake).  
CC

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Acanthophiinae; Pseudechis.  
OX NCBI\_TaxID=8671;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=89388835; PubMed=2675391;  
RA Schmidt J.J., Middlebrook J.L.;  
RT "Purification, sequencing and characterization of pseudexin  
RT phospholipases A2 from Pseudechis porphyriacus (Australian  
RT red-bellied black snake).";  
RL Toxicon 27:805-818(1989).  
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE  
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.  
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1-ACYLGLYCERYL-  
CC PHOSPHOCHOLINE + A FATTY ACID ANION.  
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.  
CC PIR; A32416; A32416.  
DR HSSP; P00608; IAE7.  
DR InterPro: IPR001211; -  
DR Pfam; PF00068; Phoslip; 1.  
DR PRINTS; PR00389; PHPLIPASEA2.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
DR PROSITE; PS00119; PA2\_ASP; 1.  
KW Hydrolase; Lipid degradation; Calcium; Multigene family; Venom.  
FT ACT\_SITE 48 48  
FT ACT\_SITE 92 92  
FT DISULFID 11 71  
FT DISULFID 27 117  
FT DISULFID 29 45  
FT DISULFID 44 98  
FT DISULFID 51 91  
FT DISULFID 60 84  
FT DISULFID 78 89  
FT CA\_BIND 49 49  
SQ SEQUENCE 117 AA; 43804BC379277D9D CRC64;  
  
Query Match 23.1%; Score 59; DB 1; Length 117;  
Best Local Similarity 32.7%; Pred. No. 1.7;  
Matches 16; Conservative 4; Mismatches 13; Indels 16; Gaps 4;  
  
QY 2 CGPGRLLLTGTDA----RCCRVHTTRCCRDYPCGCC-----SEWDC 40  
DB 29 CGWG----GSGTPVDELDRCCQTHDN--CYDQAGKGCFFKLTLYSWRC 71  
  
RESULT 10  
ID PA2L\_PSEAU STANDARD; PRT; 118 AA.  
AC P04056;  
DT 01-NOV-1986 (Rel. 03, Created)  
DT 01-NOV-1986 (Rel. 03, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE PHOSPHOLIPASE A2 ISOZYME PA-II (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-  
DE ACYLHYDROLASE).  
OS Pseudechis australis (Mulga snake) (King brown snake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Acanthophiinae; Pseudechis.  
OX NCBI\_TaxID=8670;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=85193286; PubMed=3887651;  
RA Nishida S., Terashima M., Tamiya N.;  
RT "Amino acid sequences of phospholipases A2 from the venom of an  
RT Australian elapid snake (king brown snake, Pseudechis australis).";  
RL Toxicon 23:87-104(1985).  
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE  
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.  
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1-ACYLGLYCERYL-  
CC



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-----
CC EMBL; L33416; AAA37535.1; -.
CC MGMD; MGI:103060; Ecml.
CC DR Signal; Alternative splicing; Extracellular matrix; Glycoprotein;
KW Repeat.
KW SIGNAL 1 19
FT CHAIN 20 559
FT FT DOMAIN 170 424
FT FT REPEAT 170 298
FT FT REPEAT 302 424
FT FT CARBOHYD 373 373
FT FT CARBOHYD 463 463
FT FT CARBOHYD 535 535
FT FT VARSPLIC 256 380
FT FT SEQUENCE 559 AA; 62775 MW; BBF37FAB7D67E2E8 CRC64;
SQ
Query Match 24.1%; Score 61.5; DB 1; Length 559;
Best Local Similarity 37.8%; Pred. No. 2.9;
Matches 14; Conservative 3; Mismatches 19; Indels 1; Gaps 1;
QY 2 CGGCRLLLTGTGTCARCRVHTTRCCR-DYPGEECCSE 37
|| ||| : ||| : |||
DB 445 CGSGRVLSRKHKQGLTQNTVRCCCLPYEQACCGE 481
RESULT 6
PA25_PSEAU STANDARD; PRT; 118 AA.
ID PA25_PSEAU AC P20252;
AC AC
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2 ISOZYME PA-5 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-
DE ACYLHYDROLASE).
OS Pseudechis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Pseudechis.
OX NCBI_Taxid=8670;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90260881; PubMed=2343456;
RA Takasaki C., Yutani F., Kajiyashiki T.:
RT "Amino acid sequences of eight phospholipases A2 from the venom of
RT Australian king brown snake, Pseudechis australis.";
RL Toxicon 28:329-339(1990).
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- MISCELLANEOUS: LD(50) IS 0.09 MG/KG BY INTRAVENOUS INJECTION.
CC -1- MISCELLANEOUS: THERE ARE MANY PROTEIN COMPONENTS WITH
CC PHOSPHOLIPASE A2 ACTIVITY IN THE MULGA SNAKE VENOM AND SOME OF
CC THEM ARE MYOTOXIC.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
CC PIR; C34860; C34860.
DR HSSP; P00608; 1AE7.
DR InterPro; IPR001211; -.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR PROSITE; PS00118; PA2_HIS; 1.
DR PROSITE; PS00119; PA2_ASP; FALSE_NEG.
KW Hydrolyase; Lipid degradation; Calcium; Multigene family; Venom.
FT ACT_SITE 48 48
FT ACT_SITE 92 92
FT DISULFID 11 71
FT DISULFID 27 117
FT DISULFID 29 45
FT DISULFID 44 98

```



OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Acanthophiinae; Pseudechis.  
OX NCBI\_TaxID=8671;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=89388835; PubMed=2675391;  
RA Schmidt J.J., Middlebrook J.L.;  
FT "Purification, sequencing and characterization of pseudexin

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:24 ; Search time 43.78 Seconds  
(without alignments)  
32.080 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_73

Perfect score: 255

Sequence: 1 GCGPGRLLLTGTGDARCRV.....TTRCCRDYPGECCSEWDCM 41

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	70	27.5	118	1	PA20_PSEAU
2	69	27.1	118	1	PA2D_PSEAU
3	63	24.7	118	1	PA2E_PSEAU
4	62	24.3	117	1	PA2B_PSEPO
5	61.5	24.1	559	1	ECM1_MOUSE
6	61	23.9	118	1	PA25_PSEAU
7	60	23.5	119	1	PA22_NOTSC
8	59.5	23.3	227	1	AG1_ORYSA
9	59	23.1	117	1	PA2A_PSEPO
10	59	23.1	118	1	PA21_PSEAU
11	59	23.1	118	1	PA22_OXYSC
12	59	23.1	118	1	PA2A_PSEAU
13	59	23.1	151	1	KR2C_SHEEP
14	59	23.1	156	1	KR2B_SHEEP
15	59	23.1	181	1	KR2D_SHEEP
16	59	23.1	212	1	AG1_HORVU
17	58.5	22.9	2482	1	VWF_FIG
18	58	22.7	133	1	PA23_OXYSC
19	58	22.7	171	1	KR2A_SHEEP
20	57.5	22.5	99	1	NIC1_HUMAN
21	57.5	22.5	145	1	PA2_LATLA
22	57.5	22.5	4289	1	TENX_HUMAN
23	57	22.4	118	1	PA23_PSEAU
24	57	22.4	2907	1	FBN2_MOUSE
25	57	22.4	3083	1	POLG_ZYMYR
26	56.5	22.2	60	1	TXW3_NAJHA
27	56.5	22.2	61	1	TXW4_NAJHA
28	56.5	22.2	1063	1	POLS_RUBVH
29	56.5	22.2	1063	1	POLS_RUBVH
30	56	22.0	118	1	PA21_LATSE
31	56	22.0	118	1	PA26_BUNFA
32	56	22.0	118	1	PA2A_BUNFA
33	56	22.0	118	1	PA2B_BUNFA

34 56 22.0 121 1 PA22\_BOTAS  
35 56 22.0 145 1 PA20\_NOTSC  
36 56 22.0 374 1 MTB1\_BACBR  
37 56 22.0 1799 1 LMB2\_MOUSE  
38 56 22.0 1801 1 LMB2\_RAT  
39 55.5 21.8 677 1 SP87\_DICDI  
40 55.5 21.8 3106 1 LMA2\_MOUSE  
41 55.5 21.8 4544 1 LRP1\_HUMAN  
42 55 21.6 118 1 PA2C\_PSEAU  
43 55 21.6 138 1 PA25\_TRIGA  
44 55 21.6 275 1 VA16\_VACCV  
45 55 21.6 377 1 VA16\_VARV

#### ALIGNMENTS

RESULT 1  
ID PA20\_PSEAU STANDARD; PRT; 118 AA.  
AC P20254:  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE PHOSPHOLIPASE A2 ISOZYME PA-10A (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-DE ACYLHYDROLASE).  
OS Pseudechis australis (Mulga snake) (King brown snake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Acanthophiinae; Pseudechis.  
OX NCBI\_TaxID=8670;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90260881; PubMed=2343466;  
RA Takasaki C., Yutani F., Kajiyashiki T.;  
RT "Amino acid sequences of eight phospholipases A2 from the venom of Australian king brown snake, Pseudechis australis.";  
RT Toxicon 28:329-339(1990).  
RL  
CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.  
CC -!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-PHOSPHOCHOLINE + A FATTY ACID ANION.  
CC -!- MISCELLANEOUS: THERE ARE MANY PROTEIN COMPONENTS WITH PHOSPHOLIPASE A2 ACTIVITY IN THE MULGA SNAKE VENOM AND SOME OF THEM ARE MYOTOXIC.  
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.  
DR PIR: E34860; E34860.  
DR HSP: P00608; LAE7.  
DR InterPro: IPR001211; .  
DR Pfam: PF00068; phoslip; 1.  
DR PRINTS: PR00389; PHPLIPASEA2.  
DR PROSITE: PS00118; PA2\_HIS; 1.  
DR PROSITE: PS00119; PA2\_ASP; 1.  
KW Hydrolase; Lipid degradation; Calcium; Multigene family; Venom.  
FT ACT\_SITE 48 48 BY SIMILARITY.  
FT ACT\_SITE 92 92 BY SIMILARITY.  
FT DISULFID 11 71 BY SIMILARITY.  
FT DISULFID 27 117 BY SIMILARITY.  
FT DISULFID 29 45 BY SIMILARITY.  
FT DISULFID 44 98 BY SIMILARITY.  
FT DISULFID 51 91 BY SIMILARITY.  
FT DISULFID 60 84 BY SIMILARITY.  
FT DISULFID 78 89 BY SIMILARITY.  
FT CA\_BIND 49 49 BY SIMILARITY.  
SQ SEQUENCE 118 AA; 13027 MW; 884D1D3A6E2B5FCB CRC64;

Query Match 27.5%; Score 70; DB 1; Length 118;  
Best Local Similarity 36.7%; Pred. No. 0.087;  
Matches 18; Conservative 4; Mismatches 11; Indels 16; Gaps 4;

OY 2 CGPGRLLLTGTGTD-----RCRVHTTRCCRDYPGECC-----SEWDC 40



5/L: 1724/1; 1771/1; 1819/1; 1874/1; 1888/1; 2021/3; 2086/1; 2200/1; 2266/3; 2303/1

C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von C keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicated

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-763/Product: von Willebrand antigen II #status predicted <MAI>

F:34-386/Domain: type D repeat 1 <DD1>

F:387-745/Domain: type D repeat 2 <DD2>

F:698-700/Region: cell attachment (R-G-D) motif

F:764-2813/Product: von Willebrand factor #status predicted <MA2>

F:784-865/Domain: D' <DDD>

F:788-833; 2216-2261/Region: duplication

F:826-853; 2400-2515; 2544-2662/Region: duplication

F:842-1130; 1934-2203/Region: duplication

F:866-1241/Domain: type D repeat 3 <DD3>

F:1275-1413/Domain: von Willebrand factor type A repeat homology <VWA1>

F:1496-1634/Domain: von Willebrand factor type A repeat homology <VWA2>

F:1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>

F:1947-2295/Domain: type D repeat 4 <DD4>

F:2296-2330/Domain: type B repeat 1 <VB1>

F:2340-2365/Domain: type B repeat 2 <VB2>

F:2375-2399/Domain: type B repeat 3 <VB3>

F:2430-2497/Domain: von Willebrand factor type C repeat homology <VWC1>

F:2507-2509/Region: cell attachment (R-G-D) motif

F:2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>

F:2587; 1231; 1515; 1574; 2223; 2290; 2357; 2400; 2546; 2585; 2790/Binding site: carbohydrate (Asn)

F:1147/Binding site: carbohydrate (Asn) (covalent) #status atypical

F:1248; 1255; 1256; 1468; 1477; 1487; 1679; 2298/Binding site: carbohydrate (Thr) (covalent) #S

F:1263; 1486/Binding site: carbohydrate (Ser)(covalent) #status experimental

Query Match	23.6%	Score 59.5;	DB 1;	Length 2813;
Best Local Similarity	30.8%;	Pred. No. 60;		
Matches 16;	Conservative	3;	Mismatches 18;	Indels 15;
				Gaps 2;

QY 3 QPEFHGDPCCCTTCR--HHP-----CPPGGVQSQGKFSFGTQC 39  
 656 QWYLOCGTPTCNLTCSRSLSPDPEECNEACLEGCFPPGLVMDERGDGCVPAOC 707  
 Db

RESULT	13
SMKD1S	

metallothionein 1 - mud crab  
C:Species: Scyllia serrata (mud crab)  
C:Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 13-Sep-1996  
C:Accession: A03283  
R:Lersch, K.; Ammer, D.; Olafson, R.W.  
J. Biol. Chem. 257, 2420-2426, 1982  
A:Title: Crab metallothionein. Primary structures of metallothioneins 1 and 2  
A:Reference number: A92363; MUID:821422340

A; Names: the five Cys-X-Cys sequences are believed to be the principal metal-binding sites  
 C; Superfamily: metallothionein  
 C; Keywords: metal binding

Query Match	23.4%	Score 59;	DB 1;	Length 58;
Best Local Similarity	37.5%;	Pred. No. 4;		
Matches 15;	Conservative	3;	Mismatches 12;	Indels 10;
				Gaps 2;

QY 1 CVQPEFHCGDPC-CTTCRHHPCPGQGVQSQGKSFQFC 39  
||| : ||| ||| ||| : ||| :  
Db 9 CVCKEGCKEGCOCTSCRSPCE-----KSSGCKC 39

RESULT	14
\$65778	

503776  
chitinase class IV precursor - rape (fragment)  
C:Species: Brassica napus (rape)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 22-Jun-1999  
C:Accession: S65778  
R:Hanfrey, C.; Fife, M.; Buchanan-Wollaston, V.

Plant Mol. Biol. 30, 597-609, 1996  
A: Title: Leaf senescence in *Brassica napus*: expression of genes encoding pathogenesis  
A: Reference number: S65777; MUID:96189271  
A: Accession: S65778  
A: Status: preliminary; nucleic acid sequence not shown  
A: Molecule type: mRNA  
A: Residues: 1-266 <H>  
A: Cross-references: EMBL:U21848; NID:g722271; PIDN:AB01665.1; PID:g722272  
A: Note: the sequence of residues 1-17 and the corresponding nucleotide sequence are n  
C: Superfamily: lectin-related plant chitinase; hevvin chitin-binding domain homology;  
F: 18-53/Domain: hevvin chitin-binding domain homology <HCB>  
F: 64-266/Domain: plant chitinase homology <PCH>

Query Match 23.4%; Score 59; DB 2; Length 266;  
Best Local Similarity 47.8%; Pred. NO. 12;  
Matches 11; Conservative 2; Mismatches 10; Indels

Qy 9 G D P C C T T C R H H P C P P G Q G V Q S Q G 31  
|| | || | || | || | || | || | : |  
Db 142 G D Y C D T T K T E F F C V P G K G Y Y G R G 164

RESULT 15  
A42032

A42032  
epidermal growth factor receptor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 31-Dec-1993 #sequence\_revision 31-  
C:Accession: A42032

R; Flickinger, T.W.; Mahle, N.J.; Kung, H.J. Mol. Cell. Biol. 12, 883-893, 1992

A;Title: An alternatively processed mRNA from the avian c-erbB gene encodes a soluble

A;Accession: A42032  
A;Reference number: A42032; MOID: 3414321

A;Molecule type: mRNA  
A;Residues: 1-527 <FL>

A; residues: 1-327; APLS:  
A; Cross-references: GB:M77637; MID:g211737; PIDN:AAA48759.1; PID:g211738  
A; Experimental source: liver  
A; Note: sequence extracted from NCBI backbone (NCBITN:76892, NCBITP:76893)  
C; Superfamily: epidermal growth factor receptor; protein kinase homology  
C; Keywords: ATP; growth factor receptor

Query Match 23.4%; Score 59; DB 2; Length 527;  
Best Local Similarity 33.3%; Pred. No. 20;  
Matches 11: Conservative 5; Mismatches 17: Indels

QY .8 CGDPCC<sup>T</sup>TCRHHPCPPGGVQSOGKFSFGQCI 40  
| | | : | : ||| :  
Db 270 CKDTPPLVLNPTTYQMDVNPEGKYSEGATCV 302

Search completed: September 4, 2001, 16:12:14  
Job time: 1111 sec

von Willebrand factor precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Dec-1986 #sequence\_revision 30-Jun-1993 #text\_change 22-Jun-1999  
 C:Accession: A34480; S02377; S23676; A25298; A25469; A25366; S23618; S23645; A94060  
 R:Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sorace, J. Biol. Chem. 264, 19514-19527, 1989  
 A:Title: Structure of the gene for human von Willebrand factor.  
 A:Reference number: A34480; MUID:90062044  
 A:Accession: A34480  
 A:Molecule type: DNA  
 A:Residues: 1-2813 <MAN>  
 A:Cross-references: EMBL:M25864  
 R:Bonthron, D.; Orkin, S.H.  
 Eur. J. Biochem. 171, 51-57, 1988  
 A:Title: The human von Willebrand factor gene. Structure of the 5' region.  
 A:Reference number: S02377; MUID:88111704  
 A:Accession: S02377  
 A:Molecule type: DNA  
 A:Residues: 1-177 <BO2>  
 A:Cross-references: EMBL:X06828  
 R:Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; Sorace, J. Biochemistry 30, 253-269, 1991  
 A:Title: Human von Willebrand factor gene and pseudogene: structural analysis and differences.  
 A:Reference number: A37139; MUID:91105089  
 A:Accession: A37139  
 A:Molecule type: DNA  
 A:Residues: 990-1947 <MAD>  
 A:Cross-references: GB:M60675; NID:g340357; PIDN:AAA61295.1; PID:g553810  
 A:Note: The authors translated the codon GCG for residue 156 as Gln  
 R:Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagian, Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987  
 A:Title: Molecular cloning of the human gene for von Willebrand factor and identification of the von Willebrand factor gene.  
 A:Reference number: S23676; MUID:87260814  
 A:Accession: S23676  
 A:Molecule type: DNA  
 A:Residues: 2731-2813 <COL>  
 A:Cross-references: EMBL:M16945  
 R:Bonthron, D.; Orr, E.C.; Mitsosk, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.  
 Nucleic Acids Res. 14, 7125-7127, 1986  
 A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.  
 A:Reference number: A25298; MUID:87016349  
 A:Accession: A25298  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-2813 <BON>  
 A:Cross-references: EMBL:X04385  
 R:Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 1839-1847, 1986  
 A:Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protein.  
 A:Reference number: A91044; MUID:87004550  
 A:Accession: A25469  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>  
 A:Cross-references: EMBL:X04146  
 A:Note: This sequence has been revised in reference A91056  
 R:Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 3074, 1986  
 A:Reference number: A91056  
 A:Accession: A25366  
 A:Molecule type: mRNA  
 A:Residues: 1021-1030 <VE2>  
 A:Note: This is a revision to the sequence from reference A91044  
 R:Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.  
 Biochem. Biophys. Res. Commun. 144, 657-665, 1987  
 A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated regions, and the von Willebrand factor gene.  
 A:Reference number: S23618; MUID:87213253  
 A:Accession: S23618  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <SH2>  
 A:Cross-references: EMBL:M17588; NID:g799330; PIDN:AAA65940.1; PID:g340316  
 A:Accession: S23645  
 A:Molecule type: protein  
 A:Residues: 23-56 <SH3>  
 R:Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985  
 A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand factor.  
 A:Reference number: A94060; MUID:86016708  
 A:Accession: A94060  
 A:Molecule type: mRNA  
 A:Residues: 'WA', 739, 'C', 744-769, 'H', 771-788, 'A', 790-803, 'S', 805-873, 1289-1471, 'D', 14  
 A:Note: The authors translated the codon TCG for residue 2168 as Cys  
 R:Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.  
 Biochemistry 25, 3164-3171, 1986  
 A:Title: cDNA sequences for human von Willebrand factor reveal five types of repeated regions.  
 A:Reference number: A90504; MUID:86269894  
 A:Accession: A90504  
 A:Molecule type: mRNA  
 A:Residues: 781-788, 'A', 790-1424 <SHE>  
 A:Note: 852-Gln, 857-Asp, and 1381-Thr were also found  
 R:Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.  
 Science 228, 1401-1406, 1985  
 A:Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clones.  
 A:Reference number: A44178; MUID:85244588  
 A:Accession: A44178  
 A:Molecule type: mRNA  
 A:Residues: 2621-2813 <GIN>  
 A:Cross-references: EMBL:X03028; NID:g340308; PIDN:AAA61293.1; PID:g340309  
 R:Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; Nucleic Acids Res. 13, 4699-4717, 1985  
 A:Title: Construction of cDNA coding for human von Willebrand factor using antibody p  
 A:Reference number: S07363; MUID:85269603  
 A:Accession: S07363  
 A:Molecule type: mRNA  
 A:Residues: 2731-2813 <VE3>  
 A:Cross-references: EMBL:X02672; NID:g37939; PIDN:CAA62503.1; PID:g37940  
 R:Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Li  
 Cell 41, 49-56, 1985  
 A:Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by  
 A:Reference number: S23678; MUID:85201687  
 A:Accession: S23678  
 A:Molecule type: mRNA  
 A:Residues: 2731-2813 <LYN>  
 A:Cross-references: EMBL:X03028  
 R:Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.  
 Biochemistry 25, 3171-3184, 1986  
 A:Title: Amino acid sequences of human von Willebrand factor.  
 A:Reference number: A90505; MUID:86269895  
 A:Accession: A90505  
 A:Molecule type: protein  
 A:Residues: 764-788, 'A', 790-1471, 'D', 1473-2813 <TIT>  
 A:Note: 789-Thr was also found  
 R:Chopek, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.  
 Biochemistry 25, 3146-3155, 1986  
 A:Title: Human von Willebrand factor: a multivalent protein composed of identical sub  
 A:Reference number: A23464; MUID:86269892  
 A:Accession: A23464  
 A:Molecule type: protein  
 A:Residues: 764-773; 2803-2813 <CHO>  
 R:DeRubeis, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990  
 A:Title: Identification of a cleavage site directing the immunochemical detection of  
 A:Reference number: A36013; MUID:90349604  
 A:Accession: A36013  
 A:Molecule type: protein  
 A:Residues: 1506-1617 <DEN>  
 R:Pay, P.J.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.  
 Science 232, 995-998, 1986  
 A:Title: Polypeptide of von Willebrand factor circulates in blood and is identical  
 A:Reference number: A60913; MUID:86208144  
 A:Accession: A60913  
 A:Molecule type: protein  
 A:Residues: 576-590 <PAY>  
 C:Genetics:  
 A:Gene: GDB:VWF  
 A:Cross-references: GDB:119125; OMIM:193400  
 A:Map position: 12p13.3-12p13.2  
 A:Introns: 19/1; 74/1; 108/2; 178/1; 219/3; 292/1; 333/1; 370/2; 386/1; 431/3; 478/1;

[illegible]

RESULT 12  
VWHJ



**RESULT** 8  
B59037 cytochrome c, tetraheme, precursor - Nitrosomonas europaea  
C:Species: Nitrosomonas europaea  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 04-Mar-2000  
C:Accession: B59037  
R:Bergmann, D.J.; Arclerio, D.M.; Hooper, A.B.  
J. Bacteriol. 176, 3148-3153, 1994  
A>Title: Organization of the hao gene cluster of Nitrosomonas europaea: genes for two  
A:Reference number: A59037; MUID:94252980  
A:Accession: B59037  
A>Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-233 <BER>  
A:Cross-references: GB:U08288; NID:g476339; PIDN:AAA19968.1; PID:g476341  
A>Note: submitted to GenBank, April 1994  
C:Keywords: chromoprotein; heme; iron; metalloprotein  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-233/Product: cytochrome c, tetraheme #status predicted <MAG>  
F:39-42/Binding site: heme (Cys) (covalent) #status predicted  
F:43/Binding site: heme iron (His) (axial ligand) #status predicted  
F:67-70/Binding site: heme (Cys) (covalent) #status predicted  
F:71/Binding site: heme iron (His) (axial ligand) #status predicted  
F:131,134/Binding site: heme (Cys) (covalent) #status predicted  
F:135/Binding site: heme iron (His) (axial ligand) #status predicted  
F:159,162/Binding site: heme (Cys) (covalent) #status predicted  
F:163/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 23.8%; Score 60; DB 2; Length 233;  
Best Local Similarity 45.0%; Pred. No. 8.5;  
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

**QY** 13 CTTCTRHPCPPGGVQSOGK 32  
| | | | |  
**DB** 131 CRTCHKKPAPGESQAHEK 150

**RESULT** 9  
A36325 epidermal growth factor receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 25-Jan-1991 #sequence\_revision 25-Jan-1991 #text\_change 10-Oct-1997  
C:Accession: A36325  
R:Petch, L.A.; Harris, J.; Raymond, V.W.; Blasband, A.; Lee, D.C.; Earp, H.S.  
Mol. Cell. Biol. 10, 2973-2982, 1990  
A>Title: A truncated, secreted form of the epidermal growth factor receptor is encoded  
A:Reference number: A36325; MUID:90258888  
A:Accession: A36325  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-644 <PET>  
A:Cross-references: GB:M37394  
C:Superfamily: epidermal growth factor receptor; protein kinase homology  
C:Keywords: alternative splicing; ATP; growth factor receptor

Query Match 23.8%; Score 60; DB 2; Length 644;  
Best Local Similarity 33.3%; Pred. No. 18;  
Matches 12; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

**QY** 5 EFHCGDPCCTTCRRHPCPPGGVQSOGKSFSGFOCI 40  
| | | | : | | : | : | : | : | : |  
**DB** 257 EATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCV 292

**RESULT** 10  
GQHUE epidermal growth factor receptor precursor - human  
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) erBB  
C:Species: Homo sapiens (man)  
C>Date: 15-Nov-1984 #sequence\_revision 27-Nov-1985 #text\_change 11-Jun-1999

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:14 ; Search time 80.15 seconds  
(without alignments)  
38.016 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_74\_113

Perfect score: 232

Sequence: 1 CVQPEFHCGDPCCTCRHHPCPPGQVQSOGKFSFGQCI 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	28.6	1574	2 T13954	MEGF6 protein - rat
2	67	26.6	256	2 B32393	T-cell antigen 4-1
3	64	23.4	1210	2 A53183	epidermal growth f
4	62.5	24.8	1077	2 T41146	probable cysteine-
5	60.5	24.0	216	2 JX0265	platelet aggregati
6	60.5	24.0	850	2 S56015	gastric mucin MUC5
7	60.5	24.0	1373	2 JE0095	gastric mucin MUC5
8	60	23.8	233	2 B59037	cytochrome c, tetr
9	60	23.8	644	2 A36325	epidermal growth f
10	60	23.8	1210	1 GQHUE	epidermal growth f
11	59.5	23.6	1104	2 I38869	transcription fact
12	59.5	23.6	2813	1 VWHU	von Willebrand fac
13	59	23.4	58	1 SKMD1S	metallothionein 1
14	59	23.4	266	2 S65778	chitinase class IV
15	59	23.4	527	2 A42032	epidermal growth f
16	59	23.4	1223	1 TVCHLV	epidermal growth f
17	58.5	23.2	437	2 C35147	integrase homolog
18	58.5	23.2	1321	2 JE0352	mucin MUC5B, trach
19	58	23.0	271	2 S12783	OX40 antigen, precu
20	58	23.0	295	2 JC5559	lectin-B - Virgini
21	58	23.0	2907	2 A57278	fibrillin-2 precu
22	58	23.0	2918	2 A54105	fibrillin-2 precu
23	57.5	22.8	305	2 A46476	B cell-associated
24	57.5	22.8	540	2 B47417	insulin receptor-r
25	57.5	22.8	961	1 TSHUP4	thrombospondin 4 p
26	57.5	22.8	1268	2 B36502	insulin receptor-r
27	57	22.6	329	2 A48805	insulin-like growt
28	57	22.6	488	2 T29562	hypothetical prote
29	57	22.6	1371	2 A33837	insulin-like growt

30	57	22.6	2318	2 S45306	notch 3 protein 2
31	56.5	22.4	277	2 A60771	B-cell activation
32	56.5	22.4	1297	2 T30274	proteolisin - se
33	56	22.2	63	2 S07127	chymotrypsin/elast
34	56	22.2	419	2 S41607	atrolysin A (EC 3.
35	55.5	22.0	62	2 A53640	metallothionein 4
36	55.5	22.0	277	2 I37552	OX40 homolog - hum
37	55.5	22.0	502	2 A48679	differentiated ker
38	55	21.8	921	2 S40495	collagen alpha 1(I
39	55	21.8	921	2 S42617	collagen alpha 1(I
40	55	21.8	931	2 S13580	collagen alpha 1(I
41	55	21.8	1106	2 T13938	gene shuttle craft
42	55	21.8	1106	2 T44598	hypothetical prote
43	55	21.8	1466	1 CGHU7L	collagen alpha 1(I
44	54.5	21.6	62	2 B53640	metallothionein IV
45	54.5	21.6	258	2 C86541	CR105 hypothetical

ALIGNMENTS

RESULT 1

T13954

MEGF6 protein - rat

C:Species: Rattus norvegicus. (Norway rat)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000

C:Accession: T13954

R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51, 27-34, 1998

A:Title: Identification of high-molecular-weight proteins with multiple EGF-like moti

A:Reference number: Z14126; MUID:98360089

A:Accession: T13954

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1574 <NAK>

A:Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294

A:Experimental source: strain Sprague-Dawley; brain

C:Genetics:

A:Gene: MEGF6

Query Match 28.6%; Score 72; DB 2; Length 1574;

Best Local Similarity 40.5%; Pred. No. 1.6;

Matches 15; Conservative 1; Mismatches 13; Indels 8; Gaps 2;

QY 1 CVQPEFHCGDPCCTT-----CRHHPCPPGQVQSOGK 32

DB 127 CASANGCEGCPCCNTGVGYCR---CPPYQLQGDGK 160

RESULT 2

B32393

T-cell antigen 4-1BB precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000

C:Accession: B32393; I48879

R:Kwon, B.S.; Weissman, S.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989

A:Title: cDNA sequence of two inducible T-cell genes.

A:Reference number: A32393; MUID:89184547

A:Accession: B32393

A:Molecule type: mRNA

A:Residues: 1-256 <KWO>

A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122

R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.

J. Immunol. 152, 2256-2262, 1994

A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B

A:Reference number: I48879; MUID:94179805

A:Accession: I48879

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-256 <RES>

A:Cross-references: EMBL:U02567; NID:gl117783; PIDN:AAA93113.1; PID:g409178

C;Genetics:  
A;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: transmembrane protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 26.6%; Score 67; DB 2; Length 256;  
Best Local Similarity 45.2%; Pred. No. 1.5;  
Matches 14; Conservative 3; Mismatches 12; Indels 2; Gaps 2;

Qy 1 CVQPEFHCGDPCCTCRHHPCPPGQGVQSQ 31  
Db 87 CIE-GFHLGPGQCTRC-EKDCRPGQELTKQ 115

RESULT 3  
A53183  
epidermal growth factor receptor precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 18-Jun-1999  
C;Accession: A53183; A43818; A24942; A28941; S45325; I49643  
R;Luetteker, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.;  
Genes Dev. 8, 399-413, 1994  
A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor  
A;Reference number: A53183; MUID:94170986  
A;Accession: A53183  
A;Molecule type: mRNA  
A;Residues: 1-1210 <LUE>  
A;Cross-references: GB:003425  
R;Aviv, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.  
Oncogene 6, 673-676, 1991  
A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding site  
A;Reference number: A43818; MUID:91232866  
A;Accession: A43818  
A;Molecule type: mRNA  
A;Residues: 1-714 <AVI>  
A;Cross-references: GB:X59698  
R;Eisinger, D.P.; Serrero, G.  
submitted to the EMBL Data Library, June 1992  
A;Reference number: S24942  
A;Accession: S24942  
A;Molecule type: mRNA  
A;Residues: 969-971, 'K', 973-1115, 'D' <EIS>  
A;Cross-references: EMBL:Z12608  
R;Heisermann, G.J.; Gill, G.N.  
J. Biol. Chem. 263, 13152-13159, 1988  
A;Title: Epidermal growth factor receptor threonine and serine residues phosphorylated in  
A;Reference number: A28941; MUID:88330814  
A;Accession: A28941  
A;Molecule type: protein  
A;Residues: 689-694, 'X', 696-704, 'L', 706-707, 989-992, 'XX', 995-996, 'X', 998-1000; 1002-1009,  
R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.  
submitted to the EMBL Data Library, April 1994  
A;Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor  
A;Reference number: S45325  
A;Accession: S45325  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-971, 'K', 973-1210 <VER>  
A;Cross-references: EMBL:X78987; NID:g488830; PIDN:CAA55567.1; PID:g488831  
R;Paria, B.C.; Das, S.K.; Andrews, G.K.; Dev, S.K.  
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993  
A;Title: Expression of the epidermal growth factor receptor gene is regulated in mouse b  
A;Reference number: I49643; MUID:93126380  
A;Accession: I49643  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 12-20, 22-132 <RES>  
A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201  
C;Genetics:  
A;Gene: EGFR

C;Superfamily: epidermal growth factor receptor; protein kinase homology  
C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phospho  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;648-670/Domain: transmembrane #status predicted <TMM>  
F;712-977/Domain: protein kinase homology <KIN>  
F;720-728/Region: protein kinase ATP-binding motif  
F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental  
F;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental  
F;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental  
F;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental  
F;1197/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 25.4%; Score 64; DB 2; Length 1210;  
Best Local Similarity 34.2%; Pred. No. 10;  
Matches 13; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 3 QPEFHCGDPCCTCRHHPCPPGQGVQSQKFSFGQCI 40  
Db 255 QDEATCKDTCPLMLNPTTYQMDVNPGEKYSFGATCV 292

RESULT 4  
T41146  
probable cysteine-rich transcription regulator - fission yeast (Schizosaccharomyces p  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Sep-2000  
C;Accession: T41146  
R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1998  
A;Reference number: Z21973  
A;Accession: T41146  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1077 <HIL>  
A;Cross-references: EMBL:AL031907; PIDN:CAA21417.1; GSPDB:GN00068; SPDB:SPCC18.03  
A;Experimental source: strain 972h-; cosmid c18  
C;Genetics:  
A;Gene: SPDB:SPCC18.03  
A;Map position: 3  
C;Superfamily: RING finger homology  
F;193-252/Domain: RING finger homology <RRN>

Query Match 24.8%; Score 62.5; DB 2; Length 1077;  
Best Local Similarity 30.0%; Pred. No. 14;  
Matches 18; Conservative 3; Mismatches 16; Indels 23; Gaps 3;

Qy 3 QPEF-----HCGDPCCTT-----CRHHPCPPGQGVQSQ-----GKFSFGQC 39  
Db 266 KPEFVKNLVPHSCGDPCKTRGQDCEHPCPLCHPGPCPTATVEKFLCGKSTHARC 325

RESULT 5  
JX0265  
platelet aggregation inhibitor - red diamond rattlesnake (fragment)  
N;Alternate names: disintegrin  
C;Species: Crotales ruber ruber (red diamond rattlesnake)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Nov-2000  
C;Accession: JX0265  
R;Takeya, H.; Nishida, S.; Nishino, N.; Makino, Y.; Omori-Sato, T.; Nikai, T.; Sug  
J. Biochem. 113, 473-483, 1993  
A;Title: Primary structures of platelet aggregation inhibitors (disintegrins) autopro  
hese enzymes.  
A;Reference number: JX0265; MUID:93293798  
A;Accession: JX0265  
A;Molecule type: protein  
A;Residues: 1-216 <TAK>  
A;Experimental source: venom  
C;Superfamily: mouse meltrin alpha; disintegrin homology  
F;7-89/Domain: disintegrin homology <DIS>



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FT DISULFID 107 122 BY SIMILARITY.
FT FT 116 127 BY SIMILARITY.
FT DISULFID 129 141 BY SIMILARITY.
FT DISULFID 147 166 BY SIMILARITY.
FT DISULFID 149 169 BY SIMILARITY.
FT DISULFID 171 179 BY SIMILARITY.
FT DISULFID 344 502 BY SIMILARITY.
FT DISULFID 508 520 BY SIMILARITY.
FT DISULFID 515 533 BY SIMILARITY.
FT DISULFID 527 542 BY SIMILARITY.
FT DISULFID 665 677 BY SIMILARITY.
FT DISULFID 672 690 BY SIMILARITY.
FT DISULFID 684 699 BY SIMILARITY.
FT DISULFID 725 737 BY SIMILARITY.
FT DISULFID 732 750 BY SIMILARITY.
FT DISULFID 744 759 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 867 867
SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;

Query Match 23.0%; Score 58; DB 1; Length 867;
Best Local Similarity 36.1%; Pred. No. 13;
Matches 13; Conservative 5; Mismatches 12; Indels 6; Gaps 1;

QY 4 PEFHCGDPCTTCRRHPCPPGQGVQSQGKFSFGQC 39
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Db 118 PDRPCGGPGCW-----CPAGQVLGAQGRCVMPRQC 147

Search completed: September 4, 2001, 16:15:26
Job time: 1138 sec

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DR Pfam; PF00094; vwd; 3.  
DR Pfam; PF01826; TIL; 3.  
DR PRINTS; PR00365; ENDOTHELIN.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR PROSITE; PS02324; VWF; 3.  
DR PROSITE; PS01208; VWF; 3.  
DR PROSITE; PS01185; CTCK\_1; 1.  
DR PROSITE; PS01225; CTCK\_2; 1.  
KW Blood coagulation; Platelet; Glycoprotein; Extracellular matrix;  
KW Plasma; Endothelial cell; Repeat; Cell adhesion.  
FT NON\_TER 1  
FT PROPEP <1 437 BY SIMILARITY.  
FT CHAIN 438 2482 VON WILLEBRAND FACTOR.  
FT DOMAIN 62 215 VWF2.  
FT DOMAIN 438 461 AMINO-TERMINAL.  
FT DOMAIN 462 507 EL.  
FT DOMAIN 500 527 CX.  
FT DOMAIN 541 687 VWF3.  
FT DOMAIN 947 1127 VWF4.  
FT DOMAIN 1167 1334 VWF5.  
FT DOMAIN 1360 1540 VWF6.  
FT DOMAIN 1619 1771 VWF7.  
FT DOMAIN 1885 1930 E2.  
FT DOMAIN 1924 1997 VWF8.  
FT DOMAIN 2048 2164 VWF9.  
FT DOMAIN 2249 2319 VWF10.  
FT DOMAIN 2393 2481 CTCK.  
FT SITE 2176 2178 CELL ATTACHMENT SITE (POTENTIAL).  
FT DISULFID 441 482 BY SIMILARITY.  
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FT DISULFID 572 667 BY SIMILARITY.  
FT DISULFID 588 595 BY SIMILARITY.  
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FT DISULFID 745 785 BY SIMILARITY.  
FT DISULFID 763 765 BY SIMILARITY.  
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FT DISULFID 833 843 BY SIMILARITY.  
FT DISULFID 800 804 BY SIMILARITY.  
FT DISULFID 870 873 BY SIMILARITY.  
FT DISULFID 908 911 BY SIMILARITY.  
FT DISULFID 942 1128 BY SIMILARITY.  
FT DISULFID 1338 1339 BY SIMILARITY.  
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FT DISULFID 1548 1573 BY SIMILARITY.  
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FT DISULFID 1641 1792 BY SIMILARITY.  
FT DISULFID 1619 1754 BY SIMILARITY.  
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FT DISULFID 2408 2457 BY SIMILARITY.  
FT DISULFID 2419 2473 BY SIMILARITY.  
FT DISULFID 2423 2475 BY SIMILARITY.  
FT DISULFID ? 2480 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 340 340 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 905 905 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1184 1184 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. .) (POTENTIAL).  
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FT CARBOHYD 2215 2215 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 2254 2254 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 2459 2459 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 2482 AA; 272394 MW; D499B7DDFBBCAEDD CRC64;

Query Match 23.2%; Score 58.5; DB 1; Length 2482;  
Best Local Similarity 30.8%; Pred. No. 26;  
Matches 16; Conservative 2; Mismatches 19; Indels 15; Gaps 2;  
QY 3 QPERHCGDPCCTTCR--HHP-----CPPGGVQSQGFSGFQC 39  
DB 330 QVYLQCGTPCNLTCRSLSPDECAEDLCGFCPPGLYLDGSGDCVPKQAC 381  
RESULT 14  
OX40\_RAT ID OX40\_RAT STANDARD; PRT; 271 AA.  
AC PI5725;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).  
GN TNFRSF4 OR TXGPIL OR OX40.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell;  
RX MEDLINE=90214614; PubMed=2157591;  
RA Mallett S., Fossum S., Barclay A.N.;  
RT Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.;  
RL EMBO J. 9:1063-1068(1990).  
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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CC -----  
CC EMBL: X17037; CAA34897.1; -  
DR PIR; S08036; S08036.  
DR PIR; S12783; S12783.  
DR HSSP; P25942; ICDF.  
DR InterPro; IPR001368; -  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
KW Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 271 OX40L RECEPTOR.  
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 211 235 POTENTIAL.  
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 164 4 X TNFR-CYS.  
FT REPEAT 25 60 TNFR-CYS 1.  
FT REPEAT 61 102 TNFR-CYS 2.  
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).  
FT REPEAT 124 164 TNFR-CYS 4.  
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;  
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Best Local Similarity 30.0%; Pred. No. 5;  
Matches 12; Conservative 3; Mismatches 9; Indels 16; Gaps 2;  
QY 1 CVOPERHCGDPCCTTCR-----H-----HPCPPG 24  
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FT	CARBOHYD	359	359	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	368	368	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	420	420	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	573	573	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	578	578	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	613	613	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	633	633	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	648	648	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	NON_TER	703	703	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SEQ	SEQUENCE	703 AA;	77427 MW;	AFF2DE11B735A690	CRC64;
Query Match 23.4%; Score 59; DB 1; Length 703;					
Best Local Similarity 33.3%; Pred. No. 8.3;					
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;					
Qy	8 CGDPCCTTCRRHPCPPGGVQSQGFSGFQCI 40				
Db	267 CKDTCPLVLNPTTYQMDVNPBGKYSFGATCV 299				
RESULT 11					
ID	INTR_SACER	STANDARD;	PRT;	437 AA.	
AC	P22877;				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-AUG-1991 (Rel. 19, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	INTRASE (RECOMBINASE).				
GN	INT.				
OS	Saccharopolyspora erythraea (Streptomyces erythraeus).				
OG	Plasmid pSE211.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Pseudonocardineae; Pseudonocardaceae;				
OC	Saccharopolyspora.				
ON	NCBI_TaxID=1836;				
RX	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90202705; PubMed=2180909;				
RA	Brown D.P., Idler K.B., Katz L.;				
RT	"Characterization of the genetic elements required for site-specific				
RT	integration of plasmid pSE211 in Saccharopolyspora erythraea.";				
RL	J. Bacteriol. 172:1877-1888(1990).				
CC	-1- FUNCTION: IS A RECOMBINASE (OR INTEGRASE), CATALYZING THE CUTTING				
CC	AND REJOINING OF THE RECOMBINATING DNA MOLECULES.				
CC	-1- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.				
CC	-----				
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CC	or send an email to license@lsb-sib.ch).				
CC	-----				
DR	EMBL; M35138; AAA98345.1; .				
DR	PIR; C35147; C35147.				
DR	InterPro; IPR002104; .				
DR	Pfam; PF00589; Phage_integrase; 1.				
KW	DNA recombination; DNA integration; Plasmid.				
FT	ACT_SITE	414	414	TRANSIENT COVALENT LINKAGE TO DNA DURING	
FT	STRAND CLEAVAGE AND REJOINING (BY				
FT	SIMILARITY).				
SEQ	SEQUENCE	437 AA;	50323 MW;	29EED7108CC5AFBD	CRC64;
Query Match 23.2%; Score 58.5; DB 1; Length 437;					
Best Local Similarity 32.4%; Pred. No. 6.4;					
Matches 11; Conservative 3; Mismatches 9; Indels 11; Gaps 2;					
Qy	1 CVQPE-----FHCGBPCTTCRRH-----PCPP 23				
Db	248 CSDPHRCGATVHKTEPCCKAACRHTACPPCP 281				

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RESULT 12
TSP4_RAT
ID TSP4_RAT STANDARD; PRT; 980 AA.
AC P49744:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE THROMBOSPONDIN 4 PRECURSOR.
GN THB4 OR TSP4 OR TSP-4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEWIS; TISSUE=Skeletal muscle;
RX MEDLINE=96074771; PubMed=7490284;
RA Arber S., Caroni P.;
RT "Thrombospondin-4, an extracellular matrix protein expressed in the
RL J. Cell Biol. 131:1083-1094(1995).
CC -!- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
CC CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,
CC LAMININ AND TYPE V COLLAGEN.
CC -!- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
CC -!- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
CC -----
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CC -----
DR EMBL; X89963; CAA62002.1; -.
DR HSP; P35444; 1VDF.
DR InterPro; IPR000561; -.
DR InterPro; IPR001881; -.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 2.
KW Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain;
KW Signal.
FT SIGNAL 1 39
FT CHAIN 40 980
FT DOMAIN 40 303
FT DOMAIN 304 343
FT DOMAIN 344 396
FT DOMAIN 397 437
FT DOMAIN 438 481
FT DOMAIN 511 546
FT DOMAIN 547 569
FT DOMAIN 570 605
FT DOMAIN 606 628
FT DOMAIN 629 666
FT DOMAIN 667 706
FT DOMAIN 707 742
FT DOMAIN 743 980
FT DISULFID 276 276
FT DISULFID 279 279
FT DISULFID 308 319
FT DISULFID 313 328
FT DISULFID 331 342
FT DISULFID 348 359
FT DISULFID 353 368
FT DISULFID 371 395
FT DISULFID 401 412
FT SIGNAL 1 39
FT CHAIN 40 980
FT DOMAIN 40 303
FT DOMAIN 304 343
FT DOMAIN 344 396
FT DOMAIN 397 437
FT DOMAIN 438 481
FT DOMAIN 511 546
FT DOMAIN 547 569
FT DOMAIN 570 605
FT DOMAIN 606 628
FT DOMAIN 629 666
FT DOMAIN 667 706
FT DOMAIN 707 742
FT DOMAIN 743 980
FT DISULFID 276 276
FT DISULFID 279 279
FT DISULFID 308 319
FT DISULFID 313 328
FT DISULFID 331 342
FT DISULFID 348 359
FT DISULFID 353 368
FT DISULFID 371 395
FT DISULFID 401 412

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FT DISULFID 406 421
FT DISULFID 424 436
FT DISULFID 442 456
FT DISULFID 450 466
FT DISULFID 468 480
FT CARBOHYD 631 631
FT CARBOHYD 960 960
SQ SEQUENCE 980 AA; 108213 MW; 036D41EB6E206FCF CRC64;

Query Match 23.2%; Score 58.5; DB 1; Length 980;
Best Local Similarity 31.9%; Pred. No. 12;
Matches 15; Conservative 6; Mismatches 9; Indels 17; Gaps 4;

Oy 6 FHCGDPC-----CT---TCRHPCPPGGQVGQSGKFSFGQC 39
   ||||| | : ||||| | : |||
Db 326 FQCG-PCPDGYTGNGTCSVDYCKYHPCYGVRCIN---LAPGPRC 368

RESULT 13
VWF_PIG
ID VWF_PIG STANDARD; PRT; 2482 AA.
AC Q28833:
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VON WILLEBRAND FACTOR PRECURSOR (VWF) (FRAGMENT).
GN F8VWF OR VWF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Seaman W.T., Read M.S., Bellinger D.A., Nichols T.C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 397-553 FROM N.A.
RX MEDLINE=93356762; PubMed=8352759;
RA Laverne J.M., Piao Y.C., Ferreira V., Kerbiriou-Nabias D.,
RA Bohnak B.R., Meyer D.;
RT "Primary structure of the factor VIII binding domain of human, porcine
RT and rabbit von Willebrand factor."
RL Biochem. Biophys. Res. Commun. 194:1019-1024(1993).
CC -!- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT
CC PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
CC NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF
CC VASCULAR INJURY (BY SIMILARITY).
CC -!- SUBUNIT: MULTIMERIC (BY SIMILARITY).
CC -!- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
CC INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 3 VWF DOMAINS.
CC -!- SIMILARITY: CONTAINS A C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
CC -----
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CC -----
DR EMBL; AF052036; AAC06229.1; -.
DR EMBL; S64541; AAB27829.2; -.
DR HSP; P04275; IATF.
DR InterPro; IPR000359; -.
DR InterPro; IPR001007; -.
DR InterPro; IPR001846; -.
DR InterPro; IPR002035; -.
DR InterPro; IPR002919; -.
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00092; vwa; 3.

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DR InterPro; IPR001374; --  
 DR Pfam; PF01424; RHH; 1.  
 DR Pfam; PF01422; zf-NF-X1; 8.  
 KW Transcription regulation; Repressor; DNA-binding; Nuclear protein;  
 KW Repeat.  
 FT DOMAIN 424 876 7 X APPROXIMATE REPEATS, CYS-RICH.  
 FT REPEAT 424 463 1.  
 FT REPEAT 424 517 2.  
 FT REPEAT 480 517 2.  
 FT REPEAT 541 580 3.  
 FT REPEAT 606 647 4.  
 FT REPEAT 695 734 5.  
 FT REPEAT 806 842 6.  
 FT REPEAT 836 876 7.  
 SQ SEQUENCE 1104 AA; 123149 MW; 36FEC4292F78130C CRC64;

Query Match 23.6%; Score 59.5; DB 1; Length 1104;  
 Best Local Similarity 43.5%; Pred. No. 10;  
 Matches 10; Conservative 0; Mismatches 12; Indels 1; Gaps 1;  
 QY 1 CVOPEFHCGDPCCTTCR-HHPCP 22  
 | | | | | | | | | |  
 DB 840 CTTPRADCGHPCWAPCHTSSPCP 862

RESULT 8  
 VWF\_HUMAN  
 ID VWF\_HUMAN STANDARD; PRT; 2813 AA.  
 AC P04275;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE VON WILLEBRAND FACTOR PRECURSOR (VWF).  
 GN F8VWF OR VWF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90062044; PubMed=2584182;  
 RA Mancuso D.J., Tuley E.A., Westfield L.A., Worrall N.K.,  
 RA Shelton-Inloes B.B., Sorace J.M., Alevis G., Sadler J.E.;  
 RT "Structure of the gene for human von Willebrand factor.";  
 RL J. Biol. Chem. 264:19514-19527(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87016349; PubMed=3489923;  
 RA Bonthron D., Orr E.C., Mitsock L.M., Ginsburg D., Handin R.I.,  
 RA Orkin S.H.;  
 RT "Nucleotide sequence of pre-pro-von Willebrand factor cDNA.";  
 RL Nucleic Acids Res. 14:7125-7128(1986).  
 RN [3]  
 RP SEQUENCE OF 1-120 FROM N.A., AND SEQUENCE OF 23-56.  
 RC TISSUE=Umbilical vein endothelial cells;  
 RX MEDLINE=87213253; PubMed=3495266;  
 RA Shelton-Inloes B.B., Broze G.J. Jr., Miletič J.P., Sadler J.E.;  
 RT "Evolution of human von Willebrand factor: cDNA sequence  
 RT polymorphisms, repeated domains, and relationship to von Willebrand  
 RT antigen II.";  
 RL Biochem. Biophys. Res. Commun. 144:657-665(1987).  
 RN [4]  
 RP SEQUENCE OF 1-1400 FROM N.A.  
 RX MEDLINE=87004550; PubMed=3019665;  
 RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;  
 RT "Full-length von Willebrand factor (vWF) cDNA encodes a highly  
 RT repetitive protein considerably larger than the mature vWF subunit.";  
 RL EMBO J. 5:1839-1847(1986).  
 RN [5]  
 RP ERRATUM.  
 RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;  
 RL EMBO J. 5:3074-3074(1986).  
 RN [6]

RP SEQUENCE OF 764-2813.  
 RX MEDLINE=86269895; PubMed=3524673;  
 RA Titani K., Kumar S., Takio K., Ericsson L.H., Wade R.D., Ashida K.,  
 RA Walsh K.A., Choepk M.W., Sadler J.E., Fujikawa K.;  
 RT "Amino acid sequence of human von Willebrand factor.";  
 RL Biochemistry 25:3171-3184(1986).  
 RN [7]  
 RP SEQUENCE OF 781-1424 FROM N.A.  
 RX MEDLINE=86269894; PubMed=3488076;  
 RA Shelton-Inloes B.B., Titani K., Sadler J.E.;  
 RT "cDNA sequences for human von Willebrand factor reveal five types of  
 RT repeated domains and five possible protein sequence polymorphisms.";  
 RL Biochemistry 25:3164-3171(1986).  
 RN [8]  
 RP SEQUENCE OF 764-873 AND 1289-2813 FROM N.A.  
 RX MEDLINE=86016708; PubMed=2864688;  
 RA Sadler J.E., Shelton-Inloes B.B., Sorace J.M., Harlan J.M.,  
 RA Titani K., Davie E.W.;  
 RT "Cloning and characterization of two cDNAs coding for human von  
 RT Willebrand factor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6394-6398(1985).  
 RN [9]  
 RP SEQUENCE OF 990-1947 FROM N.A.  
 RX MEDLINE=91105089; PubMed=1988024;  
 RA Mancuso D.J., Tuley E.A., Westfield L.A., Lester-Mancuso T.L.,  
 RA Le Beau M.M., Sorace J.M., Sadler J.E.;  
 RT "Human von Willebrand factor gene and pseudogene: structural analysis  
 RT and differentiation by polymerase chain reaction.";  
 RL Biochemistry 30:253-269(1991).  
 RN [10]  
 RP SEQUENCE OF 2731-2813 FROM N.A.  
 RX MEDLINE=85269603; PubMed=3875078;  
 RA Verweij C.L., de Vries C.J.M., Distel B., van Zonneveld A.-J.,  
 RA Geurts van Kessel A., van Mourik J.A., Pannekoek H.;  
 RT "Construction of cDNA coding for human von Willebrand factor using  
 RT antibody probes for colony-screening and mapping of the chromosomal  
 RT gene.";  
 RL Nucleic Acids Res. 13:4699-4717(1985).  
 RN [11]  
 RP SEQUENCE OF 1-177 FROM N.A.  
 RX MEDLINE=88111704; PubMed=2828057;  
 RA Bonthron D., Orkin S.H.;  
 RT "The human von Willebrand factor gene. Structure of the 5' region.";  
 RL Eur. J. Biochem. 171:51-57(1988).  
 RN [12]  
 RP SEQUENCE OF 2621-2813 FROM N.A.  
 RX MEDLINE=85244588; PubMed=3874428;  
 RA Ginsburg D., Handin R.I., Bonthron D.T., Donlon T.A., Bruns G.A.P.,  
 RA Latt S.A., Orkin S.H.;  
 RT "Human von Willebrand factor (vWF): isolation of complementary DNA  
 RT (cDNA) clones and chromosomal localization.";  
 RL Science 228:1401-1406(1985).  
 RN [13]  
 RP SEQUENCE OF 2731-2813 FROM N.A.  
 RX MEDLINE=85201687; PubMed=3873280;  
 RA Lynch D.C., Zimmerman T.S., Collins C.J., Brown M., Morin M.J.,  
 RA Ling E.H., Livingston D.M.;  
 RT "Molecular cloning of cDNA for human von Willebrand factor:  
 RT authentication by a new method.";  
 RL Cell 41:49-56(1985).  
 RN [14]  
 RP REVISIONS.  
 RA Lynch D.C.;  
 RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.  
 RN [15]  
 RP SEQUENCE OF 2731-2813 FROM N.A.  
 RX MEDLINE=87260814; PubMed=3496594;  
 RA Collins C.J., Underdahl J.P., Levene R.B., Ravera C.P.,  
 RA Morin M.J., Dombalaghi M.J., Ricca G., Livingston D.M.,  
 RA Lynch D.C.;  
 RT "Molecular cloning of the human gene for von Willebrand factor and  
 RT identification of the transcription initiation site.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4393-4397(1987).  
 RN [16]







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FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 528 528 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19- 19 C -> S (IN REF. 2).
FT CONFLICT 539 539 C -> W (IN REF. 5).
FT CONFLICT 991 991 L -> F (IN REF. 4).
FT CONFLICT 1116 1117 HP -> DR (IN REF. 6).
SQ SEQUENCE 1210 AA; 134853 MW; 650E20D46DF2D2F5 CRC64;

Query Match 25.4%; Score 64; DB 1; Length 1210;
Best Local Similarity 34.2%; Pred. No. 3.4; Indels 0; Gaps 0;
Matches 13; Conservative 5; Mismatches 20;

QY 3 QPEFHGCDPCTTCRHHPCPPGQGVQSGKFSFGFCI 40
D 255 QDEATCKDTCPLMLNPTTYQMDVNPCKYSGATCV 292

RESULT 3
VFV_BOVIN STANDARD; PRT; 937 AA.
AC P80012; Q28011;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VON WILLEBRAND FACTOR PRECURSOR (VWF) (FRAGMENT).
GN F8VWF OR VWF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97307751; PubMed=9165093;
RA Janel N., Ribba A.S., Cherel G., Kerbiriou-Nabias D., Meyer D.;
RT "Primary structure of the propeptide and factor VIII-binding domain of
RL bovine von Willebrand factor."
RL Biochim. Biophys. Acta 1339:4-8(1997).
RN [2]
RP SEQUENCE OF 1-177 FROM N.A.
RX MEDLINE=96144290; PubMed=8566794;
RA Janel N., Schwachtgen J.L., Bakhshi M.R., Barek L., Meyer D.,
RL Kerbiriou-Nabias D.;
RT "Comparison of the 5'-flanking sequences of the human and bovine von
RL Willebrand factor-encoding genes reveals alternation of highly
RL homologous domains with species-specific Alu-type repeats."
RL Gene 167:291-295(1995).
RN [3]
RP PARTIAL SEQUENCE.
RX MEDLINE=91192039; PubMed=1707363;
RA Fujisawa T., Takagi J., Sekiya F., Goto A., Miake F., Saito Y.;
RT "Monoclonal antibodies that inhibit binding of propeptide of von
RL Willebrand factor to collagen. Localization of epitopes."
RL Eur. J. Biochem. 196:673-677(1991).
RN [4]
RP PARTIAL SEQUENCE.
RX MEDLINE=96028118; PubMed=7588715;
RA Takagi J., Aoyama T., Ueki S., Ohba H., Saito Y., Lorand L.;
RT "Identification of bovine-XIIIa-reactive glutamyl residues in the
RL propeptide of factor von Willebrand factor."
RL Eur. J. Biochem. 232:773-777(1995).
CC -!- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT
CC PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
CC NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF
CC VASCULAR INJURY.
CC -!- SUBUNIT: MULTIMERIC (BY SIMILARITY).
CC -!- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
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CC INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS AT LEAST 3 VWF DOMAINS.
CC -----
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CC -----
CC EMBL; Y09353; CAA70525.1; -
CC EMBL; U28147; AAA96953.1; -
CC InterPro; IPR000359; -
CC InterPro; IPR001007; -
CC InterPro; IPR001846; -
CC InterPro; IPR002919; -
CC Pfam; PF01826; TIL; 3.
CC Pfam; PF00094; vwd; 3.
CC PROSITE; PS01185; CTCK_1; PARTIAL.
CC PROSITE; PS01225; CTCK_2; PARTIAL.
CC PROSITE; PS01208; WVFC; PARTIAL.
CC Blood coagulation; Platelet; Glycoprotein; Extracellular matrix;
KW Plasma; Endothelial cell; Cell adhesion; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 762 BY SIMILARITY.
FT CHAIN 763 >937 VON WILLEBRAND FACTOR.
FT DOMAIN 35 179 VWF 1.
FT DOMAIN 387 540 VWF 2.
FT DOMAIN 763 786 AMINO-TERMINAL.
FT DOMAIN 787 832 E1.
FT DOMAIN 825 852 CX.
FT DOMAIN 841 >937 VWF 3.
FT SITE 410 410 FACTOR XIII-A-BINDING.
FT SITE 414 414 FACTOR XIII-A-BINDING.
FT SITE 605 605 FACTOR XIII-A-BINDING.
FT DISULFID 766 807 BY SIMILARITY.
FT DISULFID 775 803 BY SIMILARITY.
FT DISULFID 913 920 BY SIMILARITY.
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 665 665 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 856 856 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 330 330 MISSING (IN REF. 3).
FT CONFLICT 523 523 MISSING (IN REF. 4).
FT CONFLICT 528 528 G -> Q (IN REF. 4).
FT NON_TER 937 937
SQ SEQUENCE 937 AA; 102599 MW; 9BF4C94A254A5629 CRC64;

Query Match 25.2%; Score 63.5; DB 1; Length 937;
Best Local Similarity 34.0%; Pred. No. 3.2;
Matches 16; Conservative 1; Mismatches 15; Indels 15; Gaps 2;

QY 8 CGDPCCTTCR--HHP-----CPPGQGVQSGKFSFGFCQ 39
D 660 CGTPCNLTCSRSLSHPBDECTVCLGCGFCPPGLFDETGSCVPKACQ 706

RESULT 4
VFV_CANFA STANDARD; PRT; 2813 AA.
AC Q28295; Q28311; Q9TS14;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VON WILLEBRAND FACTOR PRECURSOR (VWF).
GN F8VWF OR VWF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:25 ; Search time 43.78 Seconds  
(without alignments)  
31.298 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_74\_113

Perfect score: 232

Sequence: 1 CVQPEFHCGDPCTCTRHHPGPGQGVQSQKFSFGQCI 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	67	26.6	256	1 41BB_MOUSE	P20334 mus musculus
2	64	25.4	1210	1 EGFR_MOUSE	Q01279 mus musculus
3	63.5	25.2	937	1 VWF_BOVIN	P80012 bos taurus
4	60.5	24.0	2813	1 VWF_CANFA	Q28295 canis familiar
5	60	23.8	233	1 CYCX_NITEU	O50926 nitrosomona
6	60	23.8	1210	1 EGFR_HUMAN	P00533 homo sapien
7	59.5	23.6	1104	1 NF1_HUMAN	Q12986 homo sapien
8	59.5	23.6	2813	1 VWF_HUMAN	P04275 homo sapien
9	59	23.4	58	1 MT1_SCVSE	P02805 scylla serr
10	59	23.4	703	1 EGFR_CHICK	P13387 gallus gall
11	58.5	23.2	437	1 INTR_SACER	P22877 saccharopol
12	58.5	23.2	980	1 TSF4_RAT	P49744 rattus norv
13	58.5	23.2	2482	1 VWF_PIG	Q28833 sus scrofa
14	58	23.0	271	1 OX40_RAT	P15725 rattus norv
15	58	23.0	867	1 SSPO_BOVIN	P98167 bos taurus
16	58	23.0	2907	1 FBN2_MOUSE	Q61555 mus musculus
17	58	23.0	2911	1 FBN2_HUMAN	P35356 homo sapien
18	57.5	22.8	289	1 CD40_MOUSE	P27512 mus musculus
19	57.5	22.8	581	1 IRR_RAT	Q64716 rattus norv
20	57.5	22.8	961	1 TSF4_HUMAN	P35443 homo sapien
21	57.5	22.8	1297	1 IRR_HUMAN	P14616 homo sapien
22	57	22.6	60	1 MTA_THCCR	P52721 themarces
23	57	22.6	1370	1 IGR_RAT	P24062 rattus norv
24	57	22.6	1373	1 IGR_MOUSE	Q60751 mus musculus
25	57	22.6	2318	1 NTC3_MOUSE	Q61982 mus musculus
26	56.5	22.4	277	1 CD40_HUMAN	P25942 homo sapien
27	56	22.2	63	1 ICE1_ASCSU	P07851 ascaris suu
28	56	22.2	1687	1 Z142_HUMAN	P52746 homo sapien
29	55.5	22.0	62	1 MT4_HUMAN	P47944 homo sapien
30	55.5	22.0	277	1 OX40_HUMAN	P43489 homo sapien
31	55	21.8	269	1 CD40_BOVIN	Q28203 bos taurus
32	55	21.8	448	1 K1M2_HUMAN	Q14532 homo sapien
33	55	21.8	921	1 CA19_MOUSE	Q05722 mus musculus

34 55 21.8 931 1 CA19\_HUMAN P20849 homo sapien  
35 55 21.8 1106 1 STC\_DROME P40798 drosophila  
36 55 21.8 1466 1 CA13\_HUMAN P02461 homo sapien  
37 54.5 21.6 62 1 MT4\_MOUSE P47945 mus musculus  
38 54 21.4 230 1 SPIT\_DROME Q01083 drosophila  
39 54 21.4 677 1 SP87\_DICDI P54643 dictyostell  
40 54 21.4 798 1 HEPA\_HCMVA P16827 human cymom  
41 54 21.4 837 1 LDLR\_RABIT P20063 oryctolagus  
42 53.5 21.2 431 1 VMSA\_WHV8 P06432 woodchuck h  
43 53.5 21.2 1429 1 LI12\_CABEL P14585 caenorhabd1  
44 53 21.0 65 1 ICE2\_ASCSU P07852 ascaris suu  
45 53 21.0 91 1 VE4\_RHPV1 P24832 rhesus papi

## ALIGNMENTS

RESULT 1  
41BB\_MOUSE  
ID 41BB\_MOUSE STANDARD; PRT; 256 AA.  
AC P20334;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).  
GN TNFRSF9 OR IL4 OR LY63 OR CD137 OR CD157.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=69184547; Pubmed=2784565;  
RA Kwon B.S., Weissman S.M.;  
RT "CDNA sequences of two inducible T-cell genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RX MEDLINE=94179805; Pubmed=8133039;  
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;  
RT "Genomic organization and chromosomal localization of the T-cell antigen 4-1BB.";  
RL J. Immunol. 152:2256-2262(1994).  
RN [3]  
RP CHARACTERIZATION, AND SEQUENCE OF 25-29.  
RX MEDLINE=93139510; Pubmed=7678621;  
RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,  
RA Kwon B.S.;  
RT "Inducible T cell antigen 4-1BB. Analysis of expression and function.";  
RL J. Immunol. 150:771-781(1993).  
CC -I- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY ACTIVE DURING T CELL ACTIVATION.  
CC -I- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.  
CC -I- ASSOCIATES WITH P56-LCK.  
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -I- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.  
CC -I- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.  
CC -I- SIMILARITY: CONTAINS A LA-NGRP/TNFR-TYPE CYSTEINE-RICH REGION.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; J04492; AAA40167.1; -  
DR EMBL; U02567; AAA93113.1; -  
DR PIR; B32393; B32393.  
DR HSSP; P25942; ICDF.





Best Local Similarity 41.9%; Pred. No. 7.1;

---

Query Match 24.8%; Score 61; DB 2; Length 459;  
 Best Local Similarity 36.6%; Pred. No. 4.6;  
 Matches 15; Conservative 5; Mismatches 15; Indels 6; Gaps 2;

Qy 2 CASGTFSG--GHEGCKPWTCTQGFVTFPGNTHNAVC 40  
 ||||| : : : ||| : |||  
 Db 151 CAPGTFSDTSTDCRPHICS-----ILAIPGNASTDAVC 187

RESULT 7  
 A35356  
 tumor necrosis factor receptor 2 precursor [validated] - human  
 A:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Sep-1999 sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
 C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
 R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.  
 Science 248, 1019-1023, 1990  
 A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
 A:Reference number: A35356; MUID:90260639  
 A:Accession: A35356  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <SMI>  
 A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:gl89186  
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
 A:Reference number: A36475; MUID:91045991  
 A:Accession: A36475  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-195, 'R', 197-461 <KOH>  
 A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
 R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gents, R.; Brockhaus, M.  
 Cytokine 2, 231-237, 1990  
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
 A:Reference number: A48416; MUID:91370690  
 A:Accession: A48416  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 23-461 <DEM>  
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649  
 A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:63371)  
 R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra  
 A:Reference number: A36007; MUID:90349572  
 A:Accession: A36007  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HBL>  
 A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752  
 R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
 J. Biol. Chem. 265, 20131-20138, 1990  
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec  
 A:Reference number: A23666; MUID:91056048  
 A:Accession: A23666  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 23-40:65-69; 136-141:300-306 <LOE>  
 R:Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence;  
 A:Reference number: A35010; MUID:90110215  
 A:Accession: B35010  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 27-31 <ENG>  
 R:Kuhnert, P.; Kemper, O.; Wallach, D.  
 Gene 150, 381-386, 1994

Query Match 24.8%; Score 61; DB 1; Length 461;  
 Best Local Similarity 36.6%; Pred. No. 4.6;  
 Matches 15; Conservative 4; Mismatches 16; Indels 6; Gaps 2;

Qy 2 CASGTFSG--GHEGCKPWTCTQGFVTFPGNTHNAVC 40  
 ||||| : : : ||| : |||  
 Db 164 CAPGTFSTNTSSDTCRPHQICN-----VVAIPGNASMDAVC 200

RESULT 8  
 B38634  
 tumor necrosis factor receptor type 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
 C:Accession: B38634; A40254; S54816  
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
 A:Reference number: A38634; MUID:91187885  
 A:Accession: B38634  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <LEW>  
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f  
 A:Reference number: A40254; MUID:91246168  
 A:Accession: A40254  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <GOO>  
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
 R:Kisssonmerghis, M.; Fellows, R.; Feldmann, M.; Chernaiovsky, Y.  
 submitted to the EMBL Data Library, May 1995  
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor  
 A:Reference number: S54816  
 A:Accession: S54816  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-22 <KTS>  
 A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
 F:40-77/Domain: NGF receptor repeat homology <NG1>  
 F:79-120/Domain: NGF receptor repeat homology <NG2>  
 F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 24.8%; Score 61; DB 2; Length 474;  
 Best Local Similarity 36.6%; Pred. No. 4.7;  
 Matches 15; Conservative 5; Mismatches 15; Indels 6; Gaps 2;

QY 2 CASGTFSG--GHEGHCPRWDTCTQFGFLTVFPNGKTHNAV 40  
 || ||||| | : | : ||| : |||  
 Db 166 CAPGTFSDTSTSDVCRPHRCS----ILAIPGNASTDAVC 202

RESULT 9  
 JN0006  
 nerve growth factor receptor, low affinity precursor - chicken  
 N;Alternate names: NGF receptor  
 C;Species: Gallus gallus (chicken)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: JN0006; A60504  
 R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter; E.M.; Reid  
 Neuron 2, 1123-1134, 1989  
 A;Title: Structure and developmental expression of the nerve growth factor receptor in t  
 A;Reference number: JN0006; MUID:90166579  
 A;Accession: JN0006  
 A;Molecule type: mRNA  
 A;Residues: 1-416 <LAR>  
 R;Experimental source: embryonic chick brain  
 R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.  
 Dev. Biol. 137, 287-304, 1990  
 A;Title: Structure and developmental expression of the chicken NGF receptor.  
 A;Reference number: A60504; MUID:90152140  
 A;Accession: A60504  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 21-35,'Y','37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>  
 C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
 C;Comment: The cysteine-rich region of the extracellular domain may form part or all of  
 C;Comment: This protein is thought to form a high-affinity receptor when it associates w  
 C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-416/Product: nerve growth factor receptor #status predicted <MAT>  
 F;21-239/Domain: extracellular #status predicted <EXT>  
 F;24-57/Domain: NGF receptor repeat homology <NG1>  
 F;59-100/Domain: NGF receptor repeat homology <NG2>  
 F;101-139/Domain: NGF receptor repeat homology <NG3>  
 F;141-181/Domain: NGF receptor repeat homology <NG4>  
 F;189-237/Region: serine/threonine-rich  
 F;240-261/Domain: transmembrane #status predicted <MEM>  
 F;262-416/Domain: intracellular #status predicted <INT>  
 F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.6%; Score 60.5; DB 1; Length 416;  
 Best Local Similarity 35.9%; Pred. No. 4.8;  
 Matches 14; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

QY 2 CASGTFSGGHEGHCPRWDTCTQFGFLTVFPNGKTHNAV 40  
 || ||||| | : | : ||| : |||  
 Db 101 CAYGYQDELSSGCKECSIC-EVGFGLMFFCRSDQTV 138

RESULT 10  
 Q0BBB1  
 B1 protein - black beetle virus  
 C;Species: black beetle virus  
 C;Date: 30-Sep-1992 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
 C;Accession: S78471; S28728; S28729; A23243  
 R;Dasgupta, R.  
 submitted to the EMBL Data Library, July 1986  
 A;Reference number: S78471  
 A;Accession: S78471  
 A;Molecule type: genomic RNA  
 A;Residues: 1-998 <DAS>

A;Cross-references: EMBL:X02396; NID:960679; PIDN:CAA26238.1; PID:960680  
 R;Dasmahapatra, B.; Dasgupta, R.; Ghosh, A.; Kaesberg, P.  
 J. Mol. Biol. 182, 183-189, 1985  
 A;Title: Structure of the black beetle virus genome and its functional implications.  
 A;Reference number: S28728; MUID:85210903  
 A;Accession: S28728  
 A;Molecule type: genomic RNA  
 A;Residues: 1-883,'AALRRTPWTRNYQC' <DAW>  
 A;Cross-references: EMBL:X02396  
 A;Accession: S28729  
 A;Molecule type: genomic RNA  
 A;Residues: 897-998 <DAZ>  
 A;Cross-references: EMBL:X02396  
 R;Guarino, L.A.; Ghosh, A.; Dasmahapatra, B.; Dasgupta, R.; Kaesberg, P.  
 Virol. 139, 199-203, 1984  
 A;Title: Sequence of the black beetle virus subgenomic RNA and its location in the vi  
 A;Reference number: A23243; MUID:85042104  
 A;Accession: A23243  
 A;Molecule type: genomic RNA  
 A;Residues: 897-998 <GUA>  
 A;Cross-references: GB:M33065; NID:g210673; PIDN:AAA42745.1; PID:g210674  
 C;Superfamily: black beetle virus B1 protein  
 C;Keywords: RNA biosynthesis

Query Match 24.0%; Score 59; DB 1; Length 998;  
 Best Local Similarity 44.4%; Pred. No. 16;  
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 14 HCKPWTCTQFGFLTVFP 31  
 ||||| : |  
 Db 261 HCRPWTDCPDRLVVTIP 278

RESULT 11  
 S41397  
 protein A - flock house virus  
 C;Species: flock house virus  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 11-Jan-2000  
 C;Accession: S41397  
 R;Dasgupta, R.  
 submitted to the EMBL Data Library, January 1994  
 A;Description: Near identity in the polymerase gene of two serologically distinct nod  
 A;Reference number: S41397  
 A;Accession: S41397  
 A;Status: preliminary  
 A;Molecule type: genomic RNA  
 A;Residues: 1-998 <DAS>  
 A;Cross-references: EMBL:X77156; NID:g450500; PIDN:CAA54399.1; PID:g450501  
 C;Superfamily: black beetle virus B1 protein

Query Match 24.0%; Score 59; DB 2; Length 998;  
 Best Local Similarity 44.4%; Pred. No. 16;  
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 14 HCKPWTCTQFGFLTVFP 31  
 ||||| : |  
 Db 261 HCRPWTDCPDRLVVTIP 278

RESULT 12  
 JC7134  
 agkisacutacin alpha chain precursor - sharp-nosed viper  
 N;Alternate names: fibrinogenolytic venom protein  
 C;Species: Agkistrodon acutus (sharp-nosed viper)  
 C;Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 24-Oct-2000  
 C;Accession: JC7134; PC7037  
 R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.  
 Biochem. Biophys. Res. Commun. 265, 530-535, 1999  
 A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic ve  
 A;Reference number: JC7134; MUID:20025379  
 A;Accession: JC7134

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:14 ; Search time 80.15 Seconds  
(without alignments)  
38.966 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_114\_154  
Perfect score: 246  
Sequence: 1 DCASGTSGGHEGCKPWT.....TQPGFLTVPGNKNHNAVCV 41

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	39.0	272	2 I37552	Ox40 homolog - hum
2	95	38.6	272	2 I48700	gene ox40 protein
3	93	37.8	255	2 I38426	lymphocyte activat
4	84	34.1	271	2 S12783	Ox40 antigen precu
5	70.5	28.7	256	2 B32393	T-cell antigen 4-1
6	61	24.8	459	2 I48854	gene murine tumour
7	61	24.8	461	1 A35356	tumor necrosis fac
8	61	24.8	474	2 B38634	tumor necrosis fac
9	60.5	24.6	416	1 JN0006	nerve growth facto
10	59	24.0	998	1 Q0BBB1	BI protein - black
11	59	24.0	998	2 S41397	protein A - flock
12	57.5	23.4	152	2 JC7134	agkisacutacin alph
13	56	22.8	880	2 S56828	finger protein VIL
14	55.5	22.6	129	2 JC4329	coagulation factor
15	55.5	22.6	146	2 JC7105	aggreitin beta chai
16	54.5	22.2	123	2 B42972	coagulation factor
17	54.5	22.2	231	2 S55078	hypothetical prote
18	54.5	22.2	350	2 JQ1656	ethylene-forming e
19	54.5	22.2	425	1 A26431	nerve growth facto
20	54	22.0	435	1 I34182	tumor necrosis fac
21	54	22.0	612	2 T39666	WD-repeat protein
22	54	22.0	616	2 C86239	protein t10024.21
23	53.5	21.7	152	2 JC4690	coagulation factor
24	53.5	21.7	327	2 D75263	hypothetical prote
25	53	21.5	305	2 A46476	B cell-associated
26	53	21.5	420	2 T01172	GI/S transition co
27	53	21.5	504	2 T50983	probable pleiotrop
28	53	21.5	524	2 S38539	disintegrin-like m
29	53	21.5	584	2 T01173	GI/S transition co

RESULT 1  
I37552  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo  
Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen  
A:Reference number: I37552; MUID:94170844  
A:Accession: I37552  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 39.0%; Score 96; DB 2; Length 277;  
Best Local Similarity 43.6%; Pred. No. 0.00014;  
Matches 17; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 2 CASGTSGGHEGCKPWTCTQFGFLTVPGNKNHNAV 40  
DB 128 CPPGHPGDNQACKPWTNCTLAGKHTLQPASNSDAIC 166  
I48700  
RESULT 2  
I48700  
gene ox40 protein - mouse  
N:Alternate names: OX40 antigen  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
C:Accession: I48700; I48334; S34377  
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J  
J. Immunol. 151, 5261-5271, 1993  
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell  
A:Reference number: I48700; MUID:94044750  
A:Accession: I48700  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-272 <RES>  
A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828  
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.  
Eur. J. Immunol. 25, 926-930, 1995  
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX  
A:Reference number: I48334  
A:Accession: I48334  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-14, 'G', 16-272 <RES2>  
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819

30 53 21.5 670 2 I65967  
31 53 21.5 898 2 T14764  
32 53 21.5 1786 1 MMMSB1  
33 52.5 21.3 469 2 G59267  
34 52.5 21.3 1208 2 T09049  
35 52 21.1 264 2 B82619  
36 52 21.1 1321 2 JE0352  
37 52 21.1 1786 1 MMHUB1  
38 51.5 20.9 278 2 A84169  
39 51.5 20.9 579 2 S35237  
40 51 20.7 84 2 T03787  
41 50.5 20.5 327 2 S48839  
42 50.5 20.5 538 2 S76085  
43 50.5 20.5 700 2 A96690  
44 50 20.3 277 2 A60771  
45 50 20.3 415 2 T24307

#### ALIGNMENTS

gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
C:Accession: I48854  
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
Mamm. Genome 5, 726-727, 1994  
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
A:Reference number: I48854; MUID:95178848  
A:Accession: I48854  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-459 <RES>  
A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat  
C:151-188/Domain: NGF receptor repeat homology <NGF>

J. Biol. Chem. 266:14903-14911(1991).

[3]

X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

MEDLINE=97331317; PubMed=9187649;

Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;

"Structure of coagulation factors IX/X-binding protein, a heterodimer of C-type lectin domains."

Nat. Struct. Biol. 4:438-441(1997).

-!- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.

-!- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.

-!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.

-!- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.

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EMBL; D83331; BAAl1887.1; --

PIR; A39332; A39332.

PDB; 1IXX; 06-MAY-98.

InterPro; IPR001304; --

Pfam; PF00059; lectin\_c; 1.

PROSITE; PS00615; C-TYPE\_LLECTIN\_1; 1.

PROSITE; PS50041; C-TYPE\_LLECTIN\_2; 1.

Lectin; Calcium; Signal; 3D-structure.

SIGNAL 1 23

CHAIN 24 152

COAGULATION FACTOR IX/FACTOR X-BINDING

DOMAIN 24 152

C-TYPE LECTIN (LONG FORM).

DISULFID 25 36

BY SIMILARITY.

DISULFID 53 150

BY SIMILARITY.

DISULFID 102 102

INTERCHAIN (WITH C-98 OF B CHAIN).

DISULFID 125 142

BY SIMILARITY.

SEQUENCE 152 AA; 17213 MW; FB3DDDD2369009263 CRC64;

Query Match 21.7%; Score 53.5; DB 1; Length 152;  
Best Local Similarity 41.2%; Pred. No. 4.4;  
Matches 14; Conservative 2; Mismatches 5; Indels 13; Gaps 3;

QY 1 DCASGTFSGGHGHC-----KPWTD---CTQ 23  
| | | | | : | | | | |  
Db 24 DCLSGWSS--YEGHCKAFKYEKTWEDAERVCTE 55  
| | | | | : | | | | |

RESULT 15

CD40\_MOUSE

ID CD40\_MOUSE STANDARD; PRT; 289 AA.

AC P27512;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).

GN TNFRSF5 OR CD40.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92105763; PubMed=1370315;

RA Torres R.M., Clark E.A.;

RT "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";

RL J. Immunol. 148:620-626(1992).

RN [2]

RP REVIEWS.

RC STRAIN=BALB/C;

J. Biol. Chem. 266:14903-14911(1991).

[3]

X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

MEDLINE=97331317; PubMed=9187649;

Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;

"Structure of coagulation factors IX/X-binding protein, a heterodimer of C-type lectin domains.";

Nat. Struct. Biol. 4:438-441(1997).

-!- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.

-!- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.

-!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.

-!- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.

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EMBL; D83331; BAAl1887.1; ..

PIR; A39332; A39332.

PDB; 1IXX; 06-MAY-98.

InterPro; IPR001304; ..

Pfam; PF00059; lectin\_c\_1.

PROSITE; PS00615; C-TYPE\_LLECTIN\_1; 1.

PROSITE; PS50041; C-TYPE\_LLECTIN\_2; 1.

Lectin; Calcium; Signal; 3D-structure.

SIGNAL 1 23

CHAIN 24 152

COAGULATION FACTOR IX/FACTOR X-BINDING

FT DOMAIN 24 152

FT C-TYPE LECTIN (LONG FORM).

FT DISULFID 25 36

FT BY SIMILARITY.

FT DISULFID 53 150

FT BY SIMILARITY.

FT DISULFID 102 102

FT INTERCHAIN (WITH C-98 OF B CHAIN).

FT DISULFID 125 142

FT BY SIMILARITY.

SQ SEQUENCE 152 AA; 17213 MW; FB3DDDD2369009263 CRC64;

Query Match 21.7%; Score 53.5; DB 1; Length 152;  
Best Local Similarity 41.2%; Pred. No. 4.4;  
Matches 14; Conservative 2; Mismatches 5; Indels 13; Gaps 3;

QY 1 DCASGTFSGHGHC-----KPWTD---CTQ 23  
| | | | | : | | | | |  
DB 24 DCLSGWSS--YEGHCKAFKYEKTWEDAERVCTE 55  
| | | | | : | | | | |

RESULT 15

CD40\_MOUSE

ID CD40\_MOUSE STANDARD; PRT; 289 AA.

AC P27512;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).

GN TNFRSF5 OR CD40.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92105763; PubMed=1370315;

RA Torres R.M., Clark E.A.;

RT "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";

RL J. Immunol. 148:620-626(1992).

RN [2]

RP REVIEWS.

RC STRAIN=BALB/C;





```

DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW DNA-binding; Nuclear protein; Zinc-finger; Metal-binding; Repressor;
KW Transcription regulation; Repeat.
FT ZN_FING 174 196 C2H2-TYPE.
FT ZN_FING 202 226 C2H2-TYPE.
SQ SEQUENCE 231 AA; 26743 MW; 50F7E7ED4690D109 CRC64;

Query Match 22.2%; Score 54.5; DB 1; Length 231;
Best Local Similarity 33.3%; Pred. No. 4.8;
Matches 11; Conservative 3; Mismatches 8; Indels 11; Gaps 1;

Qy 2 CASGFTSGGGH-----EGHCKPWTDCQTQ 23
   ||| : || : ||| : ||| : |||
Db 179 CARGFTTSGHLARHNRIHTGEKNKCCPYKGCQTQ 211

RESULT 11
ACCO_PSESH STANDARD; PRT; 350 AA.
AC P32021:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (EC 1.-.-.-) (ACC OXIDASE)
DE (ETHYLENE-FORMING ENZYME) (EFE).
DE Pseudomonas syringae (pv. phaseolicola).
OS Plasmid pPSPI.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
ON NCBI_TaxID=319;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PK2;
RX MEDLINE=930751170; PubMed=1445325;
RA Fukuda H., Ogawa T., Ishihara K., Fujii T., Nagahama K., Omata T.,
RA Inoue Y., Tanase S., Morino Y.;
RT "Molecular cloning in Escherichia coli, expression, and nucleotide
RT sequence of the gene for the ethylene-forming enzyme of Pseudomonas
RT syringae pv. phaseolicola PK2.";
RL Biochem. Biophys. Res. Commun. 188:826-832(1992).
CC -|- CATALYTIC ACTIVITY: 1-AMINOCYCLOPROPANE-1-CARBOXYLATE + O2 =
CC ETHYLENE + HCN + CO(2) + 2 H(2)O.
CC -|- COFACTOR: IRON AND ASCORBATE.
CC -|- PATHWAY: LAST STEP IN THE BIOSYNTHESIS OF ETHYLENE.
CC -|- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
CC OXIDOREDUCTASES.
-----
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-----
CC EMBL; D13182; BAA02477.1; -.
CC PIR; JQ1656; JQ1656.
CC InterPro; IPR002419; -.
CC Pfam; PF00671; Fe_Asc_Oxidored; 1.
CC Ethylene biosynthesis; Oxidoreductase; Iron; Vitamin C; Plasmid.
CC SEQUENCE 350 AA; 39444 MW; 5FD86F07EFCDD392B CRC64;

Query Match 22.2%; Score 54.5; DB 1; Length 350;
Best Local Similarity 46.7%; Pred. No. 6.9;
Matches 14; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

Qy 5 GTFGSGGHEGCKPWTDCQTQ-PGLTVFPGN 33
   | | | | : ||| | | | | |
Db 224 GESSAGMEHDEPWTFTPTPGVWTVFPGD 253

```

FT	REPEAT	67	108	TNFR-CYS 2.
FT	REPEAT	109	148	TNFR-CYS 3.
FT	REPEAT	149	190	TNFR-CYS 4.
FT	DOMAIN	198	249	SER/THR-RICH.
FT	DOMAIN	354	419	DEATH DOMAIN.
FT	DISULFID	33	44	BY SIMILARITY.
FT	DISULFID	45	58	BY SIMILARITY.
FT	DISULFID	48	65	BY SIMILARITY.
FT	DISULFID	68	84	BY SIMILARITY.
FT	DISULFID	87	100	BY SIMILARITY.
FT	DISULFID	90	108	BY SIMILARITY.
FT	DISULFID	110	123	BY SIMILARITY.
FT	DISULFID	126	139	BY SIMILARITY.
FT	DISULFID	129	147	BY SIMILARITY.
FT	DISULFID	150	165	BY SIMILARITY.
FT	DISULFID	168	181	BY SIMILARITY.
FT	DISULFID	171	189	BY SIMILARITY..
FT	CARBOHYD	61	61	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	71	71	N-LINKED (GLCNAC. .) (POTENTIAL).
SEQ	SEQUENCE	425 AA;	45432 MW;	B2E152D94D3827F8 CRC64;

Query Match            22.2%; Score 54.5; DB 1; Length 425;  
Best Local Similarity 33.3%; Pred. No. 8.2;  
Matches 13; Conservative 4; Mismatches 21; Indels 1; Gaps 3;

QY	2	CASGTFSGHGHCWPWDCTCFGLTVFPGNKTHNAVC	40
DB	110	CAYGYQDETGHCEACSV--EVSGSLVFSCDQKQNTVC	147
		:     :	

RESULT 13  
TNRC\_HUMAN            STANDARD;         PRT;      435 AA.  
AC P3694I;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR  
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).  
GN LTB4R OR TNFCR OR TNFRSF3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=9325381; PubMed=8486360;  
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
RT "Construction and evaluation of a hncDNA library of human l2p  
RT transcribed sequences derived from a somatic cell hybrid.";  
RL Genomics 16:214-218(1993).  
RN [2]  
RP FUNCTION.  
RX MEDLINE=94225209; PubMed=8171323;  
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
RA Ehrenfels B., Browning J.B., Din W.S., Goodwin R.G., Smith C.A.;  
RT "A lymphotoxin-beta-specific receptor."  
RL Science 264:707-710(1994).  
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
CC IMMUNE DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SUBCELLULAR CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.  
-----  
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CC -----  
 DR EMBL; M32315; AAA59929.1; -;  
 DR EMBL; M35857; AAA63262.1; -;  
 DR EMBL; U52165; AAC50622.1; -;  
 DR EMBL; U52156; AAC50622.1; JOINED.  
 DR EMBL; U52157; AAC50622.1; JOINED.  
 DR EMBL; U52158; AAC50622.1; JOINED.  
 DR EMBL; U52159; AAC50622.1; JOINED.  
 DR EMBL; U52160; AAC50622.1; JOINED.  
 DR EMBL; U52161; AAC50622.1; JOINED.  
 DR EMBL; U52162; AAC50622.1; JOINED.  
 DR EMBL; U52163; AAC50622.1; JOINED.  
 DR EMBL; U52164; AAC50622.1; JOINED.  
 DR EMBL; M55994; AAA36755.1; -;  
 DR PIR; A35356; A35356.  
 DR PIR; A36007; A36007.  
 DR PIR; A36475; A36475.  
 DR PIR; B35010; B35010.  
 DR PIR; A23666; A23666.  
 DR POB; ICA9; 12-APR-99.  
 DR MIM; 191191; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 4.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 KW Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 258 287 POTENTIAL.  
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 201 4 X TNFR-CYS.  
 FT REPEAT 39 76 TNFR-CYS 1.  
 FT REPEAT 77 118 TNFR-CYS 2.  
 FT REPEAT 119 162 TNFR-CYS 3.  
 FT REPEAT 163 201 TNFR-CYS 4.  
 FT DISULFID 40 53 BY SIMILARITY.  
 FT DISULFID 54 67 BY SIMILARITY.  
 FT DISULFID 57 75 BY SIMILARITY.  
 FT DISULFID 78 93 BY SIMILARITY.  
 FT DISULFID 96 110 BY SIMILARITY.  
 FT DISULFID 100 118 BY SIMILARITY.  
 FT DISULFID 120 126 BY SIMILARITY.  
 FT DISULFID 134 143 BY SIMILARITY.  
 FT DISULFID 137 161 BY SIMILARITY.  
 FT DISULFID 164 179 BY SIMILARITY.  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 141 141 R -> P (IN REF. 4).  
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).  
 FT CONFLICT 363 363 A -> T (IN REF. 4).  
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

Query Match 25.68; Score 53; DB 1; Length 461;  
 Best Local Similarity 36.66; Pred. No. 0.74;  
 Matches 15; Conservative 4; Mismatches 16; Indels 6; Gaps 2;

Qy 2 CASGTFSG--GHEGCKPWTCTQFGELTVPPGNKTHNAVC 40  
 ||||| 1:1 | : ||| :|||  
 Db 164 CAPGTFSTSTSDICRPHQICN-----VVAIPGNASRAVC 200

RESULT 7  
 TNFR\_MOUSE

ID AC P25119; P97893; STANDARD; PRT; 474 AA.  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).  
 GN TNFRSF1B OR TNFR2 OR TNFR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91187885; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wong G.H., Chen E.Y., Goeddel D.V.;  
 RT "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.";  
 RL Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RC STRAIN=NOD;  
 RA Jacob C.O., Liu J.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Liver;  
 RA Kissingerhis M., Fellows R., Feldmann M., Chernajovsky Y.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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CC -----  
 DR EMBL; M60469; AAA39752.1; -;  
 DR EMBL; M59378; AAA40463.1; -;  
 DR EMBL; U39488; AAA85021.1; -;  
 DR EMBL; X87128; AAA60618.1; -;  
 DR PIR; B38634; B38634.  
 DR HSP; P19438; INCF.  
 DR MGD; MGI:1314883; Tnfrsf1b.  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 259 288 POTENTIAL.  
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 203 4 X TNFR-CYS.  
 FT REPEAT 39 77 TNFR-CYS 1.  
 FT REPEAT 78 119 TNFR-CYS 2.  
 FT REPEAT 120 164 TNFR-CYS 3.  
 FT REPEAT 165 203 TNFR-CYS 4.  
 FT DISULFID 40 54 BY SIMILARITY.



RL J. Immunol. 150:771-781(1993).  
 CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-LBBL. POSSIBLY  
 CC ACTIVE DURING T CELL ACTIVATION.  
 CC -1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.  
 CC ASSOCIATES WITH P56-LCK.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.  
 CC -1- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC -----  
 DR EMBL: J04492; AAA40167.1; -;  
 DR EMBL: U02587; AAA93113.1; -;  
 DR PIR: B32393; B32393.  
 DR HSP: P25942; ICDF.  
 DR MGD; MGI:1101059; Tnfrsf9.  
 DR InterPro: IPR001368; -;  
 DR Pfam: PF00020; TNFR\_C6; 1.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS00500; TNFR\_NGFR\_2; FALSE\_NEG.  
 KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24  
 FT CHAIN 25 256 4-LBB LIGAND RECEPTOR.  
 FT DOMAIN 25 187 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 188 208 POTENTIAL.  
 FT DOMAIN 209 236 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 17 159 4 X TNFR-CYS.  
 FT REPEAT 17 45 TNFR-CYS 1.  
 FT REPEAT 46 85 TNFR-CYS 2.  
 FT REPEAT 86 117 TNFR-CYS 3.  
 FT REPEAT 118 159 TNFR-CYS 4.  
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;  
 Query Match 28.7%; Score 70.5; DB 1; Length 256;  
 Best Local Similarity 35.0%; Pred. No. 0.049;  
 Matches 14; Conservative 8; Mismatches 17; Indels 1; Gaps 1;  
 QY 2 CASSTFGGH-EGHCKPWTDTQFGFLTVPPGNKTHNAV 40  
 DB 119 CSLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTETKDV 158  
 1: ||||: : ||: ||||: | : | : ||  
 119 CSLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTETKDV 158  
 RESULT 6  
 TNFR2\_HUMAN  
 ID TNFR2\_HUMAN STANDARD; PRT; 461 AA.  
 AC P20333;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
 DE BINDING PROTEIN 2) (TFPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90260639; PubMed-2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G.;  
 RA "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins.";

Science 248:1019-1023(1990).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE-91045991; PubMed-2172983;  
 RX Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96299745; PubMed-8661109;  
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,  
 RA Brodeur G.M.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RL Genomics 35:94-100(1996).  
 RN [4]  
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE-90349572; PubMed-2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
 RA Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
 RT and demonstration of a shed form of the receptor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
 RN [5]  
 RP SEQUENCE OF 27-31.  
 RX MEDLINE-90110215; PubMed-2153136;  
 RA Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 RT urine. Evidence for immunological cross-reactivity with cell surface  
 RT tumor necrosis factor receptors";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN [6]  
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE-91056048; PubMed-2173696;  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two  
 RT distinct tumor necrosis factor receptors from HL60 cells.";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RN [7]  
 RP CHARACTERIZATION  
 RX MEDLINE-93016040; PubMed-1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation";  
 RL J. Biol. Chem. 267:21172-21178(1992).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 RX MEDLINE-99221490; PubMed-10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 RT human TRAF2";  
 RL Nature 398:533-538(1999).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND  
 CC WYETH-AVERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING  
 CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO  
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".  
 CC -1- DATABASE: NAME=Enbrel; NOTE=clinical information on Enbrel;  
 CC WWW="http://www.enbrelinfo.com/".  
 CC -----

CC CELLS.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -1- DATABASE: NAME=PROV; NOTE=CD guide CDw137 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".

CC -----

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CC -----

CC EMBL; U03397; AAA53133.1; -

CC EMBL; L12964; AAA62478.2; -

CC HSSP; P19438; 1EXT.

CC MIM; 602250; -

CC InterPro; IPR001368; -

CC Pfam; PF00020; TNFR\_C6; 2.

CC PROSITE; PS00652; TNFR\_NGFR\_1; 1.

CC PROSITE; PS00050; TNFR\_NGFR\_2; 1.

CC Receptor; Glycoprotein; Repeat; Signal; Transmembrane.

CC SIGNAL 1 17 POTENTIAL.

CC CHAIN 18 255 4-1BB LIGAND RECEPTOR.

CC DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 187 213 POTENTIAL.

CC DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 47 159 3 X TNFR-CYS.

CC REPEAT 47 86 TNFR-CYS 1.

CC REPEAT 87 118 TNFR-CYS 2.

CC REPEAT 119 159 TNFR-CYS 3.

CC CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC SEQUENCE 255 AA; 27899 MW; F3A563F5EF00460 CRC64;

Query Match 37.8%; Score 93; DB 1; Length 255;

Best Local Similarity 40.0%; Pred. No. 7e-05;

Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTDTQFGFLTFVFPKNTNNAVC 40

DB 119 DCCGFTNDQKRGICRPWTNGLDGSVLVNGTKERDVVC 158

RESULT 4

OX40\_RAT

ID OX40\_RAT STANDARD; PRT; 271 AA.

AC P15725;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).

GN TNFRSF4 OR TNGPIL OR OX40.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=T-cell;

RC MEDLINE=90214614; PubMed=2157591;

RA Mallett S., Fossum S., Barclay A.N.;

RT "Characterization of the MRC OX40 antigen of activated CD4 positive T

RT lymphocytes -- a molecule related to nerve growth factor receptor.";

RL EMBO J. 9:1063-1068(1990).

CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -----

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CC -----

CC EMBL; X17037; CAA34897.1; -

CC PIR; S08036; S08036.

CC PIR; S12783; S12783.

CC HSSP; P25942; 1CDF.

CC InterPro; IPR001368; -

CC Pfam; PF00020; TNFR\_C6; 3.

CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.

CC PROSITE; PS00050; TNFR\_NGFR\_2; 2.

CC Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

CC SIGNAL 1 19 POTENTIAL.

CC CHAIN 20 271 OX40L RECEPTOR.

CC DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 211 235 POTENTIAL.

CC DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 25 164 4 X TNFR-CYS.

CC REPEAT 25 60 TNFR-CYS 1.

CC REPEAT 61 102 TNFR-CYS 2.

CC REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).

CC REPEAT 124 164 TNFR-CYS 4.

CC CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC SEQUENCE 271 AA; 29895 MW; C06465136B16821 CRC64;

Query Match 34.1%; Score 84; DB 1; Length 271;

Best Local Similarity 41.0%; Pred. No. 0.001;

Matches 16; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 2 CASGTFSGGHEGCKPWTDTQFGFLTFVFPKNTNNAVC 40

DB 125 CPPGHFSPGSGNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 5

41BB\_MOUSE

ID 41BB\_MOUSE STANDARD; PRT; 256 AA.

AC P20334;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).

GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=89184547; PubMed=2784565;

RT "cDNA sequences of two inducible T-cell genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C.

RC MEDLINE=94179805; PubMed=8133039;

RA Kwon B.S., Weissman S.M.;

RT "Genomic organization and chromosomal localization of the T-cell

RT antigen 4-1BB.";

RL J. Immunol. 152:2256-2262(1994).

CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -----

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:26 ; Search time 43.78 Seconds  
(without alignments)  
32.080 Million cell updates/sec.

Title: US-09-512-363-2\_COPY\_114\_154

Perfect score: 246

Sequence: 1 DCASGTFSGHGHCCKPWT.....TOGFLTFVPGNKTHNAVCV 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	96	39.0	277	1	OX40_HUMAN
2	95	38.6	272	1	OX40_MOUSE
3	93	37.8	255	1	41BB_HUMAN
4	84	34.1	271	1	OX40_RAT
5	70.5	28.7	256	1	41BB_MOUSE
6	63	25.6	461	1	TNR2_HUMAN
7	61	24.8	474	1	TNR2_MOUSE
8	60.5	24.6	416	1	NGFR_CHICK
9	56	22.8	880	1	ZAP1_YEAST
10	54.5	22.2	231	1	NRG1_YEAST
11	54.5	22.2	350	1	ACCO_PSESH
12	54.5	22.2	425	1	NGFR_RAT
13	54	22.0	435	1	TNR2_HUMAN
14	53.5	21.7	152	1	IXA_TRIFL
15	53	21.5	289	1	CD40_MOUSE
16	53	21.5	1786	1	LMB1_MOUSE
17	52	21.1	415	1	TNR2_MOUSE
18	52	21.1	1786	1	LMB2_HUMAN
19	51.5	20.9	577	1	CCBS_OENBE
20	51.5	20.9	579	1	CCBS_DAUCA
21	51.5	20.9	1050	1	ITA5_XENLA
22	51	20.7	84	1	MT22_ORYSA
23	51	20.7	997	1	AT57_HUMAN
24	50.5	20.5	327	1	GBLP_ARATH
25	50.5	20.5	327	1	GBLP_BRANA
26	50	20.3	269	1	CD40_BOVIN
27	50	20.3	277	1	CD40_HUMAN
28	50	20.3	1790	1	LMB1_DROME
29	49.5	20.1	146	1	IXB_TRIFL
30	49.5	20.1	317	1	GBLP_BARE
31	49.5	20.1	324	1	GBLP_CAEEL
32	49.5	20.1	439	1	CK13_SCHPO
33	49.5	20.1	490	1	CPC2_RABIT

34	49.5	20.1	1168	1	LMB3_MOUSE	Q61087 mus musculus
35	49	19.9	216	1	YODA_ECOLI	P76344 escherichia
36	49	19.9	582	1	ATKA_HALNI	P57684 halobacteri
37	48.5	19.7	248	1	KLKC_HUMAN	Q9UKR0 homo sapien
38	48.5	19.7	529	1	YOU1_CAEEL	P30638 caenorhabdi
39	48.5	19.7	535	1	TYR1_CHICK	O57A05 gallus gall
40	48.5	19.7	987	1	EPB4_HUMAN	P54760 homo sapien
41	48.5	19.7	1064	1	YY08_METJA	Q60307 methanococc
42	48	19.5	1074	1	SM5A_HUMAN	Q13591 homo sapien
43	48	19.5	4655	1	LRP2_HUMAN	P98164 homo sapien
44	47.5	19.3	207	1	CYOC_PSEPU	Q94WR3 pseudomonas
45	47.5	19.3	761	1	SM3D_CHICK	Q90563 gallus gall

#### ALIGNMENTS

RESULT 1

ID	OX40_HUMAN	STANDARD:	PRT:	277 AA.
AC	P43489; Q13663;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY			
DE	ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).			
GN	TNFRSF4 OR TNXP1L			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94170844; PubMed=7510240;			
RA	Latza U., Duerkop H., Schmittger S., Ringeling J., Eitelbach F.,			
RA	Hummel M., Fonatsch C., Stein H.;			
RT	"The human OX40 homolog: cDNA structure, expression and chromosomal			
RT	assignment of the ACT35 antigen."			
RL	Eur. J. Immunol. 24:677-683(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95219871; PubMed=7704935;			
RA	Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,			
RA	Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;			
RT	"Identification of OX40 ligand and preliminary characterization of			
RT	its activities on OX40 receptor."			
RL	Circ. Shock 44:30-34(1994).			
CC	-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-!- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".			

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DR	EMBL; X75962; CAA53576.1; "			
DR	EMBL; S76792; AAB33944.1; ALT_INIT.			
DR	HSSP; P25942; ICDF.			
DR	MIM; 600315; "			
DR	InterPro; IPR001368; "			
DR	Pfam; PF00020; TNFR_C6; 3.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.			
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;			
Signal				
FT	SIGNAL	1	28	POTENTIAL.
FT	CHAIN	29	277	OX40L RECEPTOR.

FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 215 235 POTENTIAL.  
 FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 30 169 4 X TNFR-CYS:  
 FT REPEAT 30 65 TNFR-CYS 1.  
 FT REPEAT 66 107 TNFR-CYS 2.  
 FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 127 167 TNFR-CYS 4.  
 FT REPEAT 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 39.0%; Score 96; DB 1; Length 277;  
 Best Local Similarity 43.6%; Pred. No. 3.1e-05;  
 Matches 17; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 2 CASGTSGGHEGCKPWTCTQFGFLTVFPGNKTHNVC 40  
 DB 128 CPPGHFSPGDNQACKPWTNCTLKGHTLPASNSDAIC 166

RESULT 2  
 OX40\_MOUSE STANDARD; PRT; 272 AA.  
 AC P47741;

DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).  
 GN TNFRSF4 OR TXGP1 OR OX40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RX MEDLINE=94044750; PubMed=8228223;  
 RA Calderhead D.M., Buhlmann J.E., van den Bortwegh A.J.,  
 RA Claassen E., Noelle R.J., Fell H.;  
 RT Cloning of mouse OX40: a T cell activation marker that may mediate  
 RT T-B cell interactions.;  
 RL J. Immunol. 151:5261-5271(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255413; PubMed=7737295;  
 RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Barclay A.N.;  
 RT "Gene structure and chromosomal localization of the mouse homologue  
 RT of rat OX40 protein.";  
 RL Eur. J. Immunol. 25:926-930(1995).  
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/OP34 CYTOKINE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.

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 CC -----  
 DR EMBL; Z21674; CAA79772.1; -  
 DR EMBL; X85214; CAA59476.1; -  
 DR HSSP; P25942; 1CDF.  
 DR MGD; MGI:104512; Tnfrsf4.  
 DR InterPro; IPR001368; -  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

KW SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 272 OX40L RECEPTOR.  
 FT DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 212 236 POTENTIAL.  
 FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 26 165 4 X TNFR-CYS:  
 FT REPEAT 26 61 TNFR-CYS 1.  
 FT REPEAT 62 103 TNFR-CYS 2.  
 FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 125 165 TNFR-CYS 4.  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 15 15 A -> G (IN REF. 2).  
 SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 38.6%; Score 95; DB 1; Length 272;  
 Best Local Similarity 46.2%; Pred. No. 4.1e-05;  
 Matches 18; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 2 CASGTSGGHEGCKPWTCTQFGFLTVFPGNKTHNVC 40  
 DB 126 CPPGHFSPGDNQACKPWTNCTLSKQTRHPASDSLDVVC 164

RESULT 3  
 41BB\_HUMAN STANDARD; PRT; 255 AA.  
 AC Q07011;

DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)  
 DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).  
 GN TNFRSF9 OR ILA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=94374434; PubMed=8088337;  
 RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,  
 RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;  
 RT "Molecular and biological characterization of human 4-1BB and its  
 RT ligand.";  
 RL Eur. J. Immunol. 24:2219-2227(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=94085794; PubMed=8262389;  
 RA Schwarz H., Tuckwell J., Lotz M.;  
 RT "A receptor induced by lymphocyte activation (ILA): a new member of  
 RT the human nerve-growth-factor/tumor-necrosis-factor receptor  
 RT family.";  
 RL Gene 134:295-298(1993).  
 RN [3]  
 RP REVISION TO 107.  
 RA Schwarz H.;  
 RL Submitted (MAR-1999); to the EMBL/GenBank/DBDJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=95347766; PubMed=7622190;  
 RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,  
 RA Kwon B.S.;  
 RT "Characterization of human homologue of 4-1BB and its ligand.";  
 RL Immunol. Lett. 45:67-73(1995).  
 CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY  
 CC ACTIVE DURING T CELL ACTIVATION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T



## STIC-ILL

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**From:** Holleran, Anne  
**Sent:** Thursday, October 18, 2001 7:28 PM  
**To:** STIC-ILL  
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4. Handel, M.L. et al. Clinical and Experimental Pharmacology and Physiology (2000) 27(3): 139-144
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